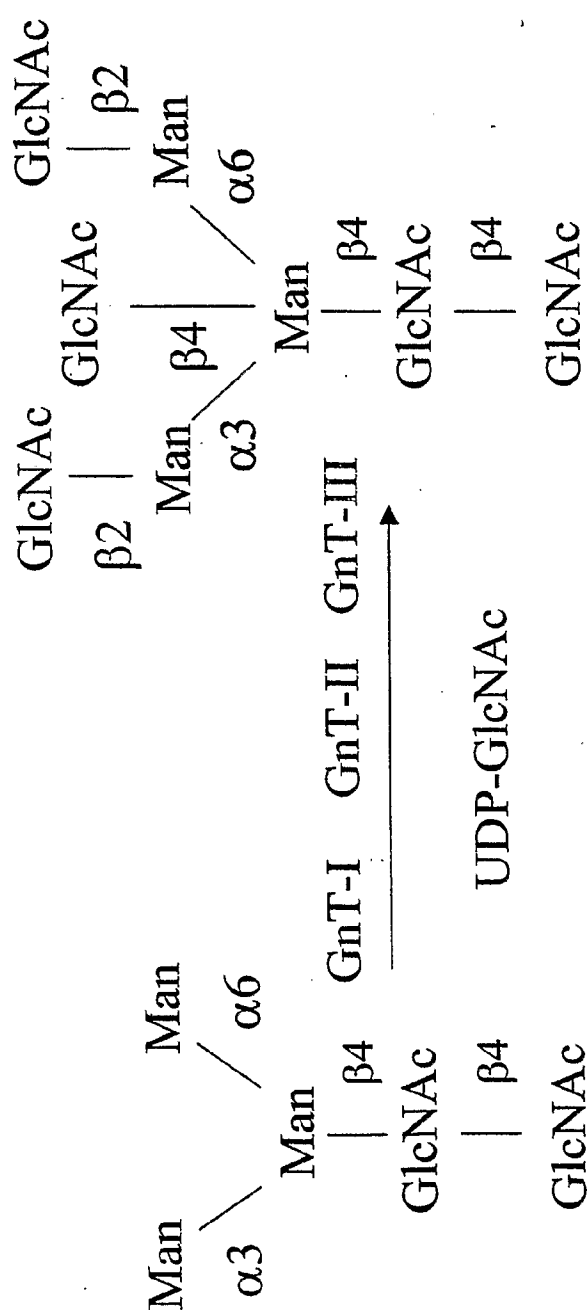


1/498



Trimannosyl core      Trimannosyl core with  
Bisecting GlcNAc

FIG. 1

2/498

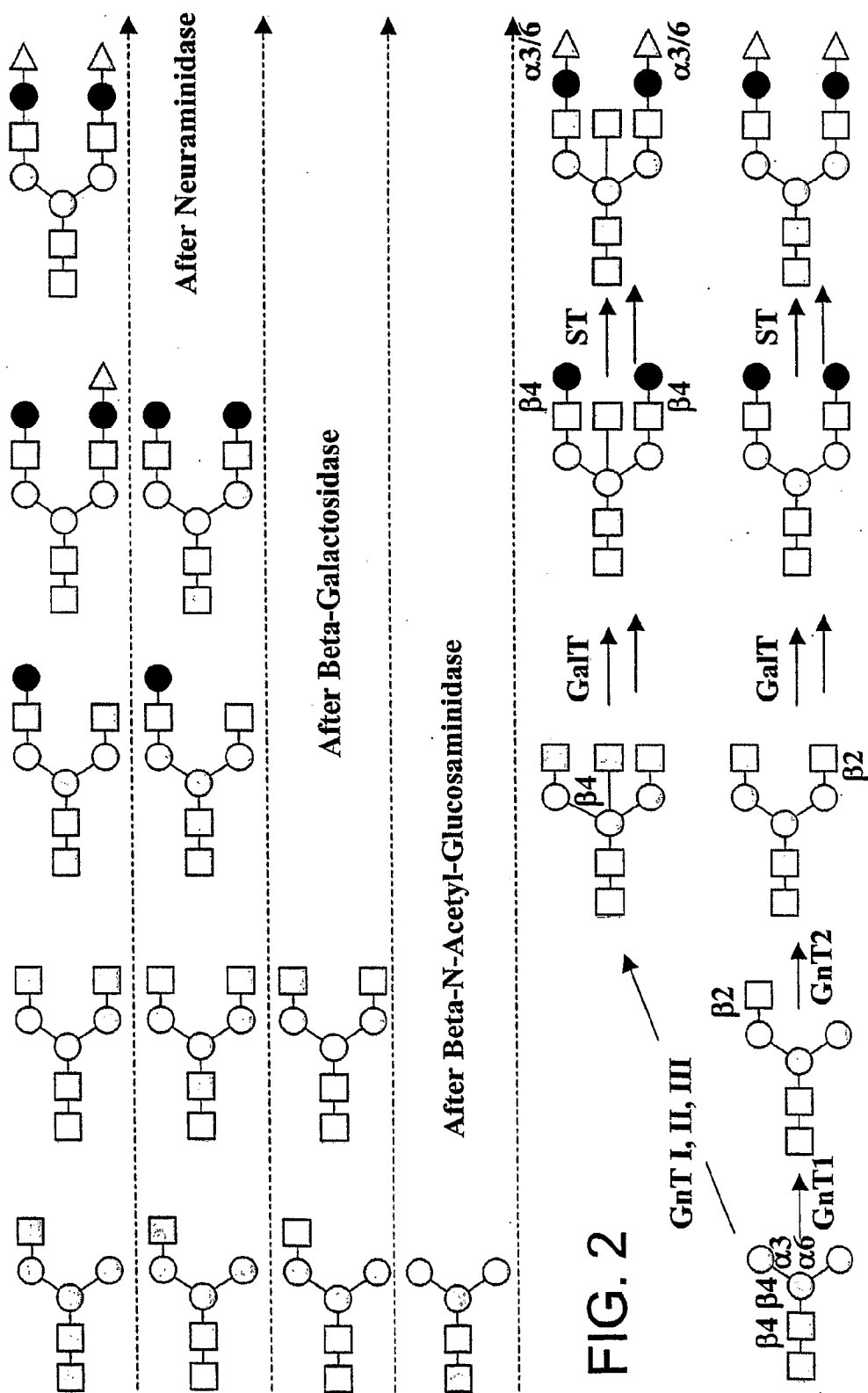
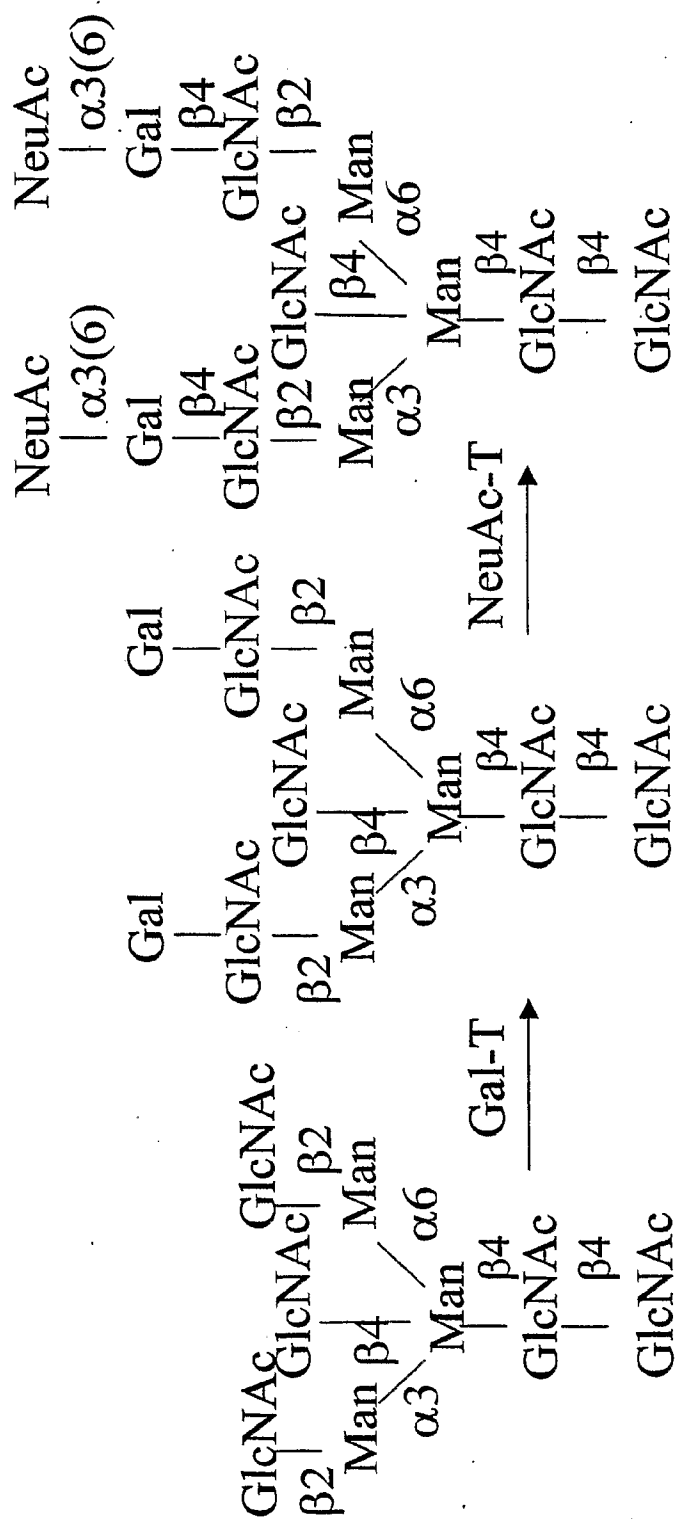


FIG. 2

3/498

3  
F/G

4/498

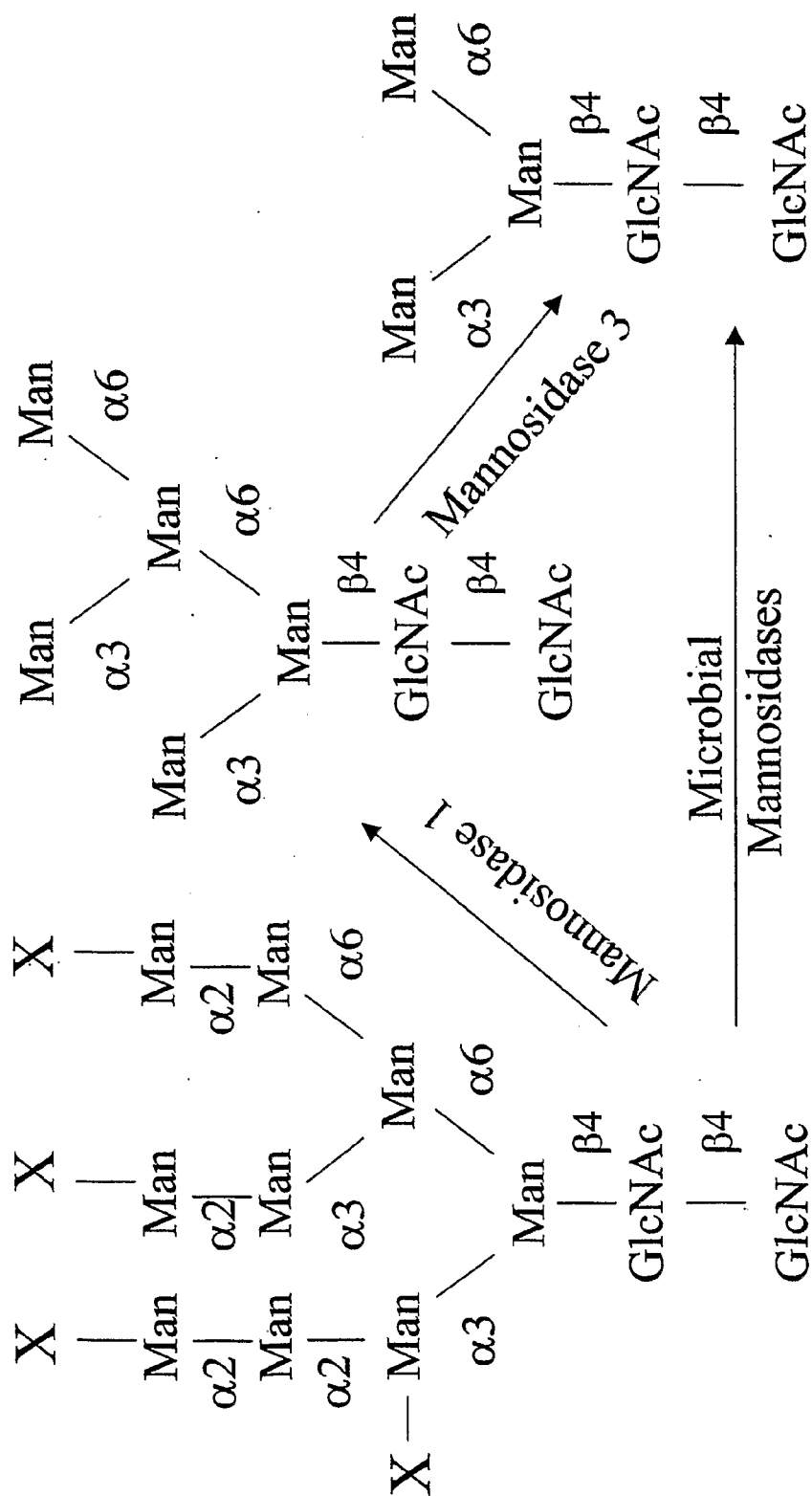


FIG. 4



5/498

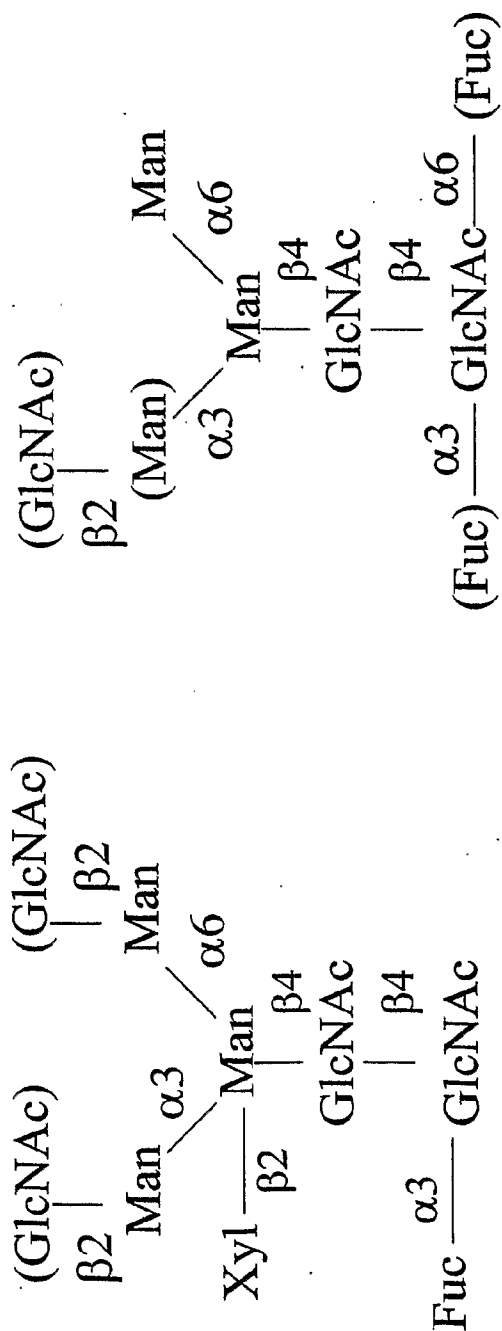


FIG. 5

FIG. 6

6/498

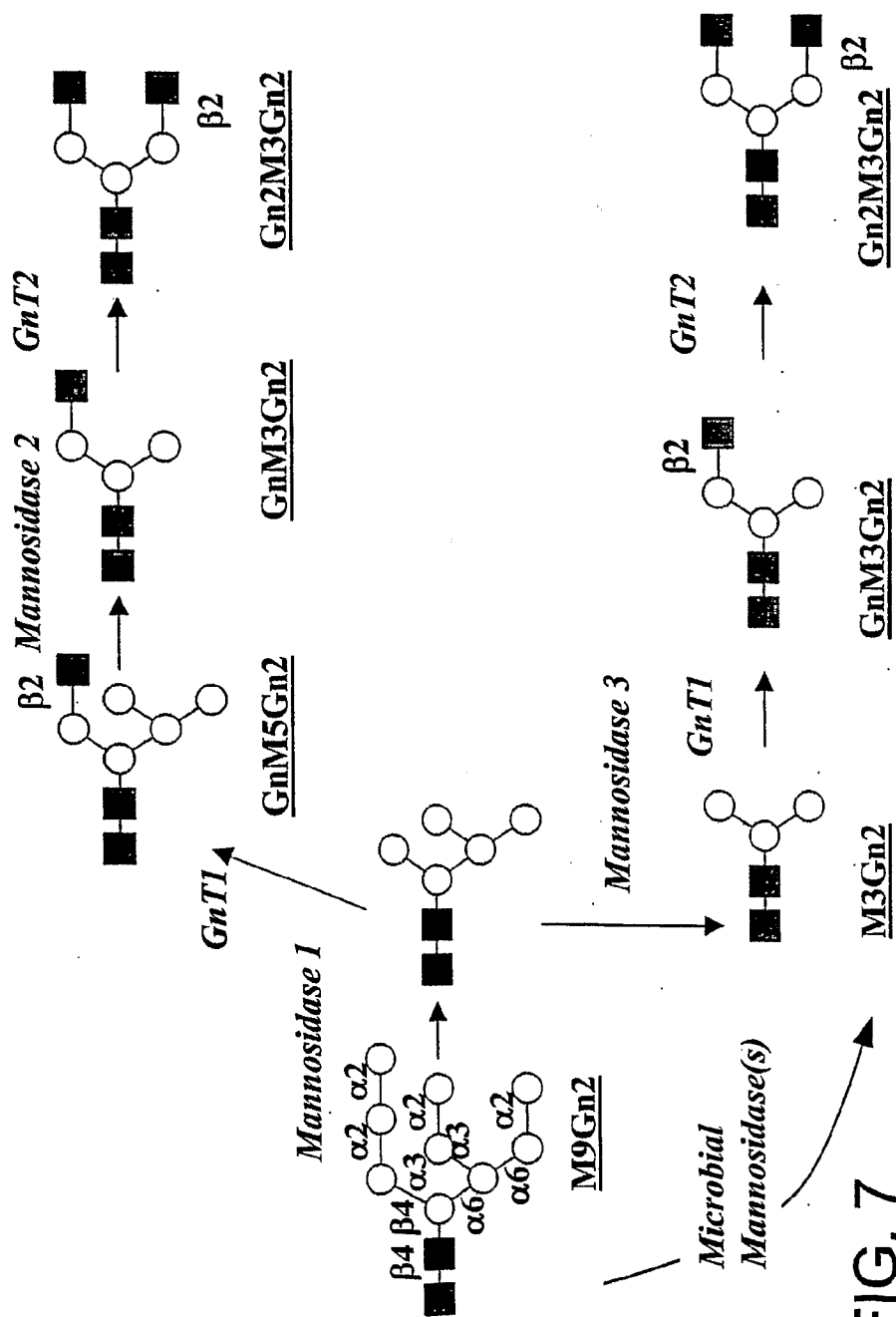


FIG. 7

7/498

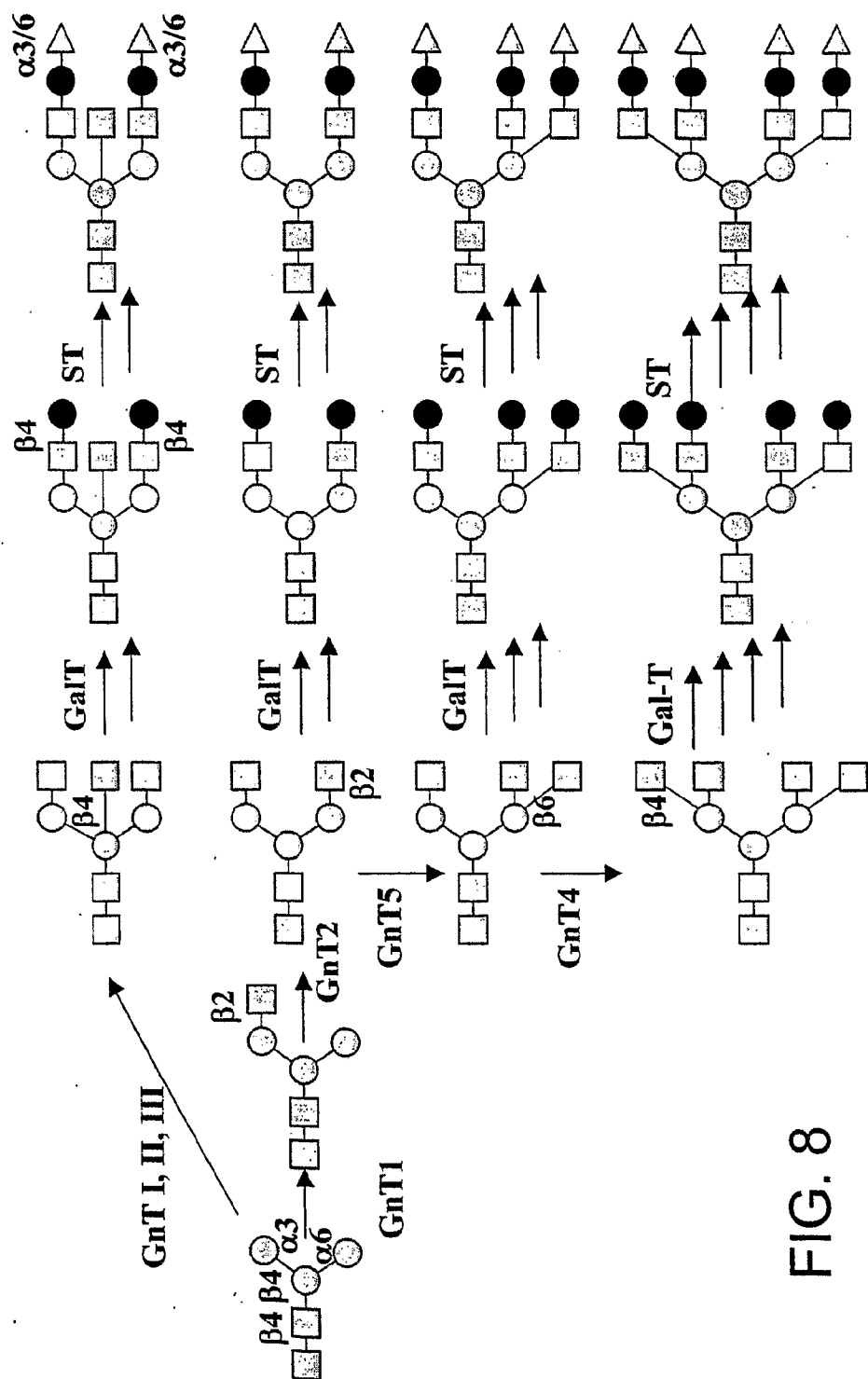


FIG. 8

8/498

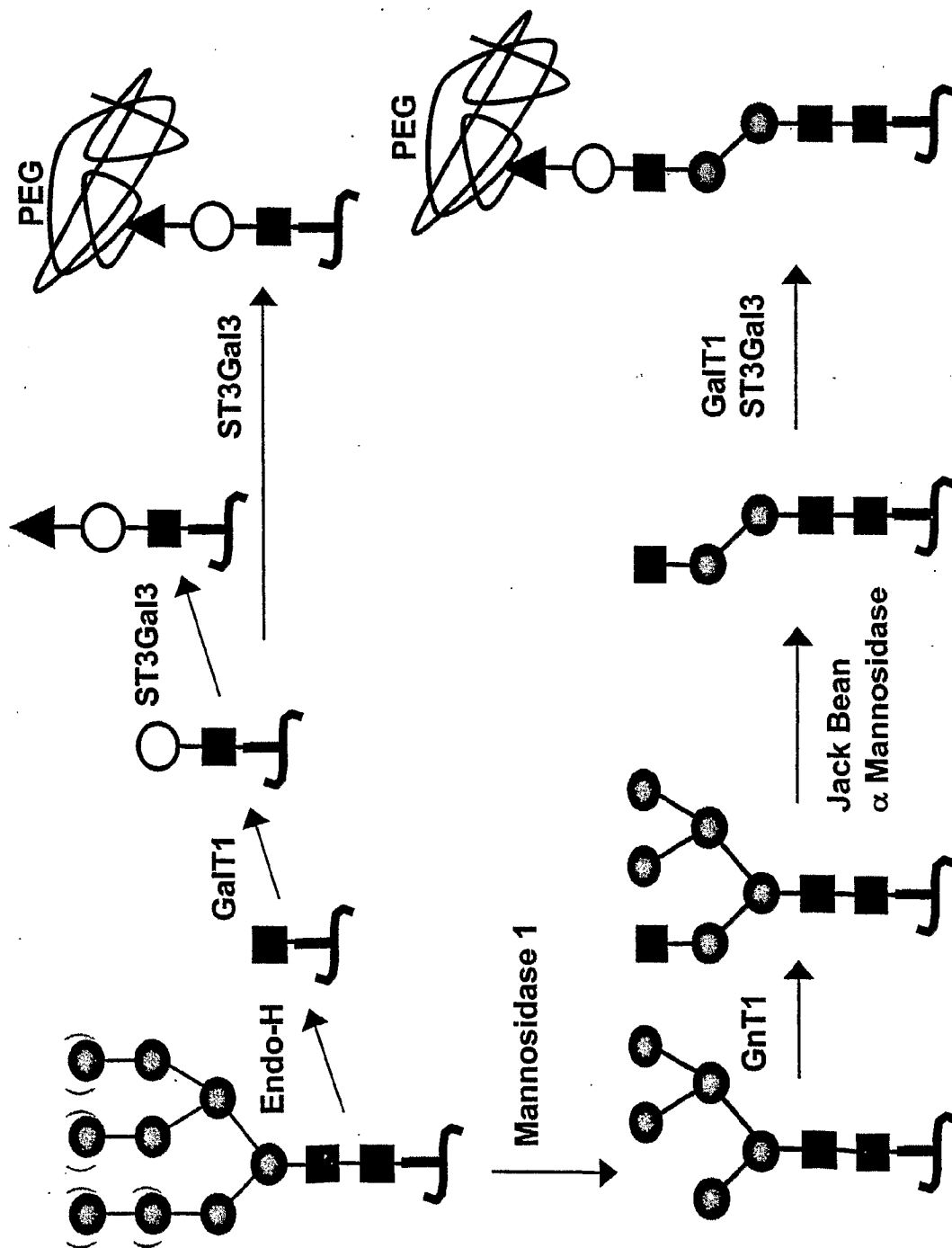


FIG. 9

9/498

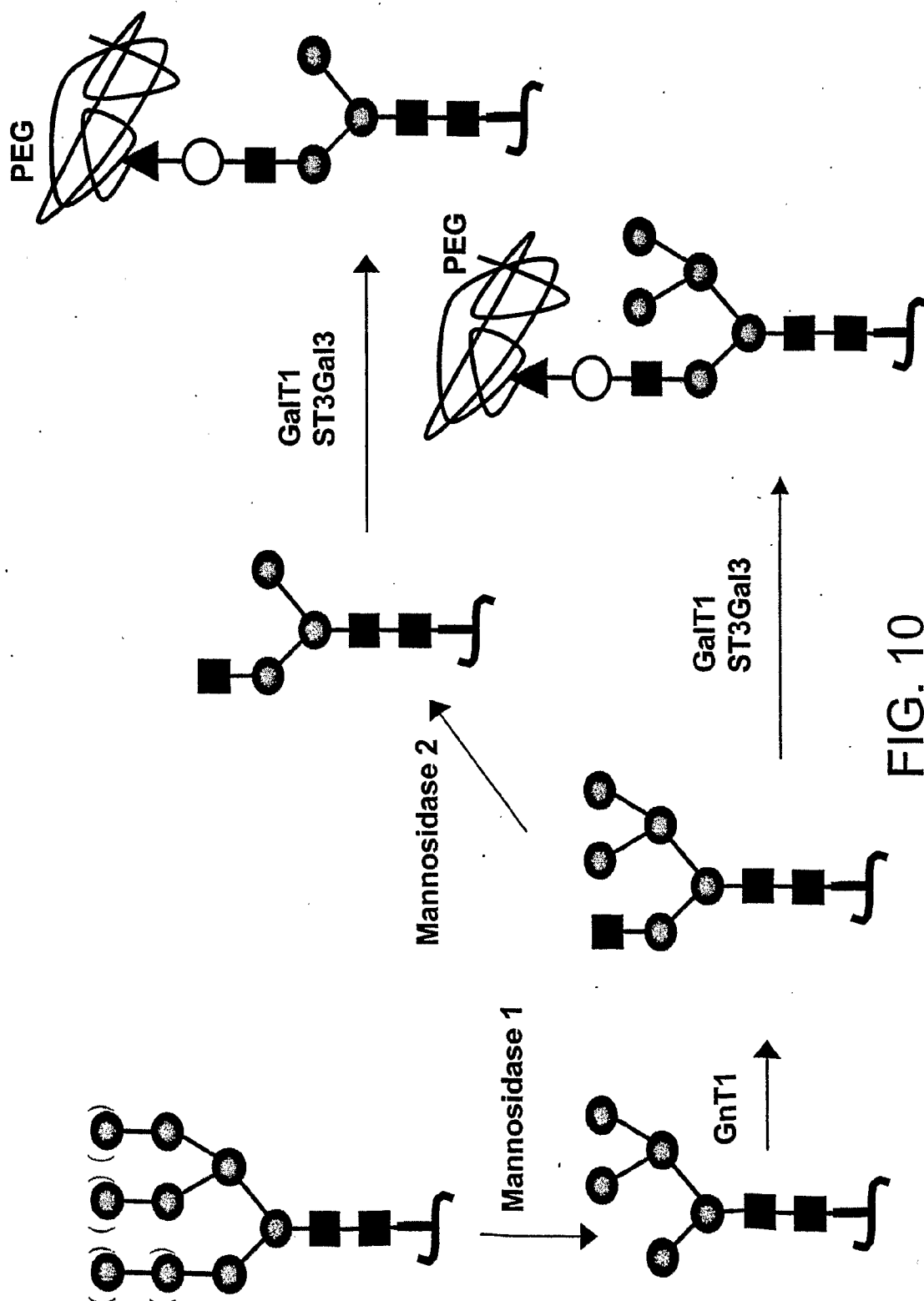


FIG. 10

10/498

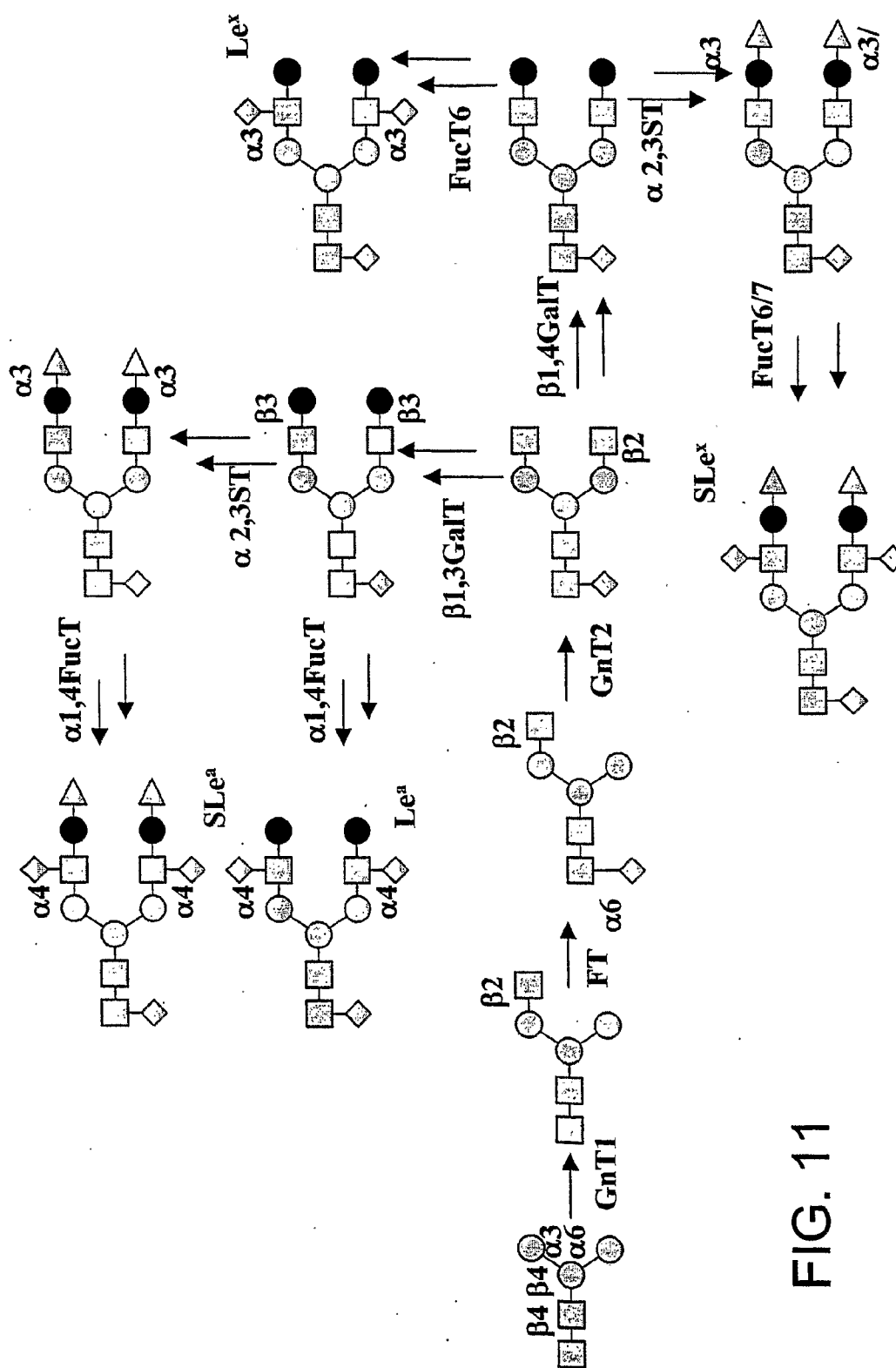


FIG. 11

11/498

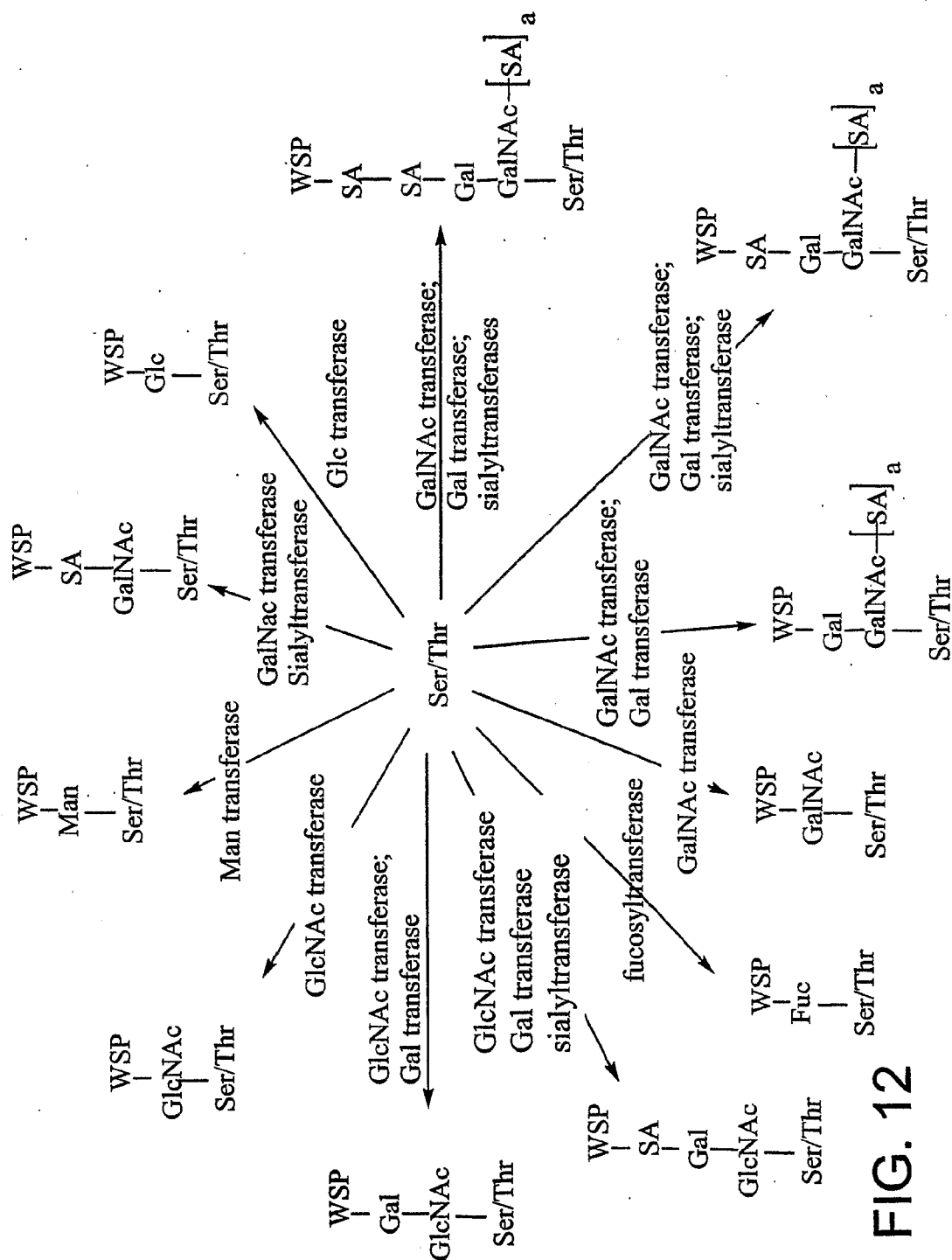
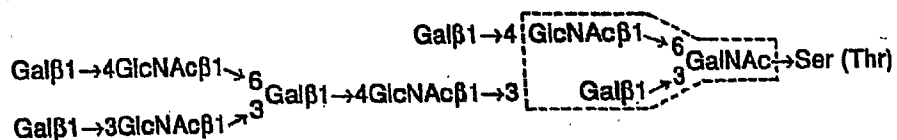
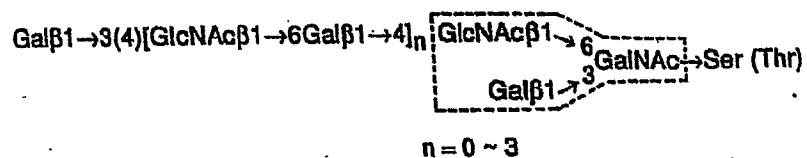
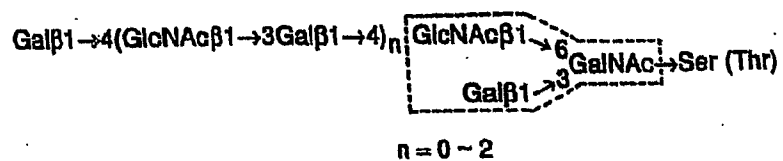
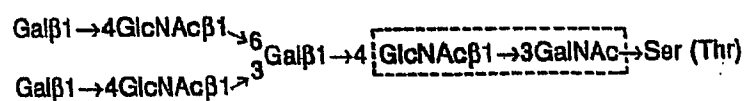
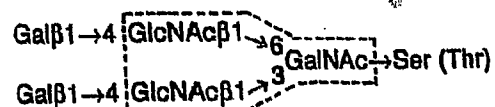


FIG. 12

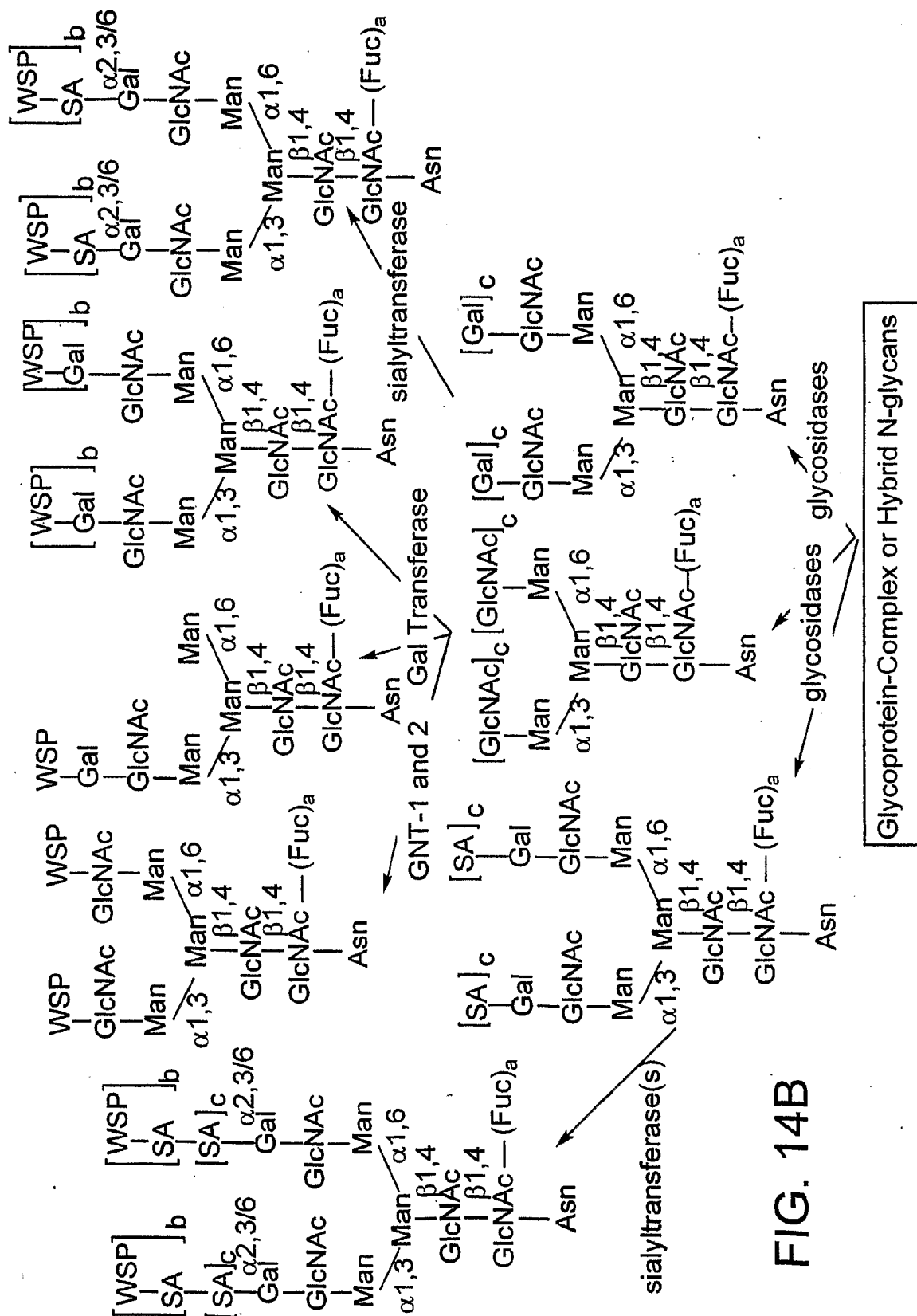
12/498

**Core 1****Core 2****Core 3****Core 4****FIG. 13**





14/498



15/498

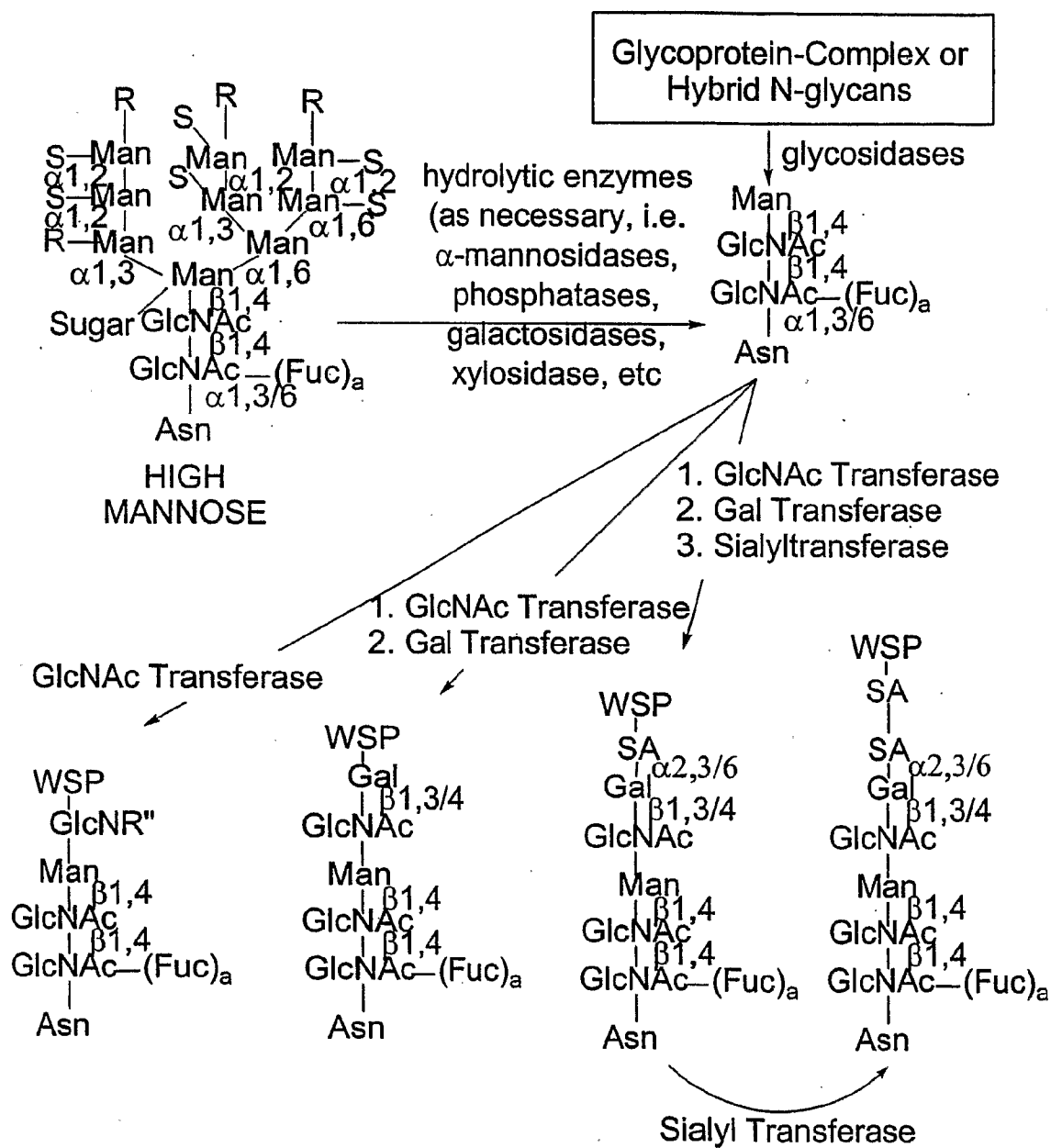


FIG. 15

16/498

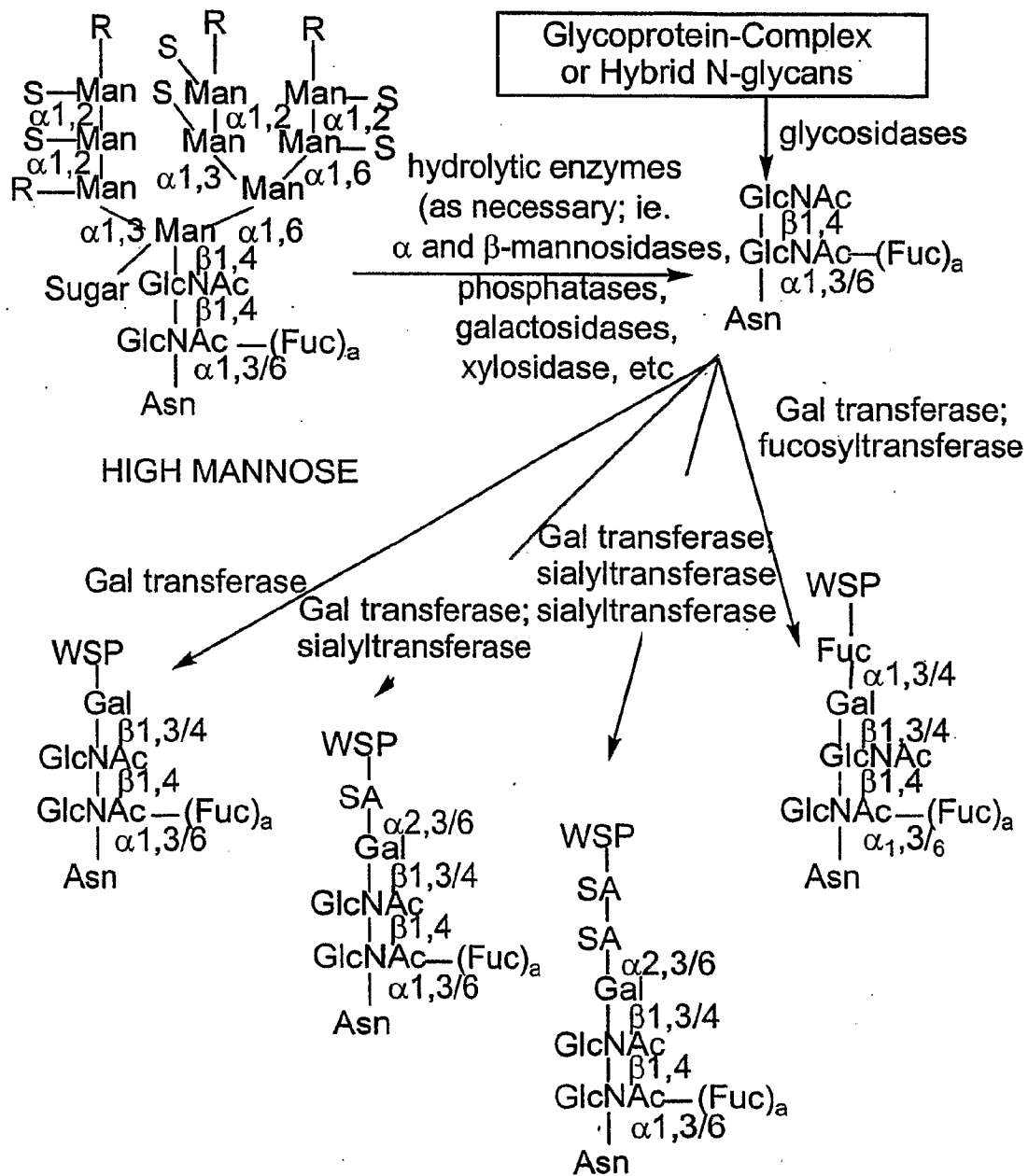


FIG. 16

17/498

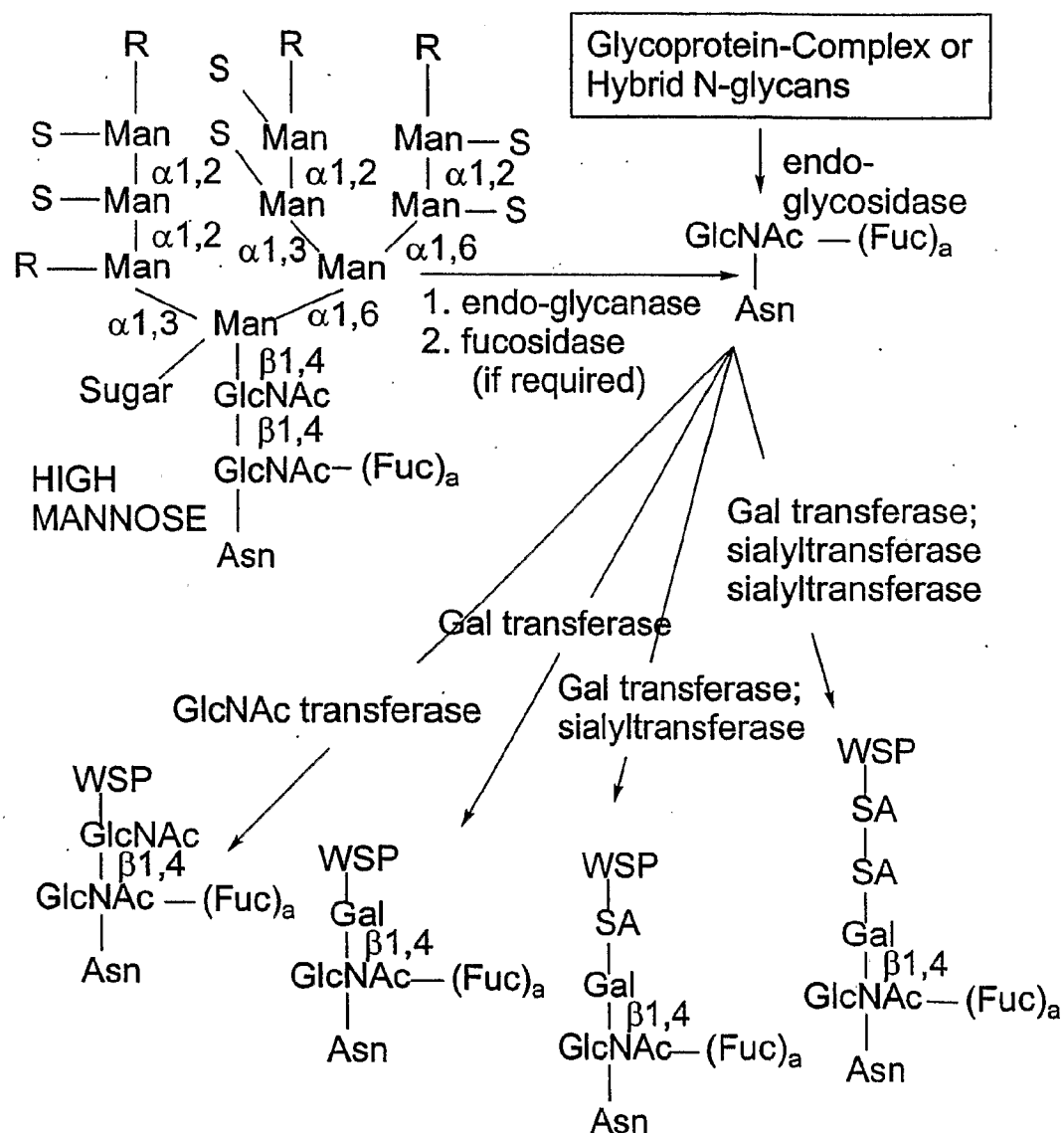
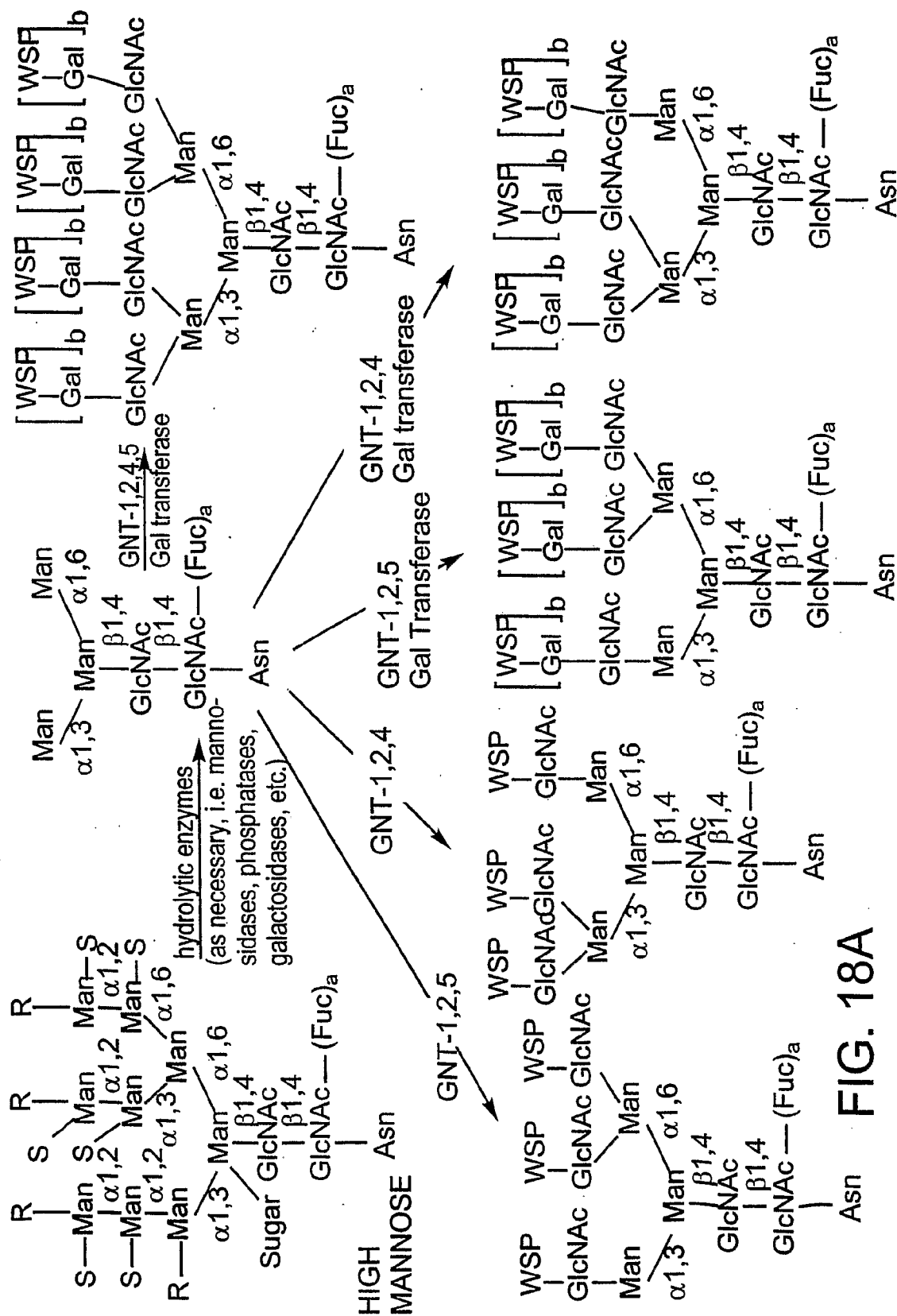


FIG. 17

18/498



19/498

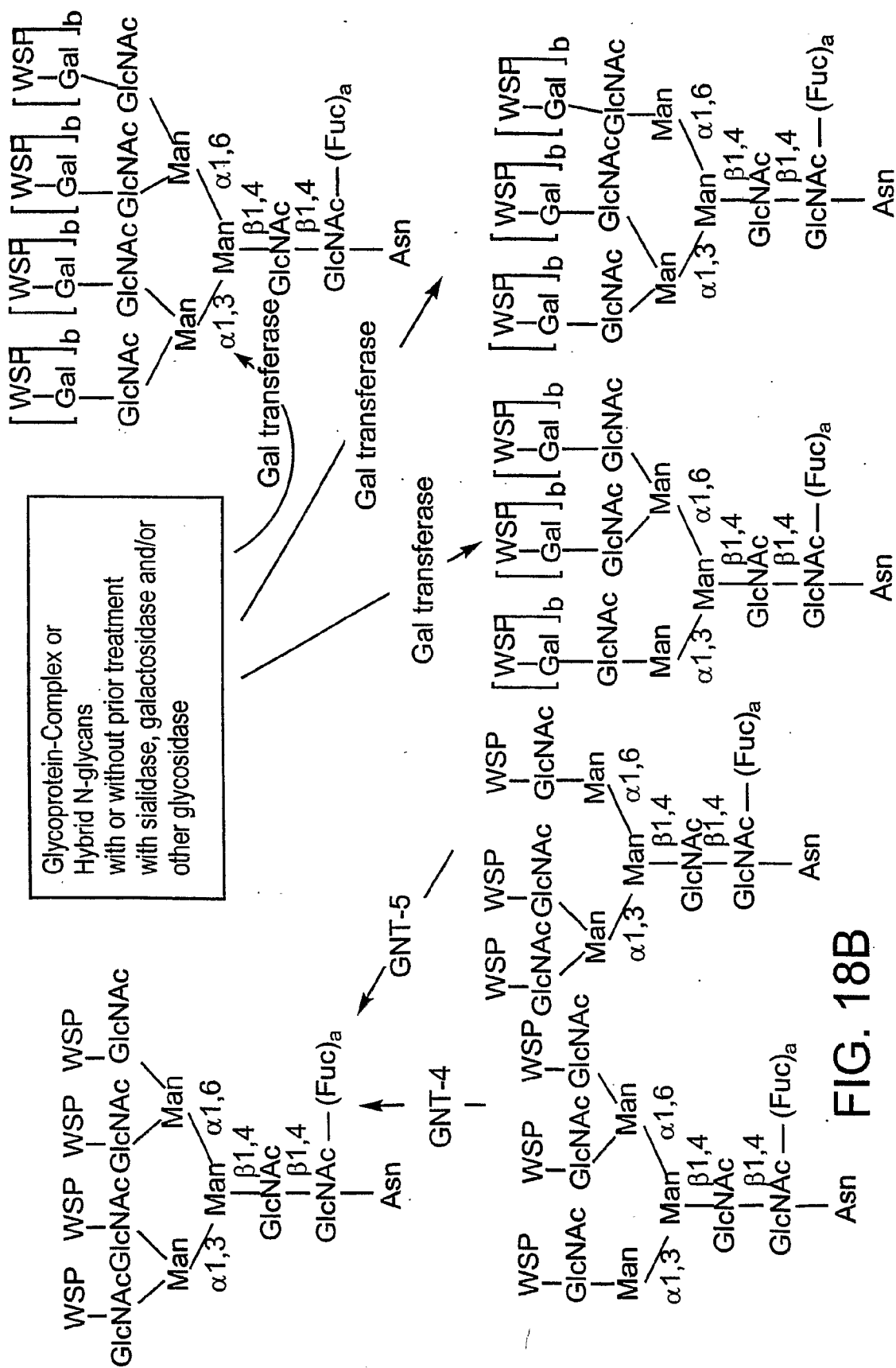
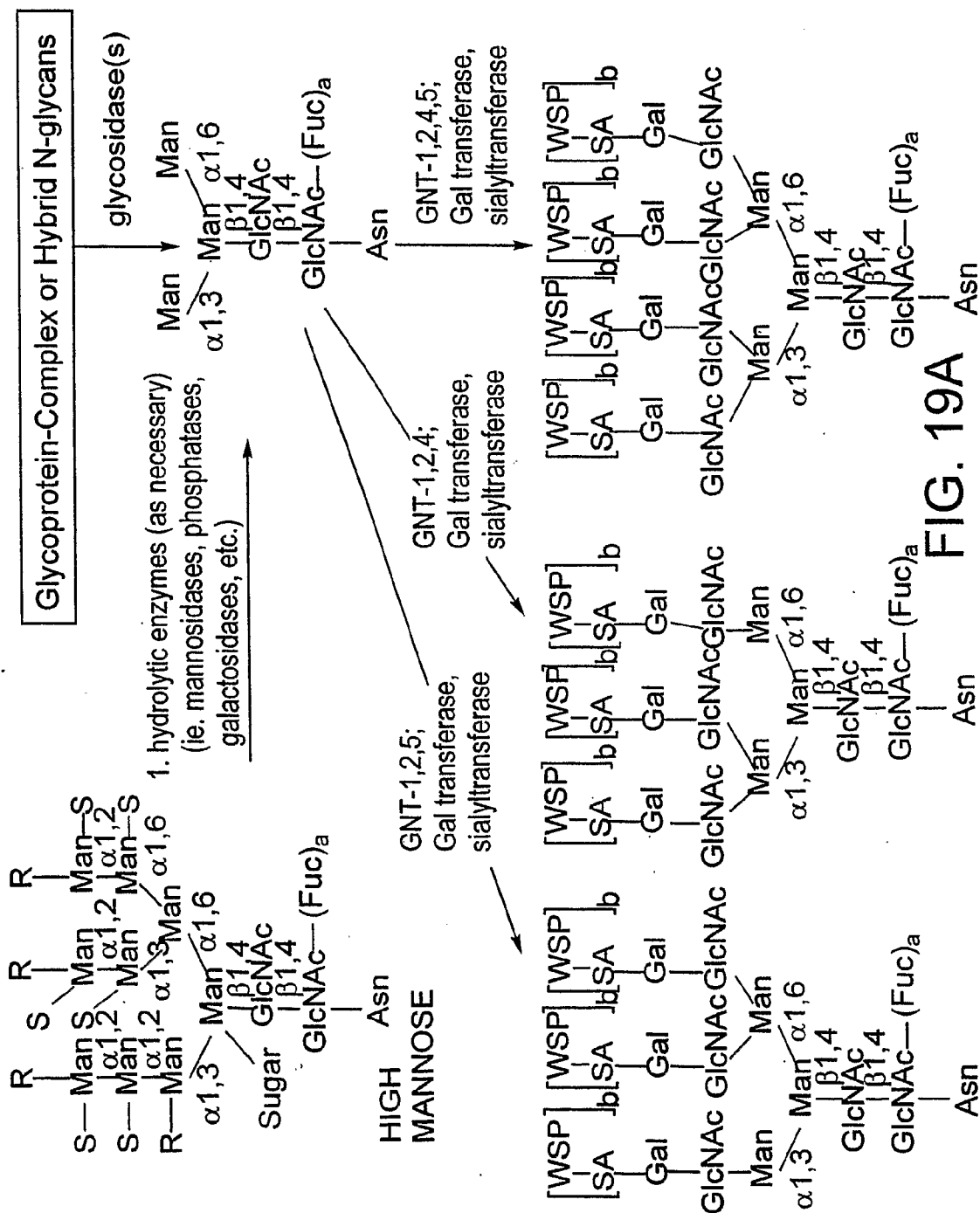


FIG. 18B

20/498





21/498

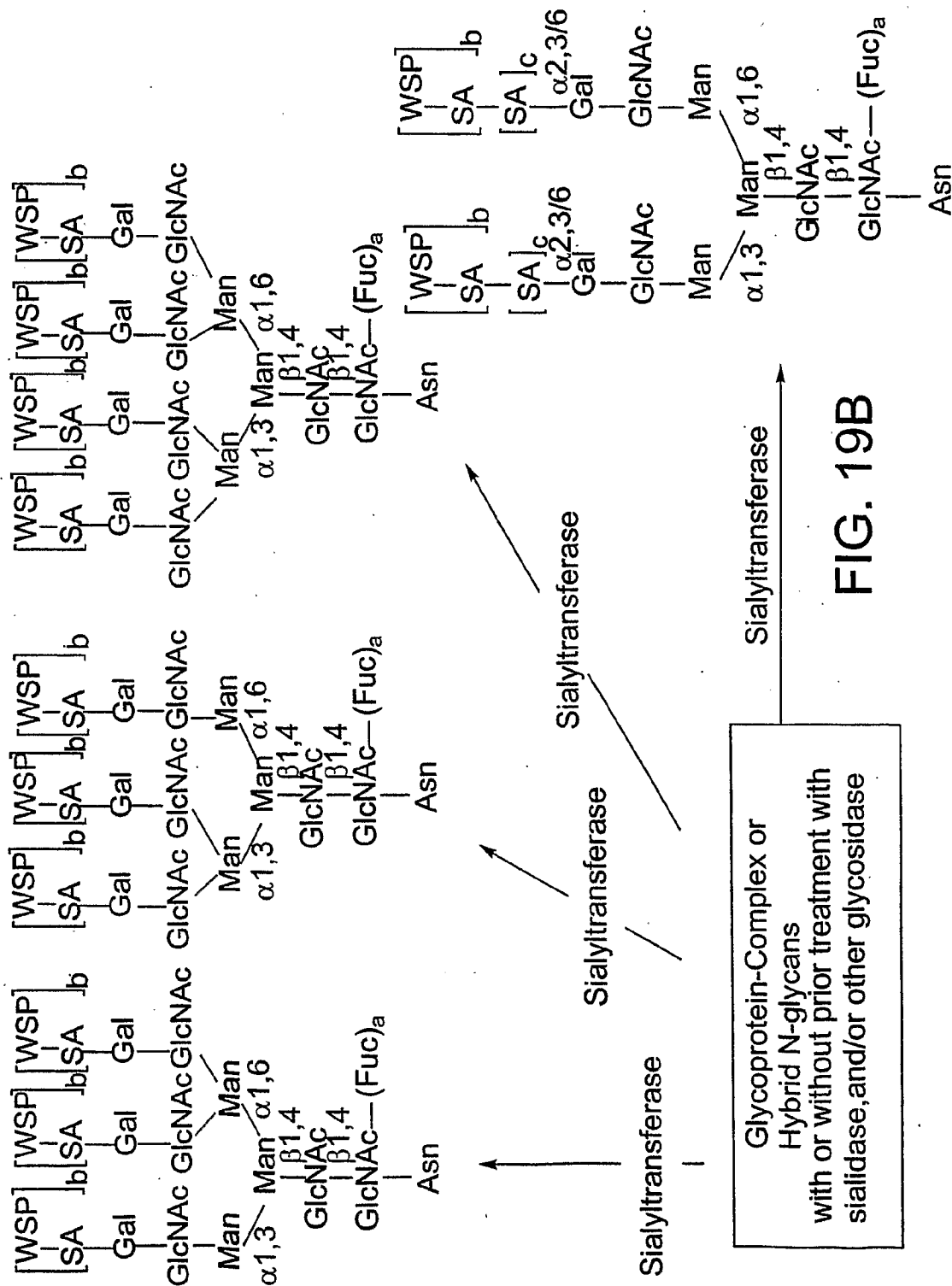


FIG. 19B

22/498

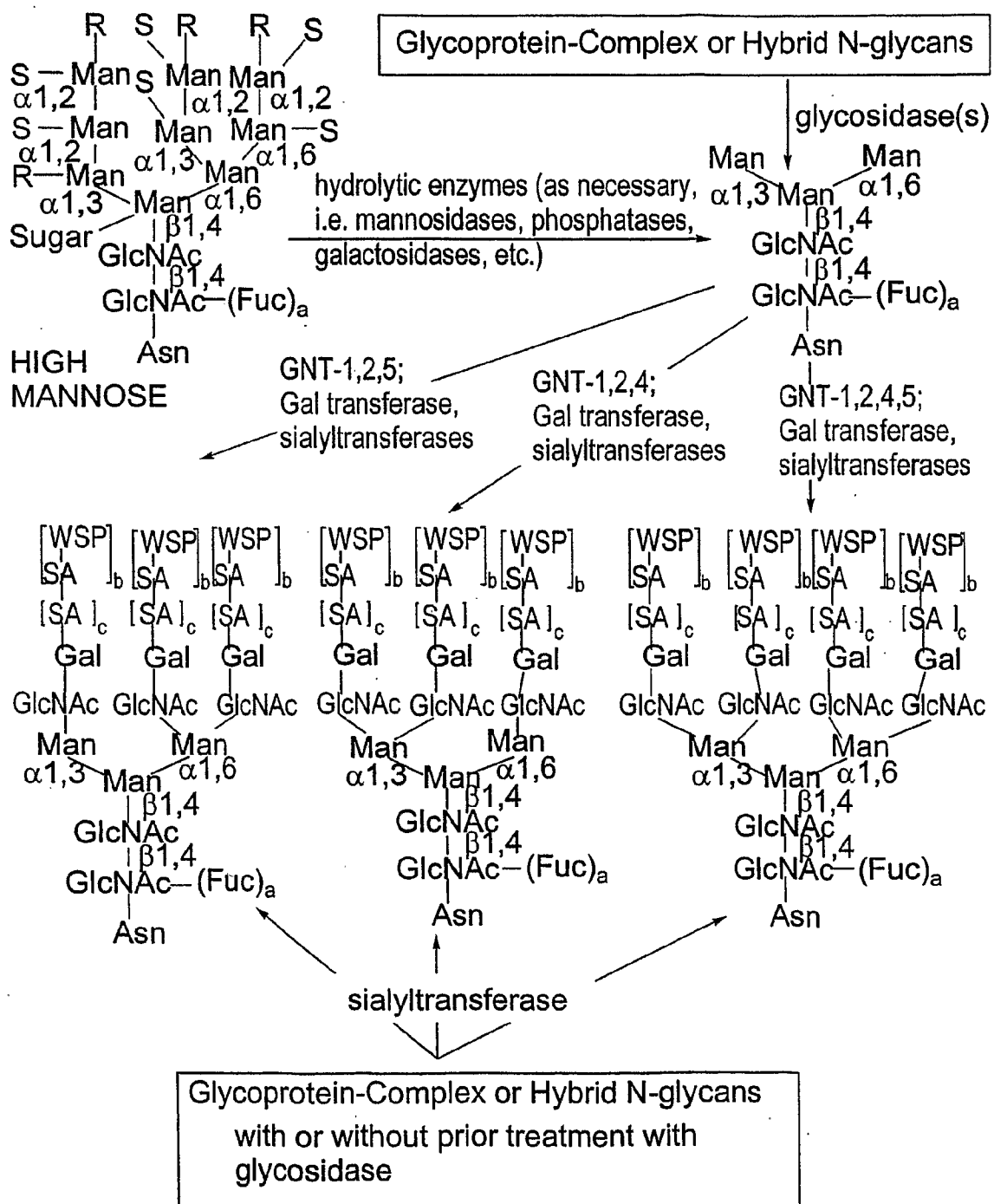
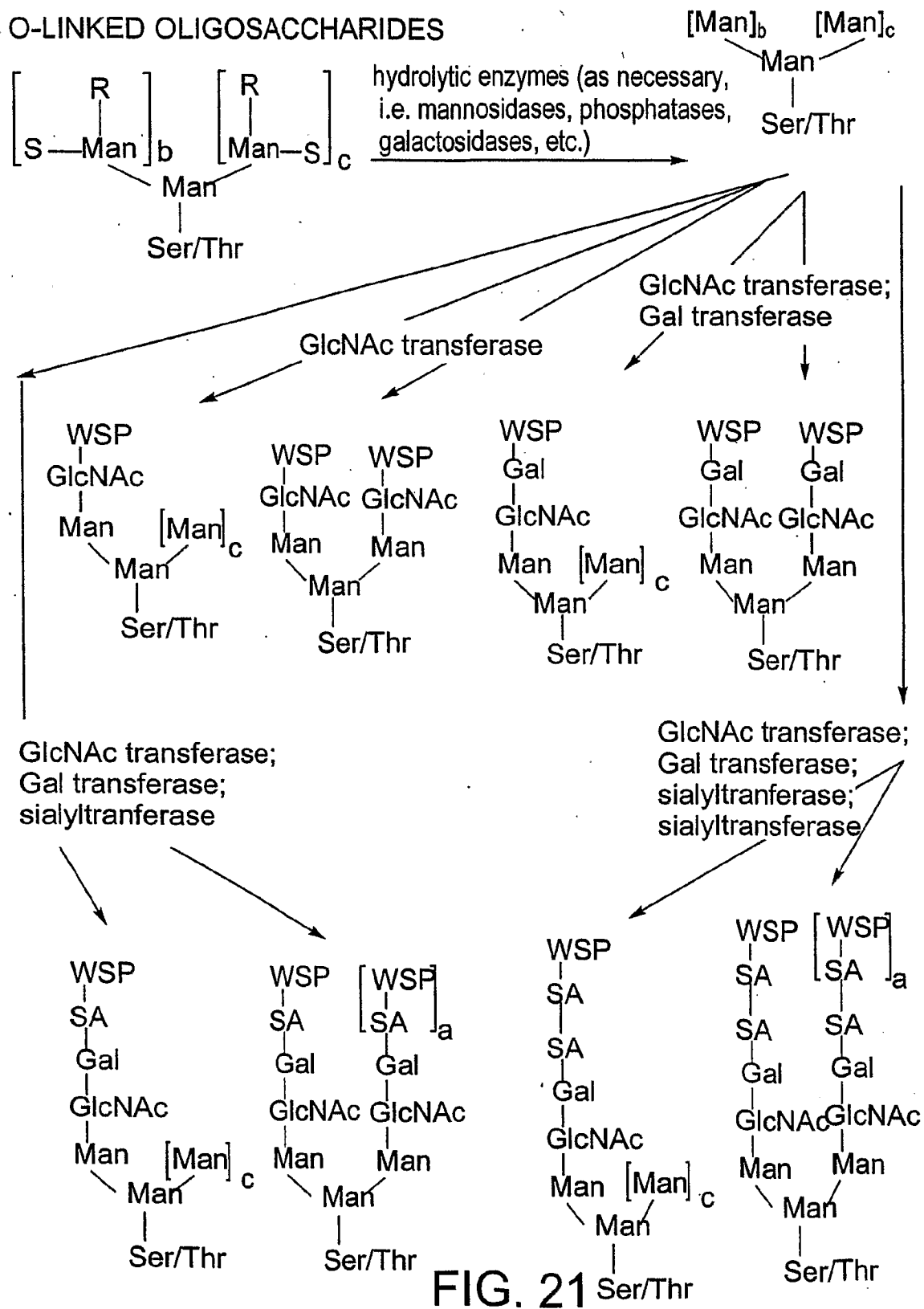


FIG. 20

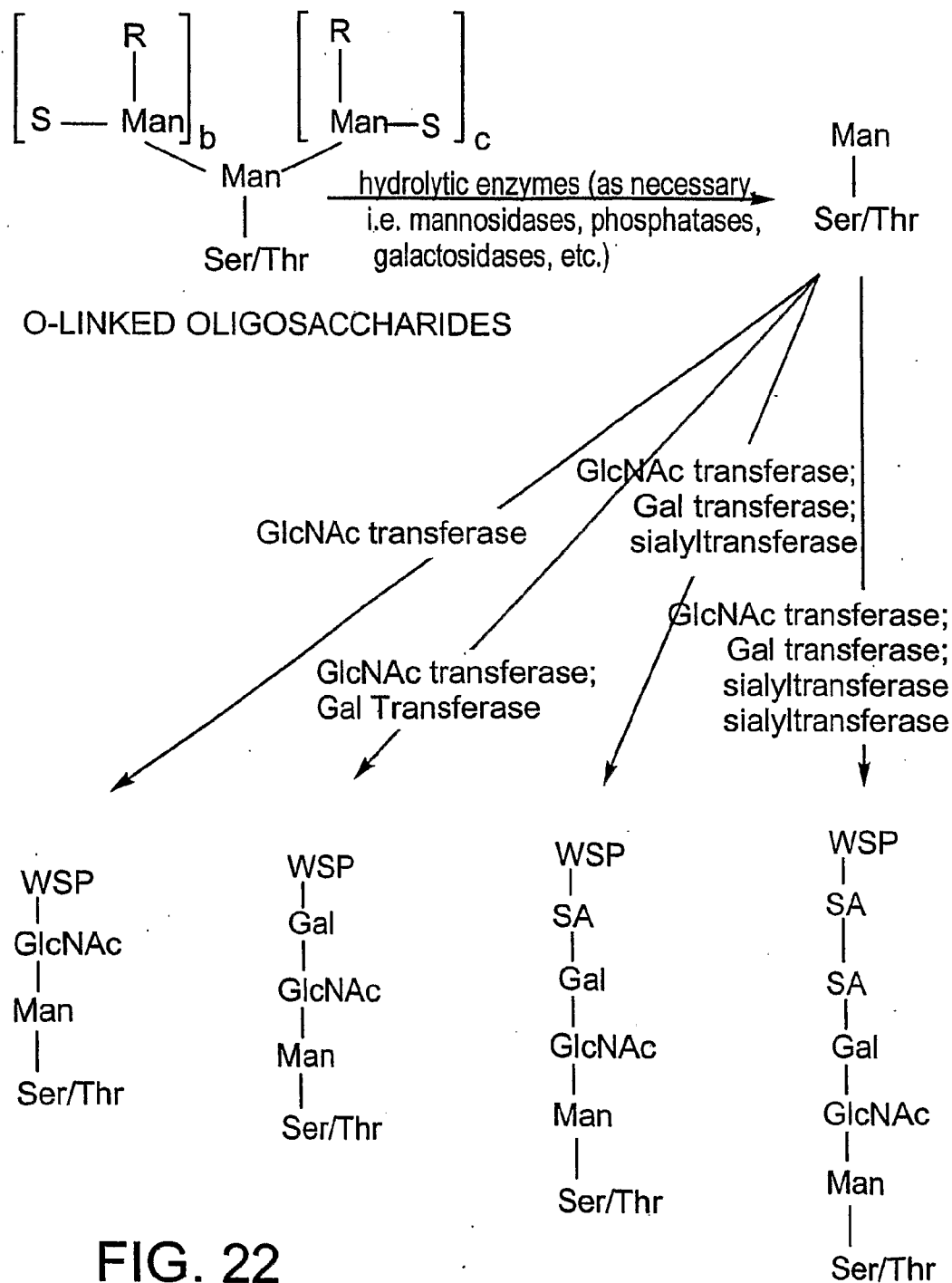
23/498

## O-LINKED OLIGOSACCHARIDES



**FIG. 21** Ser/Thr

24/498



25/498

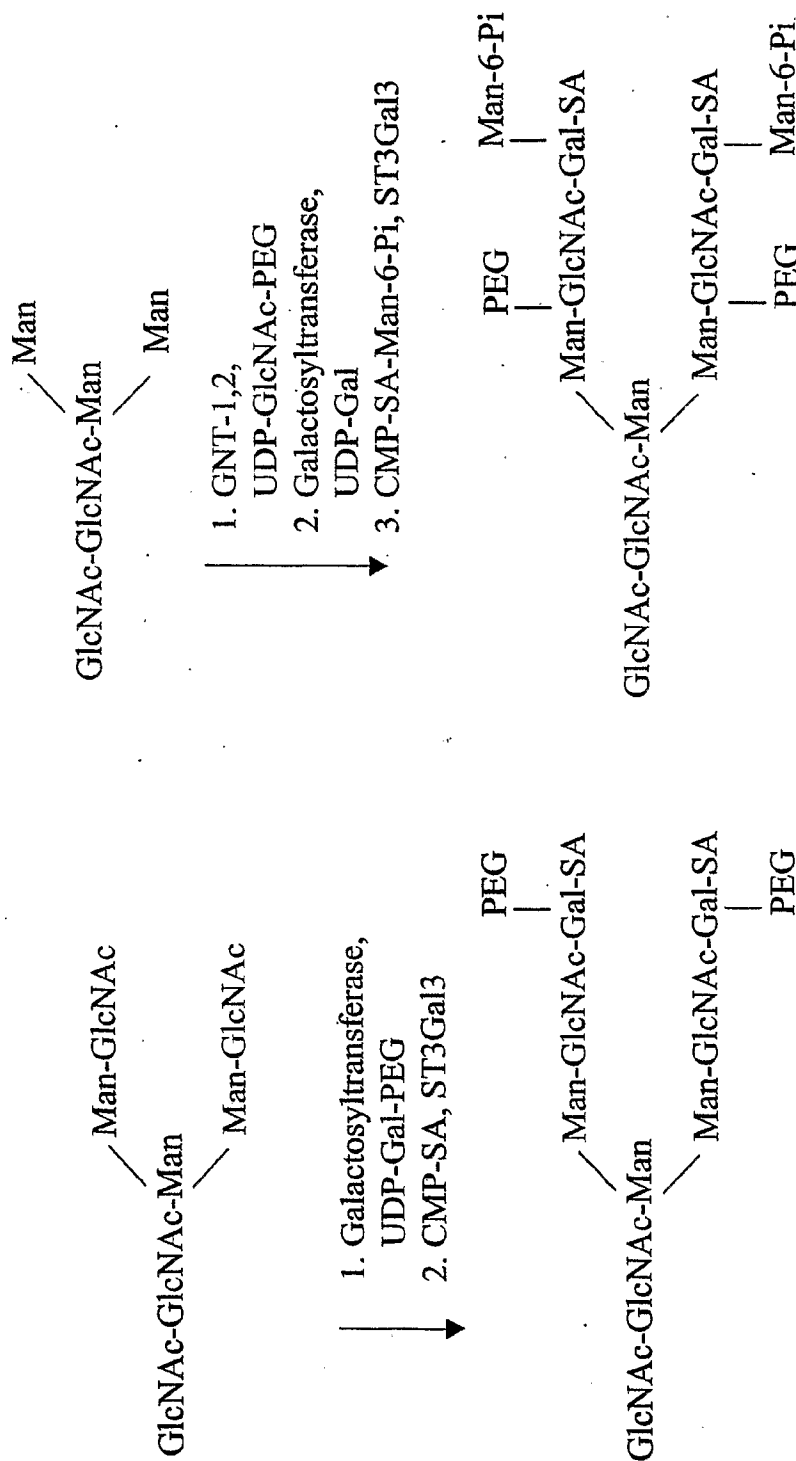


FIG. 23A

FIG. 23B

26/498

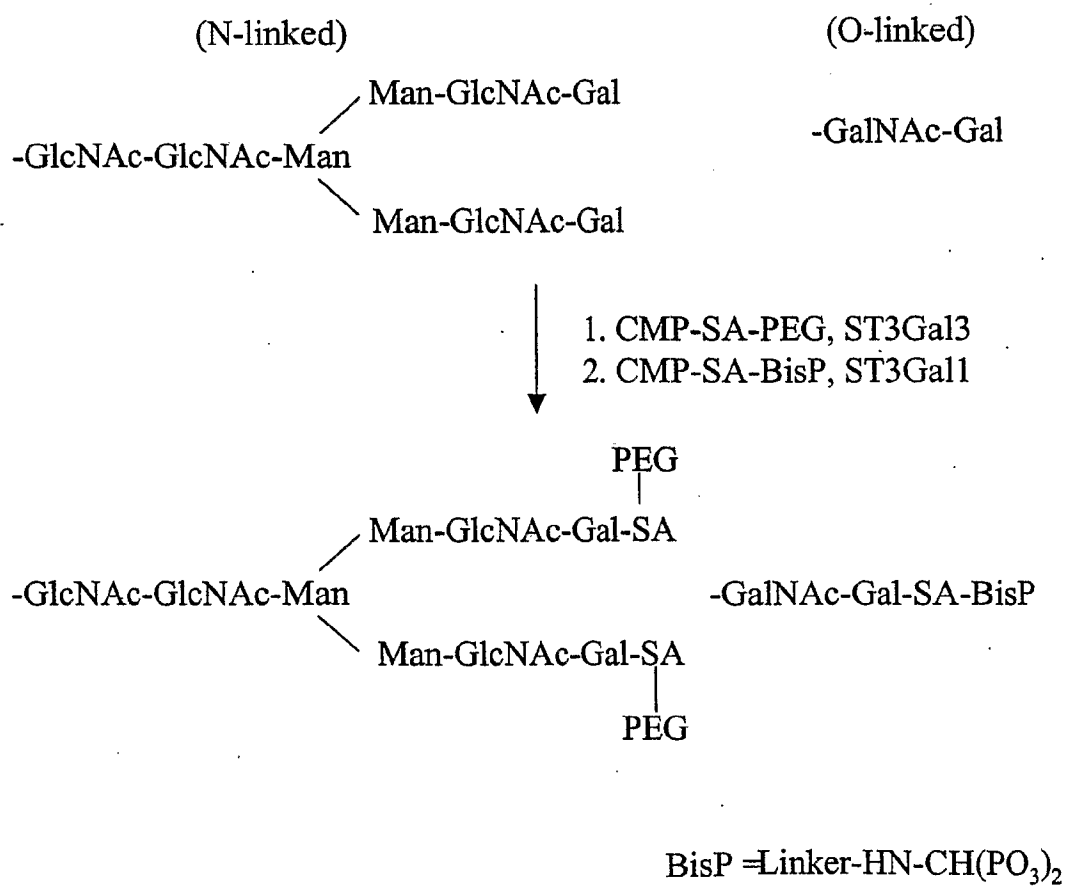


FIG. 23C

27/498

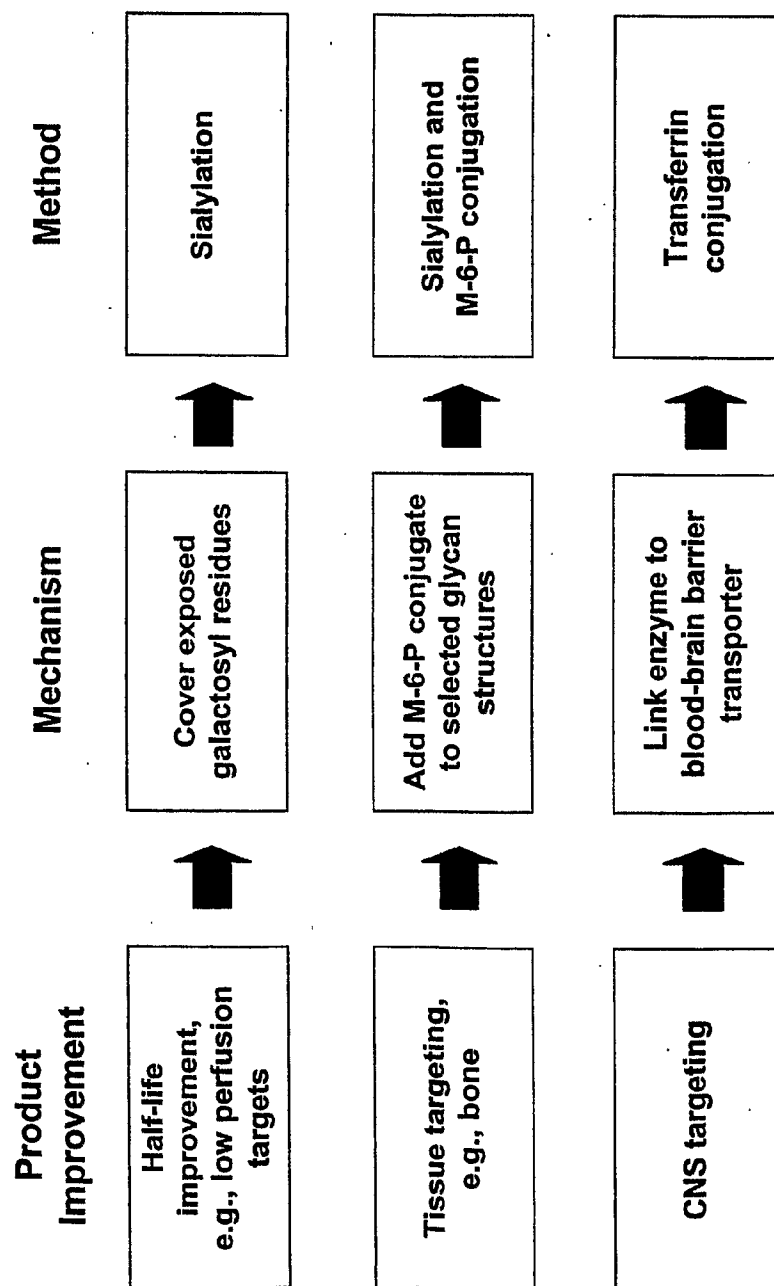


FIG. 24

28/498

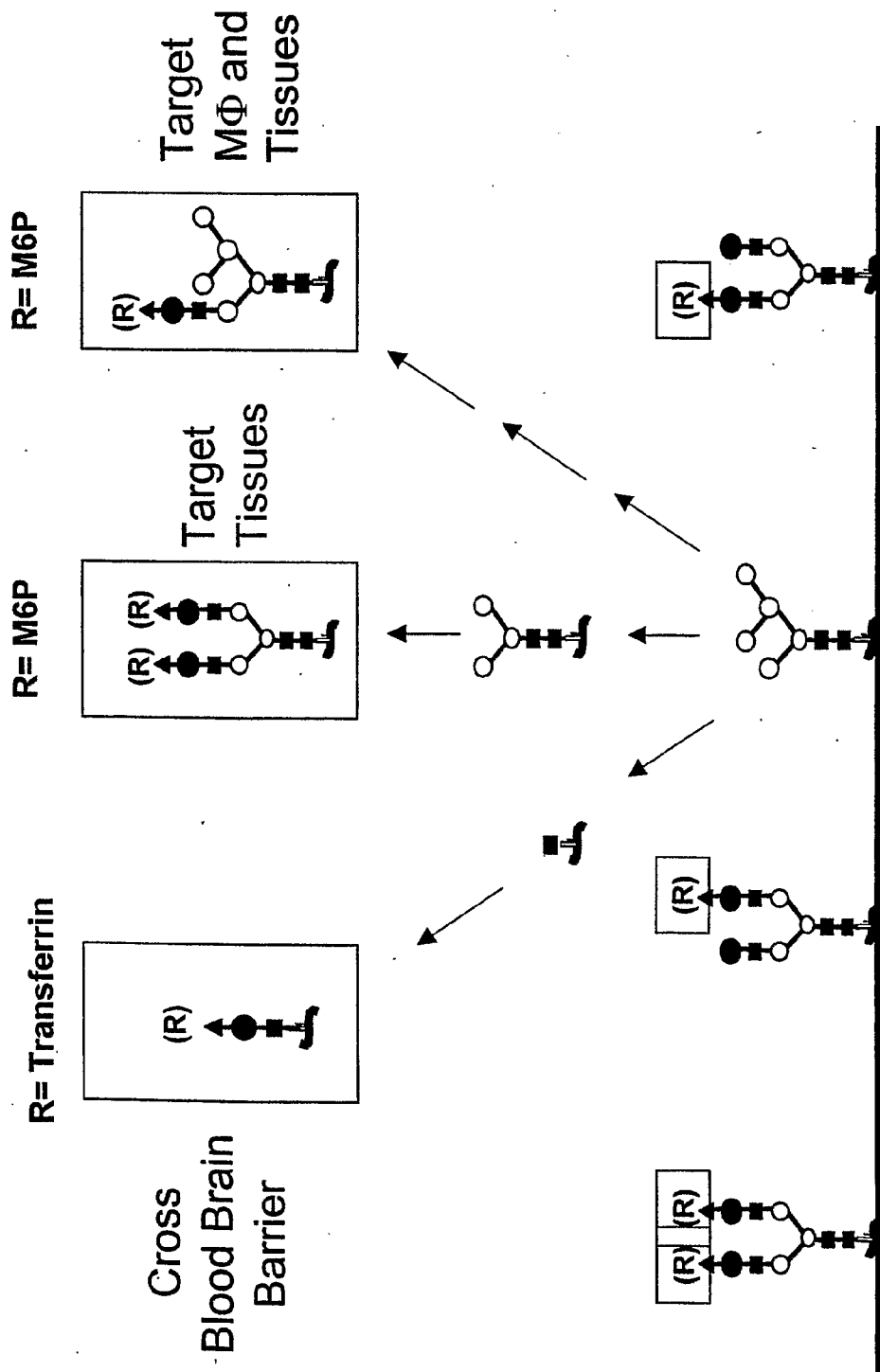


FIG. 25



29/498

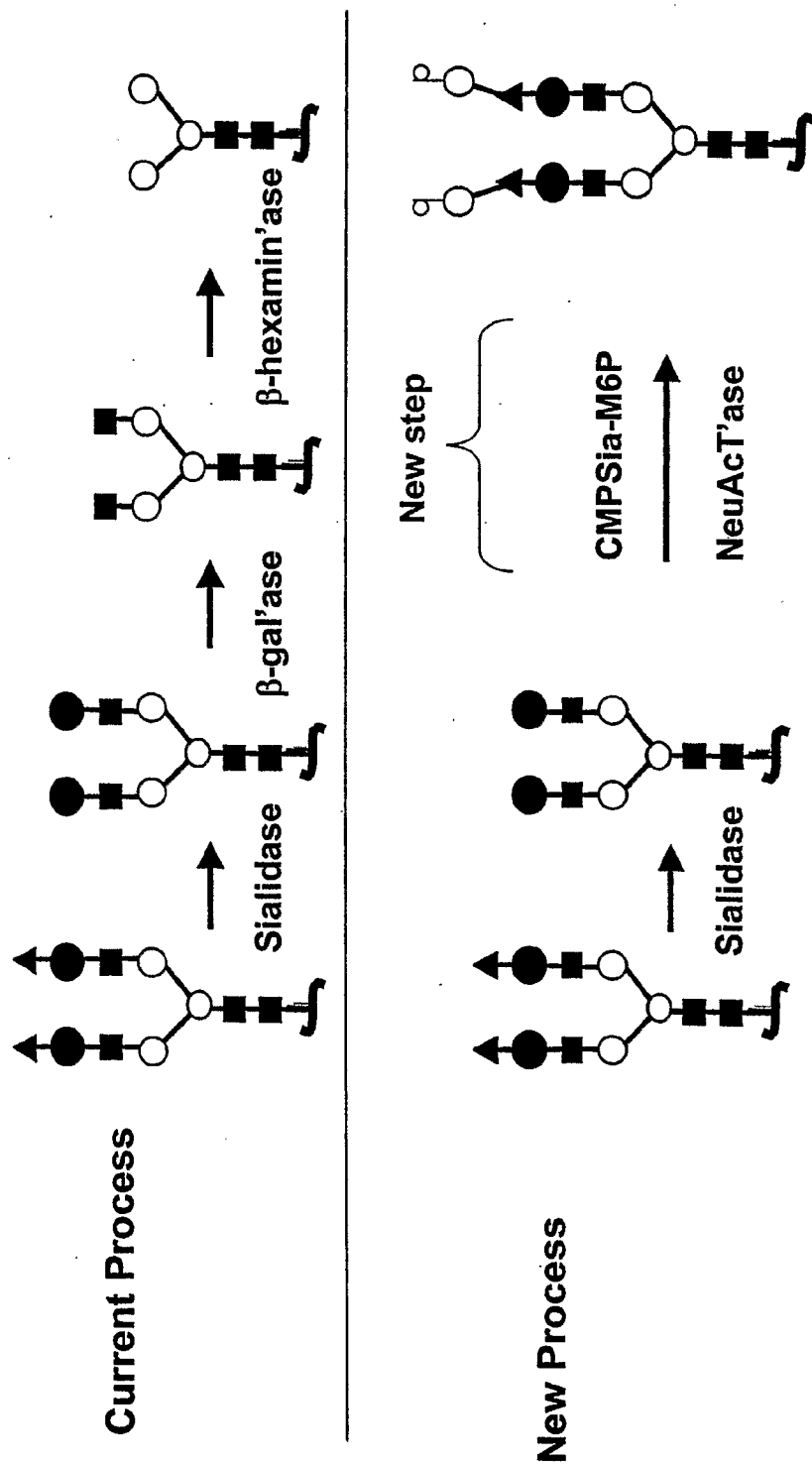


FIG. 26

30/498

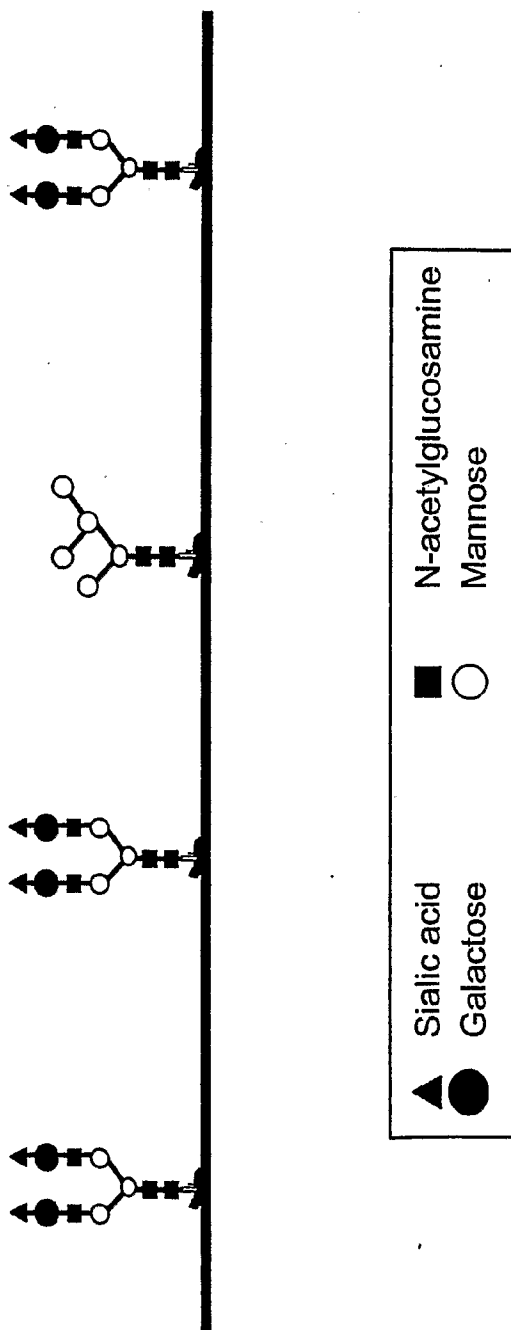


FIG. 27

## 31/498

12AP1/E5 -- Viventia Biotech	AI-201 -- AutoImmune
1964 -- Aventis	AI-301 -- AutoImmune
20K growth hormone -- AMUR	AIDS vaccine -- ANRS, CIBG, Hersed
28P6/E6 -- Viventia Biotech	Biomed, Hollis-Eden, Rome, United
3-Hydroxyphthaloyl-beta-lactoglobulin --	Biomedical, American Home Products,
4-IBB ligand gene therapy --	Maxygen
64-Cu MAb conjugate TETA-1A3 --	airway receptor ligand -- IC Innovations
Mallinckrodt Institute of Radiology	AJvW 2 -- Ajinomoto
64-Cu MAb conjugate TETA-cT84.66	AK 30 NGF -- Alkermes
64-Cu Trastuzumab TETA conjugate --	Albuferon -- Human Genome Sciences
Genentech	albumin -- Biogen, DSM Anti-Infectives,
A 200 -- Amgen	Genzyme Transgenics, PPL Therapeutics,
A10255 -- Eli Lilly	TranXenoGen, Welfide Corp.
A1PDX -- Hedral Therapeutics	aldesleukin -- Chiron
A6 -- Angstrom	alefacept -- Biogen
aaAT-III -- Genzyme	Alemtuzumab
Abciximab -- Centocor	Allergy therapy -- ALK-Abello/Maxygen,
ABI.001 -- Atlantic BioPharmaceuticals	ALK-Abello/RP Scherer
ABT-828 -- Abbott	allergy vaccines -- Allergy Therapeutics
Accutin	Alnidofibatide -- Aventis Pasteur
Actinohivin	Alnorine -- SRC VB VECTOR
activin -- Biotech Australia, Human	ALP 242 -- Gruenenthal
Therapeutics, Curis	Alpha antitrypsin -- Arriva/Hyland
AD 439 -- Tanox	Immuno/ProMetic/Protease Sciences
AD 519 -- Tanox	Alpha-1 antitrypsin -- Cutter, Bayer, PPL
Adalimumab -- Cambridge Antibody Tech.	Therapeutics, Profile, ZymoGenetics,
Adenocarcinoma vaccine -- Biomira -- NIS	Arriva
Adenosine deaminase -- Enzond	Alpha-1 protease inhibitor -- Genzyme
Adenosine A2B receptor antagonists --	Transgenics, Welfide Corp.
Adenosine Therapeutics	Alpha-galactose fusion protein --
ADP-001 -- Axis Genetics	Immunomedics
AF 13948 -- Affymax	Alpha-galactosidase A -- Research
Afelimomab -- Knoll	Corporation Technologies, Genzyme
AFP-SCAN -- Immunomedics	Alpha-glucosidase -- Genzyme, Novazyme
AG 2195 -- Corixa	Alpha-lactalbumin
agalsidase alfa -- Transkaryotic Therapies	Alpha-L-iduronidase -- Transkaryotic
agalsidase beta -- Genzyme	Therapies, BioMarin
AGENT-- Antisoma	alteplase -- Genentech
AI 300 -- AutoImmune	alvircept sudotox -- NIH
AI-101 -- Teva	ALX-0600, a GLP-2 agonist -- NPS Allelix
AI-102 -- Teva	Corp.

FIG. 28A

## 32/498

ALX1-11 --sNPS Pharmaceuticals	Anti-alphav $\beta$ 3 integrin MAb -- Applied
Alzheimer's disease gene therapy	Molecular Evolution
AM-133 -- AMRAD	Anti-angiogenesis monoclonal antibodies --
Amb a 1 immunostim conj. -- Dynavax	KS Biomedix/Schering AG
AMD 3100 -- AnorMED -- NIS	Anti-B4 MAb-DC1 conjugate -- ImmunoGen
AMD 3465 -- AnorMED -- NIS	Anti-B7 antibody PRIMATIZED -- IDEC
AMD 3465 -- AnorMED -- NIS	Anti-B7-1 MAb 16-10A1
AMD Fab -- Genentech	Anti-B7-1 MAb 1G10
Amediplase -- Menarini, Novartis	Anti-B7-2 MAb GL-1
AM-F9	Anti-B7-2-gelonin immunotoxin --
Amoebiasis vaccine	Antibacterials/antifungals --
Amphiregulin -- Octagene	Diversa/IntraBiotics
anakinra -- Amgen	Anti-beta-amyloid monoclonal antibodies --
analgesic -- Nobex	Cambridge Antibody Tech., Wyeth-Ayerst
ancestim -- Amgen	Anti-BLyS antibodies -- Cambridge
AnergiX.RA -- Corixa, Organon	Antibody Tech. /Human Genome Sciences
Angiocidin -- InKine	Antibody-drug conjugates -- Seattle
angiogenesis inhibitors -- ILEX	Genetics/Eos
AngioMab -- Antisoma	Anti-C5 MAb BB5-1 -- Alexion
Angiopoietins -- Regeneron/Procter &	Anti-C5 MAb N19-8 -- Alexion
Gamble	Anti-C8 MAb
angiostatin -- EntreMed	anticancer cytokines -- BioPulse
Angiostatin/endostatin gene therapy --	anticancer matrix -- Telios Integra
Genetix Pharmaceuticals	Anticancer monoclonal antibodies -- ARIUS,
angiotensin-II, topical -- Maret	Immunex
Anthrax -- EluSys Therapeutics/US Army	anticancer peptides -- Maxygen, Micrologix
Medical Research Institute	Anticancer prodrug Tech. -- Alexion
Anthrax vaccine	Antibody Technologies
Anti platelet-derived growth factor D human	anticancer Troy-Bodies -- Affite -- Affitech
monoclonal antibodies -- CuraGen	anticancer vaccine -- NIH
Anti-17-1A MAb 3622W94 --	anticancers -- Epimmune
GlaxoSmithKline	Anti-CCR5/CXCR4 sheep MAb -- KS
Anti-2C4 MAb -- Genentech	Biomedix Holdings
anti-4-1BB monoclonal antibodies -- Bristol-	Anti-CD11a MAb KBA --
Myers Squibb	Anti-CD11a MAb M17
Anti-Adhesion Platform Tech. -- Cytovax	Anti-CD11a MAb TA-3 --
Anti-adipocyte MAb -- Cambridge Antibody	Anti-CD11a MAb WT.1 --
Tech./ObeSys	Anti-CD11b MAb -- Pharmacia
antiallergics -- Maxygen	Anti-CD11b MAb LM2
antiallergy vaccine -- Acambis	Anti-CD154 MAb -- Biogen
Anti-alpha-4-integrin MAb	Anti-CD16-anti-CD30 MAb -- Biotest

FIG. 28B

## 33/498

Anti-CD18 MAb -- Pharmacia	Anti-CD4 MAb -- Centocor, IDEC
Anti-CD19 MAb B43 --	Pharmaceuticals, Xenova Group
Anti-CD19 MAb -liposomal sodium butyrate conjugate --	Anti-CD4 MAb 16H5
Anti-CD147	Anti-CD4 MAb 4162W94 -- GlaxoSmithKline
Anti-CD19 MAb-saporin conjugate --	Anti-CD4 MAb B-F5 -- Diaclone
Anti-CD19-dsFv-PE38-immunotoxin --	Anti-CD4 MAb GK1-5
Anti-CD2 MAb 12-15 --	Anti-CD4 MAb KT6
Anti-CD2 MAb B-E2 -- Diaclone	Anti-CD4 MAb OX38
Anti-CD2 MAb OX34 --	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb OX54 --	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX55 --	Anti-CD4 MAb W3/25
Anti-CD2 MAb RM2-1	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb RM2-2	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-4	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD20 MAb BCA B20	Anti-CD40 MAb
Anti-CD20-anti-Fc alpha RI bispecific MAb -- Medarex, Tenovus	Anti-CD40 MAb 5D12 -- Tanox
Anti-CD22 MAb-saporin-6 complex --	Anti-CD44 MAb A3D8
Anti-CD3 immunotoxin --	Anti-CD44 MAb GKWA3
Anti-CD3 MAb 145-2C11 -- Pharming	Anti-CD44 MAb IM7
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD44 MAb KM81
Anti-CD3 MAb humanised -- Protein Design, RW Johnson	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb WT32	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb-ricin-chain-A conjugate --	Anti-CD45RB MAb
Anti-CD3 MAb-xanthine-oxidase conjugate --	Anti-CD48 MAb HuLy-m3
Anti-CD30 MAb BerH2 -- Medac	Anti-CD48 MAb WM-63
Anti-CD30 MAb-saporin conjugate	Anti-CD5 MAb -- Becton Dickinson
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD5 MAb OX19
Anti-CD38 MAb AT13/5	Anti-CD6 MAb
Anti-CD38 MAb-saporin conjugate	Anti-CD7 MAb-PAP conjugate
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb -- Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-MOV18 MAb -- Centocor	Anti-CD8 MAb OX8
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD80 MAb P16C10 -- IDEC
Anti-CD4 idiotype vaccine	Anti-CD80 MAb P7C10 -- ID Vaccine
	Anti-CD8-idarubicin conjugate
	Anti-CEA MAb CE-25
	Anti-CEA MAb MN 14 -- Immunomedics

FIG. 28C

34/498

Anti-CEA MAb MN14-PE40 conjugate -- Immunomedics	Anti-heparanase human monoclonal antibodies -- Oxford Glycosciences/Medarex
Anti-CEA MAb T84.66-interleukin-2 conjugate	Anti-hepatitis C virus human monoclonal antibodies -- XTL Biopharmaceuticals
Anti-CEA sheep MAb -- KS Biomedix Holdings	Anti-HER-2 antibody gene therapy
Anti-cell surface monoclonal antibodies -- Cambridge Antibody Tech. /Pharmacia	Anti-herpes antibody -- Epicyte
Anti-c-erbB2-anti-CD3 bifunctional MAb -- Otsuka	Anti-HIV antibody -- Epicyte
Anti-CMV MAb -- Scotgen	anti-HIV catalytic antibody -- Hesed Biomed
Anti-complement	anti-HIV fusion protein -- Idun
Anti-CTLA-4 MAb	anti-HIV proteins -- Cangene
Anti-EGFR catalytic antibody -- Hesed Biomed	Anti-HM1-24 MAb -- Chugai
anti-EGFR immunotoxin -- IVAX	Anti-hR3 MAb
Anti-EGFR MAb -- Abgenix	Anti-Human-Carcinoma-Antigen MAb -- Epicyte
Anti-EGFR MAb 528	Anti-ICAM-1 MAb -- Boehringer Ingelheim
Anti-EGFR MAb KSB 107 -- KS Biomedix	Anti-ICAM-1 MAb 1A-29 -- Pharmacia
Anti-EGFR MAb-DM1 conjugate -- ImmunoGen	Anti-ICAM-1 MAb HA58
Anti-EGFR MAb-LA1 --	Anti-ICAM-1 MAb YN1/1.7.4
Anti-EGFR sheep MAb -- KS Biomedix	Anti-ICAM-3 MAb ICM3 -- ICOS
Anti-FAP MAb F19-I-131	Anti-idiotype breast cancer vaccine 11D10
Anti-Fas IgM MAb CH11	Anti-idiotype breast cancer vaccine ACA14C5 --
Anti-Fas MAb Jo2	Anti-idiotype cancer vaccine -- ImClone Systems/Merck KGaA ImClone, Viventia Biotech
Anti-Fas MAb RK-8	Anti-idiotype cancer vaccine 1A7 -- Titan
Anti-Flt-1 monoclonal antibodies -- ImClone	Anti-idiotype cancer vaccine 3H1 -- Titan
Anti-fungal peptides -- State University of New York	Anti-idiotype cancer vaccine TriAb -- Titan
antifungal tripeptides -- BTG	Anti-idiotype Chlamydia trachomatis vaccine
Anti-ganglioside GD2 antibody-interleukin-2 fusion protein -- Lexigen	Anti-idiotype colorectal cancer vaccine -- Novartis
Anti-GM2 MAb -- Kyowa	Anti-idiotype colorectal cancer vaccine -- Onyvax
Anti-GM-CSF receptor monoclonal antibodies -- AMRAD	Anti-idiotype melanoma vaccine -- IDEC Pharmaceuticals
Anti-gp130 MAb -- Tosoh	Anti-idiotype ovarian cancer vaccine ACA 125
Anti-HCA monoclonal antibodies -- AltaRex/Epigen	Anti-idiotype ovarian cancer vaccine AR54 - AltaRex
Anti-hCG antibodies -- Abgenix/AVI BioPharma	

**FIG. 28D**

## 35/498

Anti-idiotypic ovarian cancer vaccine CA-125 – AltaRex, Biomira	Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University
Anti-IgE catalytic antibody -- Hersed Biomed	Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital
Anti-IgE MAb E26 -- Genentech	Anti-MHC monoclonal antibodies
Anti-IGF-1 MAb	Anti-MIF antibody humanised – IDEC, Cytokine PharmaSciences
anti-inflammatory -- GeneMax	Anti-MRSA/VRSA sheep MAb -- KS Biomedix Holdings
anti-inflammatory peptide -- BTG	Anti-mu MAb -- Novartis
anti-integrin peptides -- Burnha	Anti-MUC-1 MAb
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC 18
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb IN1
Anti-interferon-gamma polyclonal antibody - Advanced Biotherapy	Anti-nuclear autoantibodies -- Procyon
Anti-interleukin-10 MAb –	Anti-ovarian cancer monoclonal antibodies - Dompe
Anti-interleukin-12 MAb –	Anti-p185 monoclonal antibodies
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Anti-p43 MAb
Anti-interleukin-2 receptor MAb 2A3	Antiparasitic vaccines
Anti-interleukin-2 receptor MAb 33B3-1 -- Immunotech	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAb ART-18	Anti-properdin monoclonal antibodies -- Abgenix/Gliatech
Anti-interleukin-2 receptor MAb LO-Tact-1	Anti-PSMA (prostate specific membrane antigen)
Anti-interleukin-2 receptor MAb Mikbeta1	Anti-PSMA MAb J591 -- BZL Biologics
Anti-interleukin-2 receptor MAb NDS61	Anti-Rev MAb gene therapy –
Anti-interleukin-4 MAb 11B11	Anti-RSV antibodies – Epicyte, Intracell
Anti-interleukin-5 MAb -- Wallace Laboratories	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-6 MAb – Centocor, Diaclone, Pharmadigm	Anti-RSV MAb, inhalation -- Alkermes/MedImmune
Anti-interleukin-8 MAb -- Abgenix	Anti-RT gene therapy
Anti-interleukin-8 MAb – Xenotech	Antisense K-ras RNA gene therapy
Anti-JL1 MAb	Anti-SF-25 MAb
Anti-Klebsiella sheep MAb -- KS Biomedix Holdings	Anti-sperm antibody -- Epicyte
Anti-Laminin receptor MAb-liposomal doxorubicin conjugate	Anti-Tac(Fv)-PE38 conjugate
Anti-LCG MAb -- Cytoclonal	Anti-TAPA/CD81 MAb AMP1
Anti-lipopolysaccharide MAb -- VitaResc	Anti-tat gene therapy

FIG. 28E

## 36/498

Anti-TCR-alphabeta MAb H57-597	AOP-RANTES -- Senetek
Anti-TCR-alphabeta MAb R73	Apan-CH -- Praecis Pharmaceuticals
Anti-tenascin MAb BC-4-I-131	APC-8024 -- Demegen
Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme	ApoA-1 -- Milano, Pharmacia
Anti-TGF-beta MAb 2G7 -- Genentech	Apogen -- Alexion
Antithrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad	apolipoprotein A1 -- Avanir
Anti-Thy1 MAb	Apolipoprotein E -- Bio-Tech. General
Anti-Thy1.1 MAb	Applaggin -- Biogen
Anti-tissue factor/factor VIIA sheep MAb -- KS Biomedix	aprotinin -- ProdiGene
Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharacia, Serono	APT-070C -- AdProTech
Anti-TNF sheep MAb -- KS Biomedix Holdings	AR 177 -- Aronex Pharmaceuticals
Anti-TNFalpha MAb -- Genzyme	AR 209 -- Aronex Pharmaceuticals, Antigenics
Anti-TNFalpha MAb B-C7 -- Diaclone	AR545C
Anti-tooth decay MAb -- Planet BioTech.	ARGENT gene delivery systems -- ARIAD
Anti-TRAIL receptor-1 MAb -- Takeda	Arresten
Antitumour RNases -- NIH	ART-123 -- Asahi Kasei
Anti-VCAM MAb 2A2 -- Alexion	arylsulfatase B -- BioMarin
Anti-VCAM MAb 3F4 -- Alexion	Arylsulfatase B, Recombinant human -- BioMarin
Anti-VCAM-1 MAb	AS 1051 -- Ajinomoto
Anti-VEC MAb -- ImClone	ASI-BCL -- Intracell
Anti-VEGF MAb -- Genentech	Asparaginase - Merck
Anti-VEGF MAb 2C3	ATL-101 -- Alizyme
Anti-VEGF sheep MAb -- KS Biomedix Holdings	Atrial natriuretic peptide -- Pharis
Anti-VLA-4 MAb HP1/2 -- Biogen	Aurintricarboxylic acid-high molecular weight
Anti-VLA-4 MAb PS/2	Autoimmune disorders -- GPC Biotech/MorphoSys
Anti-VLA-4 MAb R1-2	Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme
Anti-VLA-4 MAb TA-2	Tra
Anti-VAP-1 human MAb	Autoimmune disorders/cancer -- Abgenix/Chiron, CuraGen
Anti-VRE sheep MAb -- KS Biomedix Holdings	Autotaxin
ANUP -- TranXenoGen	Avicidin -- NeoRx
ANUP-1 -- Pharis	axogenesis factor-1 -- Boston Life Sciences
	Axokine -- Regeneron
	B cell lymphoma vaccine -- Biomira
	B7-1 gene therapy --
	BABS proteins -- Chiron

FIG. 28F



37/498

BAM-002 -- Novelos Therapeutics	BMP 2 -- Genetics Institute/Medtronic-
Basiliximab (anti CD25 MAb) -- Novartis	Sofamor Danek, Genetics Institute/
Bay-16-9996 -- Bayer	Collagenesis, Genetics
Bay-39-9437 -- Bayer	Institute/Yamanouch
Bay-50-4798 -- Bayer	BMP 2 gene therapy
BB-10153 -- British Biotech	BMP 52 -- Aventis Pasteur, Biopharm
BBT-001 -- Bolder BioTech.	BMP-2 -- Genetics Institute
BBT-002 -- Bolder BioTech.	BMS 182248 -- Bristol-Myers Squibb
BBT-003 -- Bolder BioTech.	BMS 202448 -- Bristol-Myers Squibb
BBT-004 -- Bolder BioTech.	bone growth factors -- IsoTis
BBT-005 -- Bolder BioTech.	BPC-15 -- Pfizer
BBT-006 -- Bolder BioTech.	brain natriuretic peptide --
BBT-007 -- Bolder BioTech.	Breast cancer -- Oxford
BCH-2763 -- Shire	GlycoSciences/Medarex
BCSF -- Millenium Biologix	Breast cancer vaccine -- Therion Biologics,
BDNF -- Regeneron -- Amgen	Oregon
Becaplermin -- Johnson & Johnson, Chiron	BSSL -- PPL Therapeutics
Bectumomab -- Immunomedics	BST-2001 -- BioStratum
Beriplast -- Aventis	BST-3002 -- BioStratum
Beta-adrenergic receptor gene therapy --	BTI 322 --
University of Arkansas	butyrylcholinesterase -- Shire
bFGF -- Scios	C 6822 -- COR Therapeutics
BI 51013 -- Behringwerke AG	C1 esterase inhibitor -- Pharming
BIBH 1 -- Boehringer Ingelheim	C3d adjuvant -- AdProTech
BIM-23190 -- Beaufour-Ipsen	CAB-2.1 -- Millennium
birch pollen immunotherapy -- Pharmacia	calcitonin -- Inhale Therapeutics Systems,
bispecific fusion proteins -- NIH	Aventis, Genetronics, TranXenoGen,
Bispecific MAb 2B1 -- Chiron	Unigene, Rhone Poulenc Rohrer
Bitistatin	calcitonin -- oral -- Nobex, Emisphere,
BIWA 4 -- Boehringer Ingelheim	Pharmaceutical Discovery
blood substitute -- Northfield, Baxter Intl.	Calcitonin gene-related peptide -- Asahi
BLP-25 -- Biomira	Kasei -- Unigene
BLS-0597 -- Boston Life Sciences	calcitonin, human -- Suntory
BLyS -- Human Genome Sciences	calcitonin, nasal -- Novartis, Unigene
BLyS radiolabelled -- Human Genome	calcitonin, Panoderm -- Elan
Sciences	calcitonin, Peptitrol -- Shire
BM 06021 -- Boehringer Mannheim	calcitonin, salmon -- Therapicon
BM-202 -- BioMarin	calin -- Biopharm
BM-301 -- BioMarin	Calphobindin I
BM-301 -- BioMarin	calphobindin I -- Kowa
BM-302 -- BioMarin	calreticulin -- NYU

**FIG. 28G**

## 38/498

Campath-1G	CD4 fusion toxin -- Senetek
Campath-1M	CD4 IgG -- Genentech
cancer therapy -- Cangene	CD4 receptor antagonists --
cancer vaccine -- Aixlie, Aventis Pasteur,	Pharmacoepia/Progenics
Center of Molecular Immunology ,YM	CD4 soluble -- Progenics
BioSciences, Cytos, Genzyme,	CD4, soluble -- Genzyme Transgenics
Transgenics, GlobelImmune, Igeneon,	CD40 ligand -- Immunex
ImClone, Virogenetics, InterCell, Iomai,	CD4-ricin chain A -- Genentech
Jenner Biotherapies, Memorial Sloan-	CD59 gene therapy -- Alexion
Kettering Cancer Center, Sydney Kimmel	CD8 TIL cell therapy -- Aventis Pasteur
Cancer Center, Novavax, Protein	CD8, soluble -- Avidex
Sciences, Argonex, SIGA	CD95 ligand -- Roche
Cancer vaccine ALVAC-CEA B7.1 --	CDP 571 -- Celltech
Aventis Pasteur/Therion Biologics	CDP 850 -- Celltech
Cancer vaccine CEA-TRICOM -- Aventis	CDP-860 (PEG-PDGF MAb) -- Celltech
Pasteur/Therion Biologics	CDP 870 -- Celltech
Cancer vaccine gene therapy -- Cantab	CDS-1 -- Ernest Orlando
Pharmaceuticals	Cedelizumab -- Ortho-McNeil
Cancer vaccine HER-2/neu -- Corixa	Cetermin -- Insmad
Cancer vaccine THERATOPE -- Biomira	CETP vaccine -- Avant
cancer vaccine, PolyMASC -- Valentis	Cetrorelix
Candida vaccine -- Corixa, Inhibitex	Cetuximab
Canstatin -- ILEX	CGH 400 -- Novartis
CAP-18 -- Panorama	CGP 42934 -- Novartis
Cardiovascular gene therapy -- Collateral	CGP 51901 -- Tanox
Therapeutics	CGRP -- Unigene
carperitide -- Suntory	CGS 27913 -- Novartis
Casocidin-1 -- Pharis	CGS 32359 -- Novartis
CAT 152 -- Cambridge Antibody Tech.	Chagas disease vaccine -- Corixa
CAT 192 -- Cambridge Antibody Tech.	chemokines -- Immune Response
CAT 213 -- Cambridge Antibody Tech.	CHH 380 -- Novartis
Catalase-- Enzon	chitinase -- Genzyme, ICOS
Cat-PAD -- Circassia	Chlamydia pneumoniae vaccine -- Antex
CB 0006 -- Celltech	Biologics
CCK(27-32)-- Akzo Nobel	Chlamydia trachomatis vaccine -- Antex
CCR2-64I -- NIH	Biologics
CD, Procept -- Paligent	Chlamydia vaccine -- GlaxoSmithKline
CD154 gene therapy	Cholera vaccine CVD 103-HgR -- Swiss
CD39 -- Immunex	Serum and Vaccine Institute Berne
CD39-L2 -- Hyseq	Cholera vaccine CVD 112 -- Swiss Serum
CD39-L4 -- Hyseq	and Vaccine Institute Berne

FIG. 28H

## 39/498

Cholera vaccine inactivated oral -- SBL Vaccin	CRL 1605 -- CytRx
Chrysalin -- Chrysalis BioTech.	CS-560 -- Sankyo
CI-782 -- Hitachi Kase	CSF -- ZymoGenetics
Ciliary neurotrophic factor -- Fidia, Roche	CSF-G -- Hangzhou, Dong-A, Hanmi
CIM project -- Active Biotech	CSF-GM -- Cangene, Hunan, LG Chem
CL 329753 -- Wyeth-Ayerst	CSF-M -- Zarix
CL22, Cobra -- ML Laboratories	CT 1579 -- Merck Frosst
Clenoliximab -- IDEC	CT 1786 -- Merck Frosst
Clostridium difficile antibodies -- Epicyte	CT-112 <sup>^</sup> -- BTG
clotting factors -- Octagene	CTB-134L -- Xenova
CMB 401 -- Celltech	CTC-111 -- Kaketsuken
CNTF -- Sigma-Tau	CTGF -- FibroGen
Cocaine abuse vaccine -- Cantab, ImmuLogic, Scripps	CTLA4-Ig -- Bristol-Myers Squibb
coccidiomycosis vaccine -- Arizo	CTLA4-Ig gene therapy --
collagen -- Type I -- Pharming	CTP-37 -- AVI BioPharma
Collagen formation inhibitors -- FibroGen	C-type natriuretic peptide -- Suntory
Collagen/hydroxyapatite/bone growth factor -- Aventis Pasteur, Biopharm, Orquest	CVS 995 -- Corvas Intl.
collagenase -- BioSpecifics	CX 397 -- Nikko Kyodo
Colorectal cancer vaccine -- Wistar Institute	CY 1747 -- Epimmune
Component B, Recombinant -- Serono	CY 1748 -- Epimmune
Connective tissue growth factor inhibitors -- FibroGen/Taisho	Cyanovirin-N
Contortrostatin	Cystic fibrosis therapy -- CBR/IVAX
contraceptive vaccine -- Zonagen	CYT 351
Contraceptive vaccine hCG	cytokine Traps -- Regeneron
Contraceptive vaccine male reversible -- IMMUCON	cytokines -- Enzon, Cytoclonal
Contraceptive vaccine zona pellucida -- Zonagen	Cytomegalovirus glycoprotein vaccine -- Chiron, Aquila Biopharmaceuticals, Aventis Pasteur, Virogenetics
Copper-64 labelled MAb TETA-1A3 -- NCI	Cytomegalovirus vaccine live -- Aventis Pasteur
Coralyne	Cytosine deaminase gene therapy -- GlaxoSmithKline
Corsevin M	DA-3003 -- Dong-A
C-peptide analogues -- Schwarz	DAB389interleukin-6 -- Senetek
CPI-1500 -- Consensus	DAB389interleukin-7
CRF -- Neurobiological Tech.	DAC:GLP-2 -- ConjuChem, Inc.
cRGDfV pentapeptide --	Daclizumab (anti-IL2R MAb) -- Protein Design Labs
CRL 1095 -- CytRx	DAMP <sup>^</sup> -- Incyte Genomics
CRL 1336 -- CytRx	Daniplestim -- Pharmacia
	darbepoetin alfa -- Amgen

FIG. 28I

## 40/498

DBI-3019 -- Diabetogen	dural graft matrix -- Integra
DCC -- Genzyme	Duteplase -- Baxter Intl.
DDF -- Hyseq	DWP-401 -- Daewoong
decorin -- Integra, Telios	DWP-404 -- Daewoong
defensins -- Large Scale Biology	DWP-408 -- Daewoong
DEGR-VIIa	Dx 88 (Epi-KAL2) -- Dyax
Delimmunised antibody 3B6/22 AGEN	Dx 890 (elastin inhibitors) -- Dyax
Deimmunised anti-cancer antibodies -- Biovation/Viragen	E coli O157 vaccine -- NIH
Dendroamide A	E21-R -- BresaGen
Dengue vaccine -- Bavarian Nordic, Merck	Eastern equine encephalitis virus vaccine --
denileukin diftitox -- Ligand	Echicetin --
DES-1101 -- Desmos	Echinhibin 1 --
desirudin -- Novartis	Echistatin -- Merck
desmopressin -- Unigene	Echitamine --
Desmoteplase -- Merck, Schering AG	Ecromeximab -- Kyowa Hakko
Destabilase	EC-SOD -- PPL Therapeutics
Diabetes gene therapy -- DeveloGen, Pfizer	Eculizumab (5G1.1) -- Alexion
Diabetes therapy -- Crucell	EDF -- Ajinomoto
Diabetes type 1 vaccine -- Diamyd Therapeutics	EDN derivative -- NIH
DiaCIM -- YM BioSciences	EDNA -- NIH
dialytic oligopeptides -- Research Corp	Edobacomab -- XOMA
Diamyd -- Diamyd Therapeutics	Edrecolomab -- Centocor
DiaPep227 -- Pepgen	EF 5077
DiavaX -- Corixa	Efalizumab -- Genentech
Digoxin MAb -- Glaxo	EGF fusion toxin -- Seragen, Ligand
Diphtheria tetanus pertussis-hepatitis B vaccine -- GlaxoSmithKline	EGF-P64k vaccine -- Center of Molecular Immunology
DIR therapy -- Solis Therapeutics --	EL 246 -- LigoCyte
DNase -- Genentech	elastase inhibitor -- Synergen
Dornase alfa -- Genentech	elcatonin -- Therapicon
Dornase alfa, inhalation -- Genentech	EMD 72000 -- Merck KGaA
Doxorubicin-anti-CEA MAb conjugate -- Immunomedics	Emdogain -- BIORA
DP-107 -- Trimeris	emfilermin -- AMRAD
drotrecogin alfa -- Eli Lilly	Emoctakin -- Novartis
DTctGMCSF	enamel matrix protein -- BIORA
DTP-polio vaccine -- Aventis Pasteur	Endo III -- NYU
DU 257-KM231 antibody conjugate -- Kyowa	endostatin -- EntreMed, Pharis
	Enhancins -- Micrologix
	Enlimomab -- Isis Pharm.
	Enoxaparin sodium -- Pharmuka

FIG. 28J

## 41/498

enzyme linked antibody nutrient depletion therapy -- KS Biomedix Holdings	Factor IX gene therapy -- Cell Genesys
Eosinophil-derived neutralizing agent -- EP-51216 -- Asta Medica	Factor VII -- Novo Nordisk, Bayer, Baxter Intl.
EP-51389 -- Asta Medica	Factor VIIa -- PPL Therapeutics, ZymoGenetics
EPH family ligands -- Regeneron	Factor VIII -- Bayer Genentech, Beaufour-Ipsen, CLB, Inex, Octagen, Pharmacia, Pharming
Epidermal growth factor -- Hitachi Kasei, Johnson & Johnson	Factor VIII -- PEGylated -- Bayer
Epidermal growth factor fusion toxin -- Senetek	Factor VIII fragments -- Pharmacia
Epidermal growth factor-genistein -- EPI-HNE-4 -- Dyax	Factor VIII gene therapy -- Targeted Genetics
EPI-KAL2 -- Dyax	Factor VIII sucrose formulation -- Bayer, Genentech
Epoetin-alfa -- Amgen, Dragon Pharmaceuticals, Nanjing Huaxin	Factor VIII-2 -- Bayer
Epratuzumab -- Immunomedics	Factor VIII-3 -- Bayer
Epstein-Barr virus vaccine -- Aviron/SmithKline Beecham, Bioresearch	Factor Xa inhibitors -- Merck, Novo Nordisk, Mochida
Eptacog alfa -- Novo Nordisk	Factor XIII -- ZymoGenetics
Eptifibatide -- COR Therapeutics	Factors VIII and IX gene therapy -- Genetics Institute/Targeted Genetics
erb-38 --	Famoxin -- Genset
Erlizumab -- Genentech	Fas (delta) TM protein -- LXR BioTech.
erythropoietin -- Alkermes, ProLease, Dong-A, Elanex, Genetics Institute, LG Chem, Protein Sciences, Serono, Snow Brand, SRC VB VECTOR, Transkaryotic Therapies	Fas TR -- Human Genome Sciences
Erythropoietin Beta -- Hoffman La Roche	Felvizumab -- Scotgen
Erythropoietin/Epoetin alfa -- Chugai	FFR-VIIa -- Novo Nordisk
Escherichia coli vaccine -- North American Vaccine, SBL Vaccin, Swiss Serum and Vaccine Institute Berne	FG-001 -- F-Gene
etanercept -- Immunex	FG-002 -- F-Gene
examorelin -- Mediolanum	FG-004 -- F-Gene
Exendin 4 -- Amylin	FG-005 -- F-Gene
exonuclease VII	FGF + fibrin -- Repair
F 105 -- Centocor	Fibrimage -- Bio-Tech. General
F-992 -- Fornix	fibrin-binding peptides -- ISIS Innovation
Factor IX -- Alpha Therapeutics, Welfide Corp., CSL, enetics Institute/AHP, Pharmacia, PPL Therapeutics	fibrinogen -- PPL Therapeutics, Pharming
	fibroblast growth factor -- Chiron, NYU, Ramot, ZymoGenetics
	fibrolase conjugate -- Schering AG
	Filgrastim -- Amgen
	filgrastim -- PDA modified -- Xencor
	FLT-3 ligand -- Immunex
	FN18 CRM9 --

**FIG. 28K**

## 42/498

follistatin -- Biotech Australia, Human Therapeutics	Glucocerebrosidase -- Genzyme
follitropin alfa -- Alkermes, ProLease, PowderJect, Serono, Akzo Nobel	glutamate decarboxylase -- Genzyme Transgenics
Follitropin Beta -- Bayer, Organon	Glycoprotein S3 -- Kureha
FP 59	GM-CSF -- Immuhex
FSH -- Ferring	GM-CSF tumour vaccine -- PowderJect
FSH + LH -- Ferring	GnRH immunotherapeutic -- Protherics
F-spondin -- CeNeS	Goserelin (LhRH antagonist) -- AstraZeneca
fusion protein delivery system -- UAB Research Foundation	gp75 antigen -- ImClone
fusion toxins -- Boston Life Sciences	gp96 -- Antigenics
G 5598 -- Genentech	GPI 0100 -- Galenica
GA-II -- Transkaryotic Therapies	GR 4991W93 -- GlaxoSmithKline
Gamma-interferon analogues -- SRC VB VECTOR	Granulocyte colony-stimulating factor -- Dong-A
Ganirelix -- Roche	Granulocyte colony-stimulating factor conjugate
gastric lipase -- Meristem	grass allergy therapy -- Dynavax
Gavilimomab --	GRF1-44 -- ICN
G-CSF -- Amgen, SRC VB VECTOR	Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo
GDF-1 -- CeNeS	growth factor peptides -- Biotherapeutics
GDF-5 -- Biopharm	growth hormone -- LG Chem
GDNF (glial derived neurotrophic factor) -- Amgen	growth hormone, Recombinant human -- Serono
gelsolin -- Biogen	GT 4086 -- Gliatech
Gemtuzumab ozogamicin -- Celltech	GW 353430 -- GlaxoSmithKline
Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies	GW-278884 -- GlaxoSmithKline
Glanzmann thrombasthenia gene therapy --	H 11 -- Viventia Biotech
Glatiramer acetate -- Yeda	H5N1 influenza A virus vaccine -- Protein Sciences
glial growth factor 2 -- CeNeS	haemoglobin -- Biopure
GLP-1 -- Amylin, Suntory, TheraTech, Watson	haemoglobin 3011, Recombinant -- Baxter Healthcare
GLP-1 peptide analogues -- Zealand Pharmaceuticals	haemoglobin crosfumaril -- Baxter Intl.
GLP-2 -- Novo Nordisk, Ontario, Inc., Suntory Limited	haemoglobin stabilized -- Ajinomoto
glucagon -- Eli Lilly, ZymoGenetics	haemoglobin, recombinant -- Apex
Glucagon-like peptide-1 7-36 amide -- Suntory	HAF -- Immune Response
Glucogen-like peptide -- Amylin	Hantavirus vaccine
	HB 19
	HBNF -- Regeneron
	HCC-1 -- Pharis

FIG. 28L

## 43/498

hCG -- Milkhaus	Herpes simplex glycoprotein DNA vaccine --
hCG vaccine -- Zonagen	Merck, Wyeth-Lederle Vaccines-Malvern,
HE-317 -- Hollis-Eden Pharmaceuticals	Genentech, GlaxoSmithKline, Chiron,
Heat shock protein cancer and influenza	Takeda
vaccines -- StressGen	Herpes simplex vaccine -- Cantab
Helicobacter pylori vaccine -- Acambis,	Pharmaceuticals, CEL-SCI, Henderson
AstraZeneca/CSL, Chiron, Provalis	Morley
Helistat-G -- GalaGen	Herpes simplex vaccine live -- ImClone
Hemolink -- Hemosol	Systems/Wyeth-Lederle, Aventis Pasteur
hepapoietin -- Snow Brand	HGF derivatives -- Dompe
heparanase -- InSight	hIAPP vaccine -- Crucell
heparinase I -- Ibex	Hib-hepatitis B vaccine -- Aventis Pasteur
heparinase III -- Ibex	HIC 1
Hepatitis A vaccine -- American Biogenetic	HIP-- Altachem
Sciences	Hirudins -- Biopharma, Cangene, Dongkook,
Hepatitis A vaccine inactivated	Japan Energy Corporation, Pharmacia
Hepatitis A vaccine Nothav -- Chiron	Corporation, SIR International, Sanofi-
Hepatitis A-hepatitis B vaccine --	Synthelabo, Sotragene, Rhein Biotech
GlaxoSmithKline	HIV edible vaccine -- ProdiGene
hepatitis B therapy -- Tripep	HIV gp120 vaccine -- Chiron, Ajinomoto,
Hepatitis B vaccine -- Amgen, Chiron SpA,	GlaxoSmithKline, ID Vaccine, Progenics,
Meiji Milk, NIS, Prodeva, PowderJect,	VaxGen
Rhein Biotech	HIV gp120 vaccine gene therapy --
Hepatitis B vaccine recombinant -- Evans	HIV gp160 DNA vaccine -- PowderJect,
Vaccines, Epitec Combiotech, Genentech,	Aventis Pasteur, Oncogen, Hyland
MedImmune, Merck Sharp & Dohme,	Immuno, Protein Sciences
Rhein Biotech, Shantha Biotechnics,	HIV gp41 vaccine -- Panacos
Vector, Yeda	HIV HGP-30W vaccine -- CEL-SCI
Hepatitis B vaccine recombinant TGP 943 --	HIV immune globulin -- Abbott, Chiron
Takeda	HIV peptides -- American Home Products
Hepatitis C vaccine -- Bavarian Nordic,	HIV vaccine -- Applied bioTech., Axis
Chiron, Innogenetics Acambis,	Genetics, Biogen, Bristol-Myers Squibb,
Hepatitis D vaccine -- Chiron Vaccines	Genentech, Korea Green Cross, NIS,
Hepatitis E vaccine recombinant --	Oncogen, Protein Sciences Corporation,
Genelabs/GlaxoSmithKline, Novavax	Terumo, Tonen Corporation, Wyeth-
hepatocyte growth factor -- Panorama,	Ayerst, Wyeth-Lederle Vaccines-Malvern,
Sosei	Advanced BioScience Laboratories,
hepatocyte growth factor kringle fragments -	Bavarian Nordic, Bavarian Nordic/Statens
- EntreMed	Serum Institute, GeneCure, Immune
Her-2/Neu peptides -- Corixa	Response, Progenics, Therion Biologics,
	United Biomedical, Chiron

## FIG. 28M

44/498

HIV vaccine vCP1433 -- Aventis Pasteur	Human monoclonal antibodies --
HIV vaccine vCP1452 -- Aventis Pasteur	Medarex/Northwest Biotherapeutics,
HIV vaccine vCP205 -- Aventis Pasteur	Medarex/Seattle Genetics
HL-9 -- American BioScience	human netrin-1 -- Exelixis
HM-9239 -- Cytran	human papillomavirus antibodies -- Epicyte
HML-103 -- Hemosol	Human papillomavirus vaccine -- Biotech
HML-104 -- Hemosol	Australia, IDEC, StressGen
HML-105 -- Hemosol	Human papillomavirus vaccine MEDI 501 --
HML-109 -- Hemosol	MedImmune/GlaxoSmithKline
HML-110 -- Hemosol	Human papillomavirus vaccine MEDI
HML-121 -- Hemosol	503/MEDI 504 --
hNLP -- Pharis	MedImmune/GlaxoSmithKline
Hookworm vaccine	Human papillomavirus vaccine TA-CIN --
host-vector vaccines -- Henogen	Cantab Pharmaceuticals
HPM 1 -- Chugai	Human papillomavirus vaccine TA-HPV --
HPV vaccine -- MediGene	Cantab Pharmaceuticals
HSA -- Meristem	Human papillomavirus vaccine TH-GW --
HSF -- StressGen	Cantab/GlaxoSmithKline
HSP carriers --Weizmann, Yeda, Peptor	human polyclonal antibodies -- Biosite/Eos
HSPPC-70 -- Antigenics	BioTech./ Medarex
HSPPC-96, pathogen-derived -- Antigenics	human type II anti factor VIII monoclonal
HSV 863 -- Novartis	antibodies -- ThromboGenics
HTLV-I DNA vaccine	humanised anti glycoprotein Ib murine
HTLV-I vaccine	monoclonal antibodies -- ThromboGenics
HTLV-II vaccine -- Access	HumaRAD -- Intracell
HU 901 -- Tanox	HuMax EGFR -- Genmab
Hu23F2G -- ICOS	HuMax-CD4 -- Medarex
HuHMFG1	HuMax-IL15 -- Genmab
HumaLYM -- Intracell	HYB 190 -- Hybridon
Human krebs statika -- Yamanouchi	HYB 676 -- Hybridon
human monoclonal antibodies --	I-125 MAb A33 -- Celltech
Abgenix/Biogen, Abgenix/ Corixa,	Ibritumomab tiuxetan -- IDEC
Abgenix/Immunex, Abgenix/Lexicon,	IBT-9401 -- Ibex
Abgenix/ Pfizer, Athersys/Medarex,	IBT-9402 -- Ibex
Biogen/MorphoSys, CAT/Searle,	IC 14 -- ICOS
Centocor/Medarex, Corixa/Kirin Brewery,	Idarubicin anti-Ly-2.1 --
Corixa/Medarex, Eos BioTech./Medarex,	IDEC 114 -- IDEC
Eos/Xenerex, Exelixis/Protein Design	IDEC 131 -- IDEC
Labs, ImmunoGen/ Raven, Medarex/	IDEC 152 -- IDEC
B.Twelve, MorphoSys/ImmunoGen, XTL	IDM 1 -- IDM
Biopharmaceuticals/Dyax,	IDPS -- Hollis-Eden Pharmaceuticals

**FIG. 28N**



## 45/498

iduronate-2-sulfatase -- Transkaryotic Therapies	insulin -- AutoImmune, Altea, Biobras, BioSante, Bio-Tech. General, Chong Kun Dang, Emisphere, Flamel, Provalis, Rhein Biotech, TranXenoGen
IGF/IBP-2-13 -- Pharis	insulin (bovine) -- Novartis
IGN-101 -- Igeneon	insulin analogue -- Eli Lilly
IK HIR02 -- Iketon	Insulin Aspart -- Novo Nordisk
IL-11 -- Genetics Institute/AHP	insulin detemir -- Novo Nordisk
IL-13-PE38 -- NeoPharm	insulin glargine -- Aventis
IL-17 receptor -- Immunex	insulin inhaled -- Inhale Therapeutics Systems, Alkermes
IL-18BP -- Yeda	insulin oral -- Inovax
IL-1Hy1 -- Hyseq	insulin, AeroDose -- AeroGen
IL-1 $\beta$ -- Celltech	insulin, AERx -- Aradigm
IL-1 $\beta$ adjuvant -- Celltech	insulin, BEODAS -- Elan
IL-2 -- Chiron	insulin, Biphax -- Helix
IL-2 + IL-12 -- Hoffman La-Roche	insulin, buccal -- GenereX
IL-6/sIL-6R fusion -- Hadasit	insulin, I2R -- Flemington
IL-6R derivative -- Tosoh	insulin, intranasal -- Bentley
IL-7-Dap 389 fusion toxin -- Ligand	insulin, oral -- Nobex, Unigene
IL-21 -- Novo Nordisk, ZymoGenetics	insulin, Orasome -- Endorex
IM-862 -- Cytran	insulin, ProMaxx -- Epic
IMC-1C11 -- ImClone	insulin, Quadrant -- Elan
imiglucerase -- Genzyme	insulin, recombinant -- Aventis
Immune globulin intravenous (human) -- Hoffman La Roche	insulin, Spiros -- Elan
immune privilege factor -- Proneuron	insulin, Transfersome -- IDEA
Immunocal -- Immunotec	insulin, Zymo, recombinant -- Novo Nordisk
Immunogene therapy -- Briana Bio-Tech	insulinotropin -- Scios
Immunoliposomal 5-fluorodeoxyuridine-dipalmitate --	Insulysin gene therapy --
immunosuppressant vaccine -- Aixlie	integrin antagonists -- Merck
immunotoxin -- Antisoma, NIH	interferon (Alpha2) -- SRC VB VECTOR, Viragen, Dong-A, Hoffman La-Roche, Genentech
ImmuRAIT-Re-188 -- Immunomedics	interferon -- BioMedicines, Human Genome Sciences
imreg-1 -- Imreg	interferon (Alfa-n3) -- Interferon Sciences Intl.
infertility -- Johnson & Johnson, E-TRANS	interferon (Alpha), Biphax -- Helix
Infliximab -- Centocor	
Influenza virus vaccine -- Aventis Pasteur, Protein Sciences	
inhibin -- Biotech Australia, Human Therapeutics	
Inhibitory G protein gene therapy	
INKP-2001 -- InKine	
Inolimomab -- Diaclone	

FIG. 280

46/498

interferon (Alpha)—Amgen, BioNative,	IL-2/ diphtheria toxin -- Ligand
Novartis, Genzyme Transgenics,	Interleukin-3 -- Cangene
Hayashibara, Inhale Therapeutics	Interleukin-4 -- Immunology Ventures,
Systems, Medusa, Flamel, Dong-A,	Sanofi Winthrop, Schering-Plough,
GeneTrol, Nastech, Shantha,	Immunex/ Sanofi Winthrop, Bayer, Ono
Wassermann, LG Chem, Sumitomo,	interleukin-4 + TNF-Alpha -- NIH
Aventis, Behring EGIS, Pepgen, Servier,	interleukin-4 agonist -- Bayer
Rhein Biotech,	interleukin-4 fusion toxin -- Ligand
interferon (Alpha2A)	Interleukin-4 receptor -- Immunex, Immun
interferon (Alpha2B) -- Enzon, Schering-	Interleukin-6 -- Ajinomoto, Cangene, Yeda,
Plough, Biogen, IDEA	Genetics Institute, Novartis
interferon (Alpha-N1) -- GlaxoSmithKline	interleukin-6 fusion protein
interferon (beta) -- Rentschler, GeneTrol,	interleukin-6 fusion toxin -- Ligand, Serono
Meristem, Rhein Biotech, Toray, Yeda,	interleukin-7 -- IC Innovations
Daiichi, Mochida	interleukin-7 receptor -- Immunex
interferon (Beta1A) -- Serono, Biogen	interleukin-8 antagonists -- Kyowa
interferon (beta1A),inhale -- Biogen	Hakko/Millennium/Pfizer
interferon (β1b)-- Chiron	interleukin-9 antagonists -- Genaera
interferon (tau)-- Pepgen	Interleukin-10 -- DNAX, Schering-Plough
Interferon alfacon-1 -- Amgen	Interleukin-10 gene therapy --
Interferon alpha-2a vaccine	interleukin-12 -- Genetics Institute, Hoffman
Interferon Beta 1b -- Schering/Chiron,	La-Roche
InterMune	interleukin-13 -- Sanofi
Interferon Gamma -- Boehringer Ingelheim,	interleukin-13 antagonists -- AMRAD
Sheffield, Rentschler, Hayashibara	Interleukin-13-PE38QQR
interferon receptor , Type I -- Serono	interleukin-15 -- Immunex
interferon(Gamma1B) -- Genentech	interleukin-16 -- Research Corp
Interferon-alpha-2b + ribavirin -- Biogen,	interleukin-18 -- GlaxoSmithKline
ICN	Interleukin-18 binding protein -- Serono
Interferon-alpha-2b gene therapy --	Ior-P3 -- Center of Molecular Immunology
Schering-Plough	IP-10 -- NIH
Interferon-con1 gene therapy --	IPF -- Metabolex
interleukin-1 antagonists -- Dompe	IR-501 -- Immune Response
Interleukin-1 receptor antagonist -- Abbott	ISIS 9125 -- Isis Pharmaceuticals
Bioresearch, Pharmacia	ISURF No. 1554 -- Millennium
Interleukin-1 receptor type I -- Immunex	ISURF No. 1866 -- Iowa State Univer.
interleukin-1 receptor Type II -- Immunex	ITF-1697 -- Italfarmaco
Interleukin-1 trap -- Regeneron	IxC 162 -- Ixion
Interleukin-1-alpha -- Immunex/Roche	J 695 -- Cambridge Antibody Tech.,
interleukin-2 -- SRC VB VECTOR,	Genetics Inst., Knoll
Ajinomoto, Biomira, Chiron	Jagged + FGF -- Repair

FIG. 28P

## 47/498

JKC-362 -- Phoenix Pharmaceuticals	leptin, 2nd-generation -- Amgen
JTP-2942 -- Japan Tobacco	leridistim -- Pharmacia
Juman monoclonal antibodies -- Medarex/Raven	leuprolide, ProMaxx -- Epic
K02 -- Axys Pharmaceuticals	leuprorelin, oral -- Unigene
Keliximab -- IDEC	LeuTech -- Papatin
Keyhole limpet haemocyanin	LEX 032 -- SuperGen
KGF -- Amgen	LiDEPT -- Novartis
KM 871 -- Kyowa	Lintuzumab (anti-CD33 MAb) -- Protein Design Labs
KPI 135 -- Scios	lipase -- Altus Biologics
KPI-022 -- Scios	lipid A vaccine -- EntreMed
Kringle 5	lipid-linked anchor Tech. -- ICRT, ID Biomedical
KSB 304	liposome-CD4 Tech. -- Sheffield
KSB-201 -- KS Biomedix	Listeria monocytogenes vaccine
L 696418 -- Merck	LMB 1
L 703801 -- Merck	LMB 7
L1 -- Acorda	LMB 9 -- Battelle Memorial Institute, NIH
L-761191 -- Merck	LM-CD45 -- Cantab Pharmaceuticals
lactoferrin -- Meristem, Pharming, Agennix	lovastatin -- Merck
lactoferrin cardio -- Pharming	LSA-3
LAG-3 -- Serono	LT- $\beta$ receptor -- Biogen
LAIT -- GEMMA	lung cancer vaccine -- Corixa
LAK cell cytotoxin -- Arizona	lusupultide -- Scios
lamellarins -- PharmaMar/University of Malaga	L-Vax -- AVAX
laminin A peptides -- NIH	LY 355455 -- Eli Lilly
lanotepase -- Genetics Institute	LY 366405 -- Eli Lilly
laronidase -- BioMarin	LY-355101 -- Eli Lilly
Lassa fever vaccine	Lyme disease DNA vaccine -- Vical/Aventis Pasteur
LCAT -- NIH	Lyme disease vaccine -- Aquila
LDP 01 -- Millennium	Biopharmaceuticals, Aventis, Pasteur, Symbicom, GlaxoSmithKline, Hyland
LDP 02 -- Millennium	Immuno, MedImmune
Lecithinized superoxide dismutase -- Seikagaku	Lymphocytic choriomeningitis virus vaccine
LeIF adjuvant -- Corixa	lymphoma vaccine -- Biomira, Genitope
leishmaniasis vaccine -- Corixa	LYP18
lenercept -- Hoffman La-Roche	lys plasminogen, recombinant
Lenograstim -- Aventis, Chugai	Lysosomal storage disease gene therapy -- Avigen
lepirudin -- Aventis	lysostaphin -- Nutrition 21
leptin -- Amgen, IC Innovations	
Leptin gene therapy -- Chiron Corporation	

FIG. 28Q

48/498

M 23 -- Gruenenthal	MEDI 507 -- BioTransplant
M1 monoclonal antibodies -- Acorda	melanin concentrating hormone --
Therapeutics	Neurocrine Biosciences
MA 16N7C2 -- Corvas Intl.	melanocortins -- OMRF
malaria vaccine -- GlaxoSmithKline,	Melanoma monoclonal antibodies -- Viragen
AdProTech, Antigenics, Apovia, Aventis	melanoma vaccine -- GlaxoSmithKline,
Pasteur, Axis Genetics, Behringwerke,	Akzo Nobel, Avant, Aventis Pasteur,
CDCP, Chiron Vaccines, Genzyme	Bavarian Nordic, Biovector, CancerVax,
Transgenics, Hawaii, MedImmune, NIH,	Genzyme Molecular Oncology, Humbolt,
NYU, Oxxon, Roche/Saramane, Biotech	ImClone Systems, Memorial, NYU, Oxxon
Australia, Rx Tech	Melanoma vaccine Magevac -- Therion
Malaria vaccine CDC/NIIMALVAC-1	memory enhancers -- Scios
malaria vaccine, multicomponent	meningococcal B vaccine -- Chiron
mammaglobin -- Corixa	meningococcal vaccine -- CAMR
mammastatin -- Biotherapeutics	Meningococcal vaccine group B conjugate -
mannan-binding lectin -- NatlImmu	- North American Vaccine
mannan-MUC1 -- Psiron	Meningococcal vaccine group B
MAP 30	recombinant -- BioChem Vaccines,
Marinovir -- Phytera	Microscience
MARstem -- Maret	Meningococcal vaccine group Y conjugate -
MB-015 -- Mochida	- North American Vaccine
MBP -- ImmuLogic	Meningococcal vaccine groups A B and C
MCI-028 -- Mitsubishi-Tokyo	conjugate -- North American Vaccine
MCIF -- Human Genome Sciences	Mepolizumab -- GlaxoSmithKline
MDC -- Advanced BioScience -- Akzo	Metastatin -- EntreMed, Takeda
Nobel, ICOS	Met-CkB7 -- Human Genome Sciences
MDX 11 -- Medarex	met-enkephalin -- TNI
MDX 210 -- Medarex	METH-1 -- Human Genome Sciences
MDX 22 -- Medarex	methioninase -- AntiCancer
MDX 22	Methionine lyase gene therapy --
MDX 240 -- Medarex	AntiCancer
MDX 33	Met-RANTES -- Genexa Biomedical,
MDX 44 -- Medarex	Serono
MDX 447 -- Medarex	Metreleptin
MDX H210 -- Medarex	Microtubule inhibitor MAb
MDX RA -- Houston BioTech., Medarex	Immunogen/Abgenix
ME-104 -- Pharmexa	MGDF -- Kirin
Measles vaccine	MGV -- Progenics
Mecasermin -- Cephalon/Chiron, Chiron	micrin -- Endocrine
MEDI 488 -- MedImmune	microplasmin -- ThromboGenics
MEDI 500	MIF -- Genetics Institute

FIG. 28R

## 49/498

migration inhibitory factor -- NIH	MAB 45-2D9- -- haematoporphyrin conjugate
Mim CD4.1 -- Xyte Therapies	MAB 4B4
mirostipen -- Human Genome Sciences	MAB 4E3-CPA conjugate -- BCM Oncologia
Mitumomab (BEC-2) -- ImClone Systems, Merck KGaA	MAB 4E3-daunorubicin conjugate
MK 852 -- Merck	MAB 50-6
MLN 1202 (Anti-CCR2 monoclonal antibody) -- Millenium Pharmaceuticals	MAB 50-61A -- Institut Pasteur
Mobenakin -- NIS	MAB 5A8 -- Biogen
molgramostim -- Genetics Institute, Novartis	MAB 791T/36-methotrexate conjugate
monoclonal antibodies -- Abgenix/Celltech, Immusol/ Medarex, Viragen/ Roslin Institute, Cambridge Antibody Tech./Elan	MAB 7c11.e8
MAB 108 --	MAB 7E11 C5-selenocystamine conjugate
MAB 10D5 --	MAB 93KA9 -- Novartis
MAB 14.18-interleukin-2 immunocytokine -- Lexigen	MAB A5B7-cisplatin conjugate -- Biodynamics Research, Pharmacia
MAB 14G2a --	MAB A5B7-I-131
MAB 15A10 --	MAB A7
MAB 170 -- Biomira	MAB A717 -- Exocell
MAB 177Lu CC49 --	MAB A7-zinostatin conjugate
MAB 17F9	MAB ABX-RB2 -- Abgenix
MAB 1D7	MAB ACA 11
MAB 1F7 -- Immune Network	MAB AFP-I-131 -- Immunomedics
MAB 1H10-doxorubicin conjugate	MAB AP1
MAB 26-2F	MAB AZ1
MAB 2A11	MAB B3-LysPE40 conjugate
MAB 2E1 -- RW Johnson	MAB B4 -- United Biomedical
MAB 2F5	MAB B43 Genistein-conjugate
MAB 31.1 -- International BioImmune Systems	MAB B43.13-Tc-99m -- Biomira
MAB 32 -- Cambridge Antibody Tech., Peptech	MAB B43-PAP conjugate
MAB 323A3 -- Centocor	MAB B4G7-gelonin conjugate
MAB 3C5	MAB BCM 43-daunorubicin conjugate -- BCM Oncologia
MAB 3F12	MAB BIS-1
MAB 3F8	MAB BMS 181170 -- Bristol-Myers Squibb
MAB 42/6	MAB BR55-2
MAB 425 -- Merck KGaA	MAB BW494
MAB 447-52D -- Merck Sharp & Dohme	MAB C 242-DM1 conjugate -- ImmunoGen
	MAB C242-PE conjugate
	MAB c30-6
	MAB CA208-cytorhodin-S conjugate -- Hoechst Japan
	MAB CC49 -- Enzon

FIG. 28S

## 50/498

MAB ch14.18 --	MAB LL2-I-131 -- Immunomedics
MAB CH14.18-GM-CSF fusion protein --	MAB LL2-Y-90
Lexigen	MAB LS2D617 -- Hybritech
MAB chCE7	MAB LYM-1-gelonin conjugate
MAB CI-137 -- AMRAD	MAB LYM-1-I-131
MAB cisplatin conjugate	MAB LYM-1-Y-90
MAB CLB-CD19	MAB LYM-2 -- Peregrine
MAB CLB-CD19v	MAB M195
MAB CLL-1 -- Peregrine	MAB M195-bismuth 213 conjugate --
MAB CLL-1-GM-CSF conjugate	Protein Design Labs
MAB CLL-1-IL-2 conjugate -- Peregrine	MAB M195-gelonin conjugate
MAB CLN IgG -- doxorubicin conjugates	MAB M195-I-131
MAB conjugates -- Tanox	MAB M195-Y-90
MAB D612	MAB MA 33H1 -- Sanofi
MAB Dal B02	MAB MAD11
MAB DC101 -- ImClone	MAB MGB2
MAB EA 1 --	MAB MINT5
MAB EC708 -- Biovation	MAB MK2-23
MAB EP-5C7 -- Protein Design Labs	MAB MOC31 ETA(252-613) conjugate
MAB ERIC-1 -- ICRT	MAB MOC-31-In-111
MAB F105 gene therapy	MAB MOC-31-PE conjugate
MAB FC 2.15	MAB MR6 --
MAB G250 -- Centocor	MAB MRK-16 -- Aventis Pasteur
MAB GA6	MAB MS11G6
MAB GA733	MAB MX-DTPA BrE-3
MAB Gliomab-H -- Viventia Biotech	MAB MY9
MAB HB2-saporin conjugate	MAB Nd2 -- Tosoh
MAB HD 37 --	MAB NG-1 -- Hygeia
MAB HD37-ricin chain-A conjugate	MAB NM01 -- Nissin Food
MAB HNK20 -- Acambis	MAB OC 125
MAB huN901-DM1 conjugate --	MAB OC 125-CMA conjugate
ImmunoGen	MAB OKI-1 -- Ortho-McNeil
MAB I-131 CC49 -- Corixa	MAB OX52 -- Bioproducts for Science
MAB ICO25	MAB PMA5
MAB ICR12-CPG2 conjugate	MAB PR1
MAB ICR-62	MAB prost 30
MAB IRac-ricin A conjugate	MAB R-24
MAB K1	MAB R-24 $\alpha$ Human GD3 -- Celltech
MAB KS1-4-methotrexate conjugate	MAB RFB4-ricin chain A conjugate
MAB L6 -- Bristol-Myers Squibb, Oncogen	MAB RFT5-ricin chain A conjugate
MAB LiCO 16-88	MAB SC 1

FIG. 28T

## 51/498

MAb SM-3 -- ICRT	Muc-1 vaccine -- Corixa
MAb SMART 1D10 -- Protein Design Labs	mucosal tolerance -- Aberdeen
MAb SMART ABL 364 -- Novartis	mullerian inhibiting subst
MAb SN6f	muplestim -- Genetics Institute, Novartis,
MAb SN6f-deglycosylated ricin A chain	DSM Anti-Infectives
conjugate --	murine MAb -- KS Biomedix
MAb SN6j	Mutant somatropin -- JCR Pharmaceutical
MAb SN7-ricin chain A conjugate	MV 833 -- Toagosei
MAb T101-Y-90 conjugate -- Hybritech	Mycoplasma pulmonis vaccine
MAb T-88 -- Chiron	Mycoprex -- XOMA
MAb TB94 -- Cancer ImmunoBiology	myeloperoxidase -- Henogen
MAb TEC 11	myostatin -- Genetics Institute
MAb TES-23 -- Chugai	Nacolomab tafenatox -- Pharmacia
MAb TM31 -- Avant	Nagrecor -- Scios
MAb TNT-1 -- Cambridge Antibody Tech.,	nagrestipen -- British Biotech
Peregrine	NAP-5 -- Corvas Intl.
MAb TNT-3	NAPc2 -- Corvas Intl.
MAb TNT-3 -- IL2 fusion protein --	nartograstim -- Kyowa
MAb TP3-A $\alpha$ -211	Natalizumab -- Protein Design Labs
MAb TP3-PAP conjugate --	Nateplase -- NIH, Nihon Schering
MAb UJ13A -- ICRT	nateplase -- Schering AG
MAb UN3	NBI-3001 -- Neurocrine Biosci.
MAb ZME-018-gelonin conjugate	NBI-5788 -- Neurocrine Biosci.
MAb-BC2 -- GlaxoSmithKline	NBI-6024 -- Neurocrine Biosci.
MAb-DM1 conjugate -- ImmunoGen	Nef inhibitors -- BRI
MAb-ricin-chain-A conjugate -- XOMA	Neisseria gonorrhoea vaccine -- Antex
MAb-temoporfin conjugates	Biologics
Monopharm C -- Viventia Biotech	Neomycin B-arginine conjugate
monteplase -- Eisai	Nerelimomab -- Chiron
montirelin hydrate -- Gruenenthal	Nerve growth factor -- Amgen -- Chiron,
moroctocog alfa -- Genetics Institute	Genentech
Moroctocog-alfa -- Pharmacia	Nerve growth factor gene therapy
MP 4	nesiritide citrate -- Scios
MP-121 -- Biopharm	neuregulin-2 -- CeNeS
MP-52 -- Biopharm	neurocan -- NYU
MRA -- Chugai	neuronal delivery system -- CAMR
MS 28168 -- Mitsui Chemicals, Nihon	Neurophil inhibitory Factor -- Corvas
Schering	Neuroprotective vaccine -- University of
MSH fusion toxin -- Ligand	Auckland
MSI-99 -- Genaera	neurotrophic chimaeras -- Regeneron
MT 201 -- Micromet	neurotrophic factor -- NsGene, CereMedix

FIG. 28U

## 52/498

NeuroVax -- Immune Response	Oncophage -- Antigenics
neurturin -- Genentech	Oncostatin M -- Bristol-Myers Squibb
neutral endopeptidase -- Genentech	OncoVax-CL -- Jenner Biotherapies
NGF enhancers -- NeuroSearch	OncoVax-P -- Jenner Biotherapies
NHL vaccine -- Large Scale Biology	onercept -- Yeda
NIP45 -- Boston Life Sciences	onychomycosis vaccine -- Boehringer
NKI-B20	Ingelheim
NM 01 -- Nissin Food	opebecan -- XOMA
NMI-139 -- NitroMed	opioids -- Arizona
NMMP -- Genetics Institute	Oprelvekin -- Genetics Institute
NN-2211 -- Novo Nordisk	Oregovomab -- AltaRex
Noggin -- Regeneron	Org-33408 b-- Akzo Nobel
Nonacog alfa	Orolip DP -- EpiCept
Norelin -- Biostar	oryzacystatin
Norwalk virus vaccine	OSA peptides -- GenSci Regeneration
NRLU 10 -- NeoRx	osteoblast-cadherin GF -- Pharis
NRLU 10 PE -- NeoRx	Osteocalcin-thymidine kinase gene therapy
NT-3 -- Regeneron	osteogenic protein -- Curis
NT-4/5 -- Genentech	osteopontin -- OraPharma
NU 3056	osteoporosis peptides -- Integra, Telios
NU 3076	osteoprotegerin -- Amgen, SnowBrand
NX 1838 -- Gilead Sciences	otitis media vaccines -- Antex Biologics
NY ESO-1/CAG-3 antigen -- NIH	ovarian cancer -- University of Alabama
NYVAC-7 -- Aventis Pasteur	OX40-IgG fusion protein -- Cantab, Xenova
NZ-1002 -- Novazyme	P 246 -- Diatide
obesity therapy -- Nobex	P 30 -- Alfacell
OC 10426 -- Ontogen	p1025 -- Active Biotech
OC 144093 -- Ontogen	P-113 <sup>^</sup> -- Demegen
OCIF -- Sankyo	P-16 peptide -- Transition Therapeutics
Oct-43 -- Otsuka	p43 -- Ramot
Odulimomab -- Immunotech	P-50 peptide -- Transition Therapeutics
OK PSA - liposomal	p53 + RAS vaccine -- NIH, NCI
OKT3-gamma-1-ala-ala	PACAP(1-27) analogue
OM 991	paediatric vaccines -- Chiron
OM 992	Pafase -- ICOS
Omalizumab -- Genentech	PAGE-4 plasmid DNA -- IDEC
oncoimmunin-L -- NIH	PAI-2 -- Biotech Australia, Human
Oncolysin B -- ImmunoGen	Therapeutics
Oncolysin CD6 -- ImmunoGen	Palifermin (keratinocyte growth factor) --
Oncolysin M -- ImmunoGen	Amgen
Oncolysin S -- ImmunoGen	Palivizumab -- MedImmune

FIG. 28V



## 53/498

PAM 4 -- Merck	PEG-uricase -- Mountain View
pamiteplase -- Yamanouchi	Pegvisomant -- Genentech
pancreatin, Minitabs -- Eurand	PEGylated proteins, PolyMASC -- Valentis
Pangen -- Fournier	PEGylated recombinant native human leptin
Pantarin -- Selective Genetics	-- Roche
Parainfluenza virus vaccine -- Pharmacia,	Pemtumomab
Pierre Fabre	Penetratin -- Cyclacel
paraoxanase -- Esperion	Pepscan -- Antisoma
parathyroid hormone -- Abiogen, Korea	peptide G -- Peptech, ICRT
Green Cross	peptide vaccine -- NIH, NCI
Parathyroid hormone (1-34) --	Pexelizumab
Chugai/Suntory	pexiganan acetate -- Genaera
Parkinson's disease gene therapy -- Cell	Pharmaprojects No. 3179 -- NYU
Genesys/ Ceregene	Pharmaprojects No. 3390 -- Ernest Orlando
Parvovirus vaccine -- MedImmune	Pharmaprojects No. 3417 -- Sumitomo
PCP-Scan -- Immunomedics	Pharmaprojects No. 3777 -- Acambis
PDGF -- Chiron	Pharmaprojects No. 4209 -- XOMA
PDGF cocktail -- Theratechnologies	Pharmaprojects No. 4349 -- Baxter Intl.
peanut allergy therapy -- Dynavax	Pharmaprojects No. 4651
PEG anti-ICAM MAb -- Boehringer	Pharmaprojects No. 4915 -- Avanir
Ingelheim	Pharmaprojects No. 5156 -- Rhizogenics
PEG asparaginase -- Enzon	Pharmaprojects No. 5200 -- Pfizer
PEG glucocerebrosidase	Pharmaprojects No. 5215 -- Origene
PEG hirudin -- Knoll	Pharmaprojects No. 5216 -- Origene
PEG interferon-alpha-2a -- Roche	Pharmaprojects No. 5218 -- Origene
PEG interferon-alpha-2b + ribavirin --	Pharmaprojects No. 5267 -- ML
Biogen, Enzon, ICN Pharmaceuticals,	Laboratories
Schering-Plough	Pharmaprojects No. 5373 -- MorphoSys
PEG MAb A5B7 --	Pharmaprojects No. 5493 -- Metabolex
Pegacaristim -- Amgen -- Kirin Brewery --	Pharmaprojects No. 5707 -- Genentech
ZymoGenetics	Pharmaprojects No. 5728 -- Autogen
Pegaldesleukin -- Research Corp	Pharmaprojects No. 5733 -- BioMarin
pegaspargase -- Enzon	Pharmaprojects No. 5757 -- NIH
pegfilgrastim -- Amgen	Pharmaprojects No. 5765 -- Gryphon
PEG-interferon Alpha -- Viragen	Pharmaprojects No. 5830 -- AntiCancer
PEG-interferon Alpha 2A -- Hoffman La-	Pharmaprojects No. 5839 -- Dyax
Roche	Pharmaprojects No. 5849 -- Johnson &
PEG-interferon Alpha 2B -- Schering-	Johnson
Plough	Pharmaprojects No. 5860 -- Mitsubishi-
PEG-r-hirudin -- Abbott	Tokyo
PEG-rHuMGDF -- Amgen	

FIG. 28W

## 54/498

Pharmaprojects No. 5869 -- Oxford GlycoSciences	Plasminogen activators -- Abbott Laboratories, American Home Products, Boehringer Mannheim, Chiron
Pharmaprojects No. 5883 -- Asahi Brewery	Corporation, DuPont Pharmaceuticals, Eli Lilly, Shionogi, Genentech, Genetics Institute, GlaxoSmithKline, Hemispherx Biopharma, Merck & Co, Novartis, Pharmacia Corporation, Wakamoto, Yeda
Pharmaprojects No. 5947 -- StressGen	plasminogen-related peptides -- Bio-Tech. General/MGH
Pharmaprojects No. 5961 -- Theratechnologies	platelet factor 4 -- RepliGen
Pharmaprojects No. 5962 -- NIH	Platelet-derived growth factor -- Amgen -- ZymoGenetics
Pharmaprojects No. 5966 -- NIH	plusonemin-- Hayashibara
Pharmaprojects No. 5994 -- Pharming	PMD-2850 -- Protherics
Pharmaprojects No. 5995 -- Pharming	Pneumococcal vaccine -- Antex Biologics, Aventis Pasteur
Pharmaprojects No. 6023 -- IMMUCON	Pneumococcal vaccine intranasal -- BioChem Vaccines/Biovector
Pharmaprojects No. 6063 -- Cytoclonal	PR1A3
Pharmaprojects No. 6073 -- SIDDCO	PR-39
Pharmaprojects No. 6115 -- Genzyme	pralmorelin -- Kaken
Pharmaprojects No. 6227 -- NIH	Pretarget-Lymphoma -- NeoRx
Pharmaprojects No. 6230 -- NIH	Priliximab -- Centocor
Pharmaprojects No. 6236 -- NIH	PRO 140 -- Progenics
Pharmaprojects No. 6243 -- NIH	PRO 2000 -- Procept
Pharmaprojects No. 6244 -- NIH	PRO 367 -- Progenics
Pharmaprojects No. 6281 -- Senetek	PRO 542 -- Progenics
Pharmaprojects No. 6365 -- NIH	pro-Apo A-I -- Esperion
Pharmaprojects No. 6368 -- NIH	prolactin -- Genzyme
Pharmaprojects No. 6373 -- NIH	Prosaptide TX14(A) -- Bio-Tech. General
Pharmaprojects No. 6408 -- Pan Pacific	prostate cancer antibodies -- Immunex, UroCor
Pharmaprojects No. 6410 -- Athersys	prostate cancer antibody therapy -- Genentech/UroGenesys, Genotherapeutics
Pharmaprojects No. 6421 -- Oxford GlycoSciences	prostate cancer immunotherapeutics -- The PSMA Development Company
Pharmaprojects No. 6522 -- Maxygen	prostate cancer vaccine -- Aventis Pasteur, Zonagen, Corixa, Dendreon, Jenner
Pharmaprojects No. 6523 -- Pharis	Biotherapies, Therion Biologics
Pharmaprojects No. 6538 -- Maxygen	
Pharmaprojects No. 6554 -- APALEXO	
Pharmaprojects No. 6560 -- Ardana	
Pharmaprojects No. 6562 -- Bayer	
Pharmaprojects No. 6569 -- Eos	
Phenoxazine	
Phenylase -- Ibex	
Pigment epithelium derived factor -- plasminogen activator inhibitor-1, recombinant -- DuPont Pharmaceuticals	

FIG. 28X

## 55/498

prostate-specific antigen -- EntreMed	RD 62198
protein A -- RepliGen	rDnase -- Genentech
protein adhesives -- Enzon	RDP-58 -- SangStat
protein C -- Baxter Intl., PPL Therapeutics,	RecepTox-Fce -- Keryx
ZymoGenetics	RecepTox-GnRH -- Keryx, MTR
protein C activator -- Gilead Sciences	Technologies
protein kinase R antags -- NIH	RecepTox-MBP -- Keryx, MTR
protirelin -- Takeda	Technologies
protocadherin 2 -- Caprion	recFSH -- Akzo Nobel, Organon
Pro-urokinase -- Abbott, Bristol-Myers	REGA 3G12
Squibb, Dainippon, Tosoh -- Welfide	Regavirumab -- Teijin
P-selectin glycoprotein ligand-1 -- Genetics	relaxin -- Connetics Corp
Institute	Renal cancer vaccine -- Macropharm
pseudomonal infections -- InterMune	repifermin -- Human Genome Sciences
Pseudomonas vaccine -- Cytovax	Respiratory syncytial virus PFP-2 vaccine --
PSGL-Ig -- American Home Products	Wyeth-Lederle
PSP-94 -- Procyon	Respiratory syncytial virus vaccine --
PTH 1-34 -- Nobex	GlaxoSmithKline, Pharmacia, Pierre Fabre
Quilimmune-M -- Antigenics	Respiratory syncytial virus vaccine
R 744 -- Roche	inactivated
R 101933	Respiratory syncytial virus-parainfluenza
R 125224 -- Sankyo	virus vaccine -- Aventis Pasteur,
RA therapy -- Cardion	Pharmacia
Rabies vaccine recombinant -- Aventis	Retepase -- Boehringer Mannheim,
Pasteur, BioChem Vaccines, Kaketsuken	Hoffman La-Roche
Pharmaceuticals	Retropep -- Retroscreen
RadioTheraCIM -- YM BioSciences	RFB4 (dsFv) PE38
Ramot project No. 1315 -- Ramot	RFI 641 -- American Home Products
Ramot project No. K-734A -- Ramot	RFTS -- UAB Research Foundation
Ramot project No. K-734B -- Ramot	RG 12986 -- Aventis Pasteur
Ranibizumab (Anti-VEGF fragment) --	RG 83852 -- Aventis Pasteur
Genentech	RG-1059 -- RepliGen
RANK -- Immunex	rGCR -- NIH
ranpirnase -- Alfacell	rGLP-1 -- Restoragen
ranpirnase-anti-CD22 MAb -- Alfacell	rGRF -- Restoragen
RANTES inhibitor -- Milan	rh Insulin -- Eli Lilly
RAPID drug delivery systems -- ARIAD	RHAMM targeting peptides -- Cangene
rasburicase -- Sanofi	rHb1.1 -- Baxter Intl.
rBPI-21, topical -- XOMA	rhCC10 -- Claragen
RC 529 -- Corixa	rhCG -- Serono
rCFTR -- Genzyme Transgenics	Rheumatoid arthritis gene therapy

FIG. 28Y

## 56/498

Rheumatoid arthritis vaccine -- Veterans Affairs Medical Center	SB RA 31012 --
rhLH -- Serono	SC 56929 -- Pharmacia
Ribozyme gene therapy -- Genset	SCA binding proteins -- Curis, Enzon
Rickettsial vaccine recombinant	scFv(14E1)-ETA Berlex Laboratories, Schering AG
RIGScan CR -- Neoprobe	ScFv(FRP5)-ETA --
RIP-3 -- Rigel	ScFv6C6-PE40 --
Rituximab -- Genentech	SCH 55700 -- Celltech
RK-0202 -- RxKinetix	Schistosomiasis vaccine -- Glaxo Wellcome/Medeva, Brazil
RLT peptide -- Esperion	SCPF -- Advanced Tissue Sciences
rM/NEI -- IVAX	scuPA-suPAR complex -- Hadasit
rmCRP -- Immtech	SD-9427 -- Pharmacia
RN-1001 -- Renovo	SDF-1 -- Ono
RN-3 -- Renovo	SDZ 215918 -- Novartis
RNAse conjugate -- Immunomedics	SDZ 280125 -- Novartis
RO 631908 -- Roche	SDZ 89104 -- Novartis
Rotavirus vaccine -- Merck	SDZ ABL 364 -- Novartis
RP 431 -- DuPont Pharmaceuticals	SDZ MMA 383 -- Novartis
RP-128 -- Resolution	Secretin -- Ferring, Repligen
RPE65 gene therapy --	serine protease inhbs -- Pharis
RPR 110173 -- Aventis Pasteur	sermorelin acetate -- Serono
RPR 115135 -- Aventis Pasteur	SERP-1 -- Viron
RPR 116258A -- Aventis Pasteur	sertenef -- Dainippon
rPSGL-Ig -- American Home Products	serum albumin, Recombinant human -- Aventis Behring
r-SPC surfactant -- Byk Gulden	serum-derived factor -- Hadasit
RSV antibody -- Medimmune	Sevirumab -- Novartis
Ruplizumab -- Biogen	SGN 14 -- Seattle Genetics
rV-HER-2/neu -- Therion Biologics	SGN 15 -- Seattle Genetics
SA 1042 -- Sankyo	SGN 17/19 -- Seattle Genetics
sacrosidase -- Orphan Medical	SGN 30 -- Seattle Genetics
Sant 7	SGN-10 -- Seattle Genetics
Sargramostim -- Immunex	SGN-11 -- Seattle Genetics
saruplase -- Gruenenthal	SH 306 -- DuPont Pharmaceuticals
Satumomab -- Cytogen	Shanvac-B -- Shantha
SB 1 -- COR Therapeutics	Shigella flexneri vaccine -- Avant, Acambis, Novavax
SB 207448 -- GlaxoSmithKline	Shigella sonnei vaccine --
SB 208651 -- GlaxoSmithKline	sICAM-1 -- Boehringer Ingelheim
SB 240683 -- GlaxoSmithKline	Silteplase -- Genzyme
SB 249415 -- GlaxoSmithKline	
SB 249417 -- GlaxoSmithKline	
SB 6 -- COR Therapeutics	

FIG. 28Z

## 57/498

SIV vaccine -- Endocon, Institut Pasteur	Staphylococcus aureus vaccine conjugate --
SK 896 -- Sanwa Kagaku Kenkyusho	Nabi
SK-827 -- Sanwa Kagaku Kenkyusho	Staphylococcus therapy -- Tripep
Skeletex -- CellFactors	Staphylokinase -- Biovation, Prothera,
SKF 106160 -- GlaxoSmithKline	Thrombogenetics
S-nitroso-AR545C --	Streptococcal A vaccine -- M6
SNTP -- Active Biotech	Pharmaceuticals, North American Vaccine
somatomedin-1 -- GroPep, Mitsubishi-	Streptococcal B vaccine -- Microscience
Tokyo, NIH	Streptococcal B vaccine recombinant --
somatomedin-1 carrier protein -- Insmed	Biochem Vaccines
somatostatin -- Ferring	Streptococcus pyogenes vaccine
Somatotropin/	STRL-33 -- NIH
Human Growth Hormone -- Bio-Tech.	Subalin -- SRC VB VECTOR
General, Eli Lilly	SUIS -- United Biomedical
somatropin -- Bio-Tech. General, Alkermes,	SUIS-LHRH -- United Biomedical
ProLease, Aventis Behring, Biovector,	SUN-E3001 -- Suntory
Cangene, Dong-A, Eli Lilly, Emisphere,	super high affinity monoclonal antibodies --
Enact, Genentech, Genzyme Transgenics,	YM BioSciences
Grandis/InfiMed, CSL, InfiMed, MacroMed,	Superoxide dismutase -- Chiron, Enzon,
Novartis, Novo Nordisk, Pharmacia	Ube Industries, Bio-Tech, Yeda
Serono, TranXenoGen	superoxide dismutase-2 -- OXIS
somatropin derivative -- Schering AG	suppressin -- UAB Research Foundation
somatropin, AIR -- Eli Lilly	SY-161-P5 -- ThromboGenics
Somatropin, inhaled -- Eli Lilly/Alkermes	SY-162 -- ThromboGenics
somatropin, Kabi -- Pharmacia	Systemic lupus erythematosus vaccine --
somatropin, Orasome -- Novo Nordisk	MedClone/VivoRx
Sonermin -- Dainippon Pharmaceutical	T cell receptor peptides -- Xoma
SP(V5.2)C -- Supertek	T cell receptor peptide vaccine
SPf66	T4N5 liposomes -- AGI Dermatics
sphingomyelinase -- Genzyme	TACI, soluble -- ZymoGenetics
SR 29001 -- Sanofi	targeted apoptosis -- Antisoma
SR 41476 -- Sanofi	tasonermin -- Boehringer Ingelheim
SR-29001 -- Sanofi	TASP
SS1(dsFV)-PE38 -- NeoPharm	TASP-V
$\beta$ 2 microglobulin -- Avidex	Tat peptide analogues -- NIH
$\beta$ 2-microglobulin fusion proteins -- NIH	TBP I -- Yeda
$\beta$ -amyloid peptides -- CeNeS	TBP II
$\beta$ -defensin -- Pharis	TBV25H -- NIH
Staphylococcus aureus infections --	Tc 99m ior cea1 -- Center of Molecular
Inhibitex/ZLB	Immunology
	Tc 99m P 748 -- Diatide

FIG. 28AA

## 58/498

Tc 99m votumumab -- Intracell	Tissue factor -- Genentech
Tc-99m rh-Annexin V -- Theseus Imaging	Tissue factor pathway inhibitor
teceleukin -- Biogen	TJN-135 -- Tsumura
tenecteplase -- Genentech	TM 27 -- Avant
Teriparatide -- Armour Pharmaceuticals, Asahi Kasei, Eli Lilly	TM 29 -- Avant
terlipressin -- Ferring	TMC-151 -- Tanabe Seiyaku
testisin -- AMRAD	TNF tumour necrosis factor -- Asahi Kasei
Tetrafibricin -- Roche	TNF Alpha -- Cytimmune
TFPI -- EntreMed	TNF antibody -- Johnson & Johnson
tgD-IL-2 -- Takeda	TNF binding protein -- Amgen
TGF-Alpha -- ZymoGenetics	TNF degradation product -- Oncotech
TGF- $\beta$ -- Kolon	TNF receptor -- Immunex
TGF- $\beta$ 2 -- Insmad	TNF receptor 1, soluble -- Amgen
TGF- $\beta$ 3 -- OSI	TNF Tumour necrosis factor-alpha -- Asahi Kasei, Genetech, Mochida
Thalassaemia gene therapy -- Crucell	TNF-Alpha inhibitor -- Tripep
TheraCIM-h-R3 -- Center of Molecular Immunology, YM BioSciences	TNFR:Fc gene therapy -- Targeted Genetics
Theradigm-HBV -- Epimmune	TNF-SAM2
Theradigm-HPV -- Epimmune	Tolerimab -- Innogenetics
Theradigm-malaria -- Epimmune	Toxoplasma gondii vaccine -- GlaxoSmithKline
Theradigm-melanoma -- Epimmune	TP 9201 -- Telios
TheraFab -- Antisoma	TP10 -- Avant
ThGRF 1-29 -- Theratechnologies	TP20 -- Avant
ThGRF 1-44 -- Theratechnologies	tPA -- Centocor
Thrombin receptor activating peptide -- Abbott	trafermin -- Scios
thrombomodulin -- Iowa, Novocastra	TRAIL/Apo2L -- Immunex
Thrombopoietin -- Dragon Pharmaceuticals, Genentech	TRAIL-R1 MAb -- Cambridge Antibody Technologies
thrombopoietin, Pliva -- Recepton	transferrin-binding proteins -- CAMR
Thrombospondin 2 --	Transforming growth factor-beta-1 -- Genentech
thrombostatin -- Thromgen	transport protein -- Genesis
thymalfasin -- SciClone	Trastuzumab -- Genetech
thymocartin -- Gedeon Richter	TRH -- Ferring
thymosin Alpha1 -- NIH	Triabin -- Schering AG
thyroid stimulating hormone -- Genzyme	Triconal
tICAM-1 -- Bayer	Triflavin
Tick anticoagulant peptide -- Merck	troponin I -- Boston Life Sciences
TIF -- Xoma	TRP-2 <sup>A</sup> -- NIH
Tifacogin -- Chiron, NIS, Pharmacia	trypsin inhibitor -- Mochida

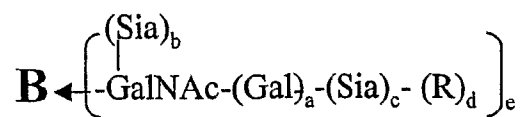
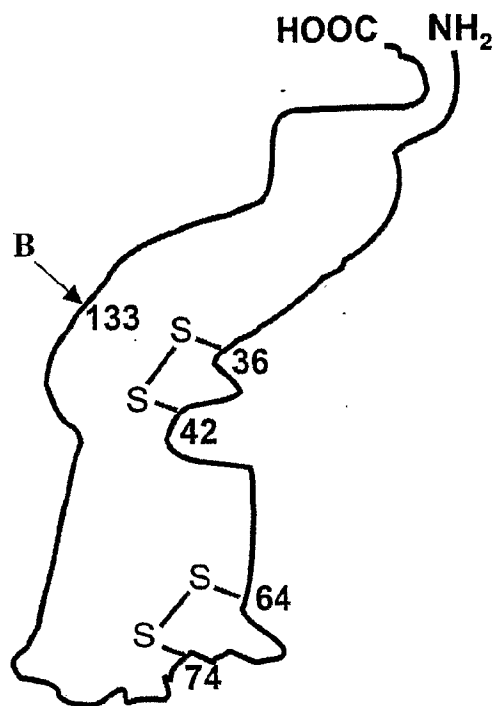
FIG. 28BB

## 59/498

TSP-1 gene therapy --	Vascular endothelial growth factors -- R&D
TT-232	Systems
TTS-CD2 -- Active Biotech	vascular targeting agents -- Peregrine
Tuberculosis vaccine -- Aventis Pasteur,	vasopermeation enhancement agents --
Genesis	Peregrine
Tumor Targeted Superantigens -- Active	vasostatin -- NIH
Biotech -- Pharmacia	VCL -- Bio-Tech. General
tumour vaccines -- PhotoCure	VEGF -- Genentech, Scios
tumour-activated prodrug antibody	VEGF inhibitor -- Chugai
conjugates -- Millennium/ImmunoGen	VEGF-2 -- Human Genome Sciences
tumstatin -- ILEX	VEGF-Trap -- Regeneron
Tuvirumab -- Novartis	viscumin, recombinant -- Madaus
TV-4710 -- Teva	Vitaxin
TWEAK receptor -- Immunex	Vitrage -- ISTA Pharmaceuticals
TXU-PAP	West Nile virus vaccine -- Bavarian Nordic
TY-10721 -- TOA Eiyo	WP 652
Type I diabetes vaccine -- Research Corp	WT1 vaccine -- Corixa
Typhoid vaccine CVD 908	WX-293 -- Willex BioTech.
U 143677 -- Pharmacia	WX-360 -- Willex BioTech.
U 81749 -- Pharmacia	WX-UK1 -- Willex BioTech.
UA 1248 -- Arizona	XMP-500 -- XOMA
UGIF -- Sheffield	XomaZyme-791 -- XOMA
UIC 2	XTL 001 -- XTL Biopharmaceuticals
UK 101	XTL 002 -- XTL Biopharmaceuticals
UK-279276 -- Corvas Intl.	yeast delivery system -- GlobelImmune
urodilatin -- Pharis	Yersinia pestis vaccine
urofollitrophin -- Serono	YIGSR-Stealth -- Johnson & Johnson
Urokinase -- Abbott	Yisum Project No. D-0460 -- Yisum
uteroferin-- Pepgen	YM 207 -- Yamanouchi
V 20 -- GLYCODESIGN	YM 337 -- Protein Design Labs
V2 vasopressin receptor gene therapy	Yttrium-90 labelled biotin
vaccines -- Active Biotech	Yttrium-90-labeled anti-CEA MAb T84.66 --
Varicella zoster glycoprotein vaccine --	ZD 0490 -- AstraZeneca
Research Corporation Technologies	ziconotide -- Elan
Varicella zoster virus vaccine live -- Cantab	ZK 157138 -- Berlex Laboratories
Pharmaceuticals	Zolimomab aritox
Vascular endothelial growth factor --	Zorcell -- Immune Response
Genentech, University of California	ZRXL peptides -- Novartis

FIG. 28CC

60/498



a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, sialyl or  
oligosialyl

FIG. 29A



61/498

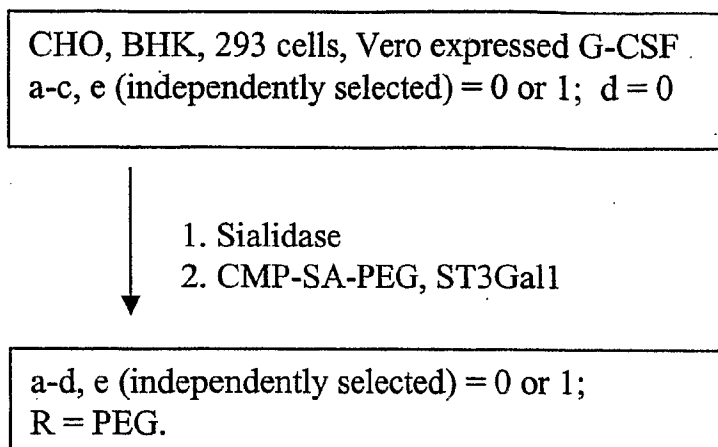


FIG. 29B

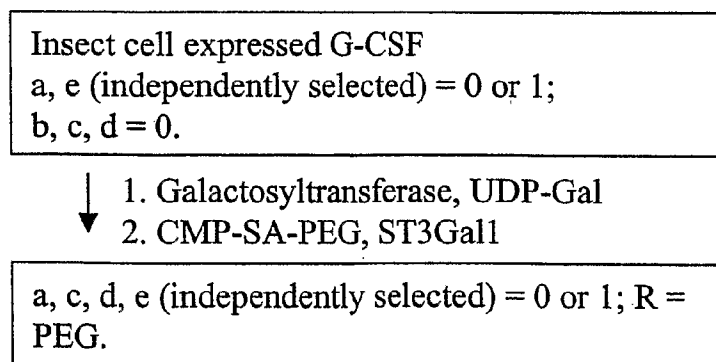


FIG. 29C

62/498

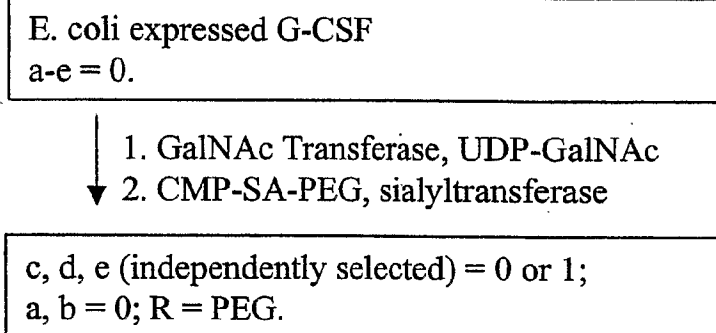


FIG. 29D

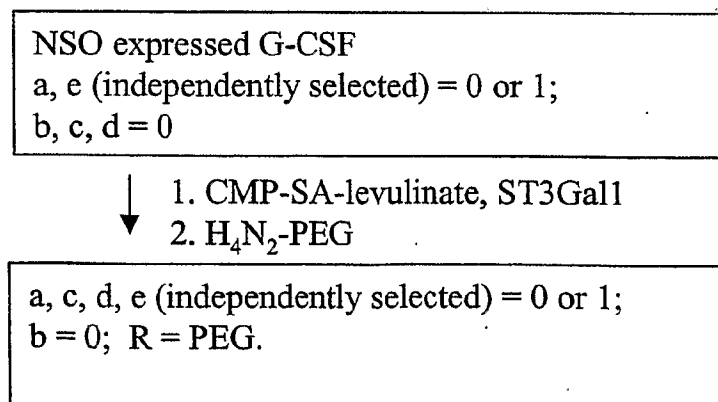


FIG. 29E

63/498

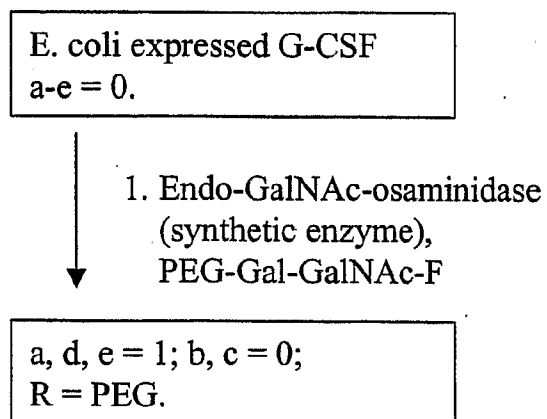


FIG. 29F

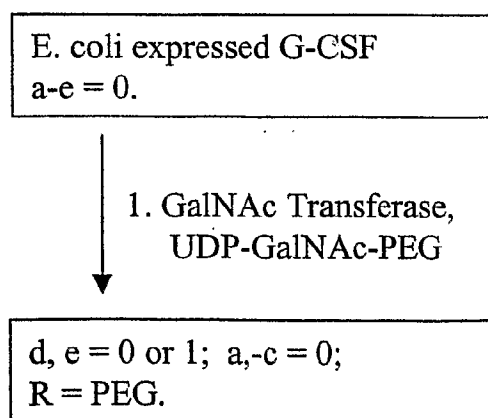
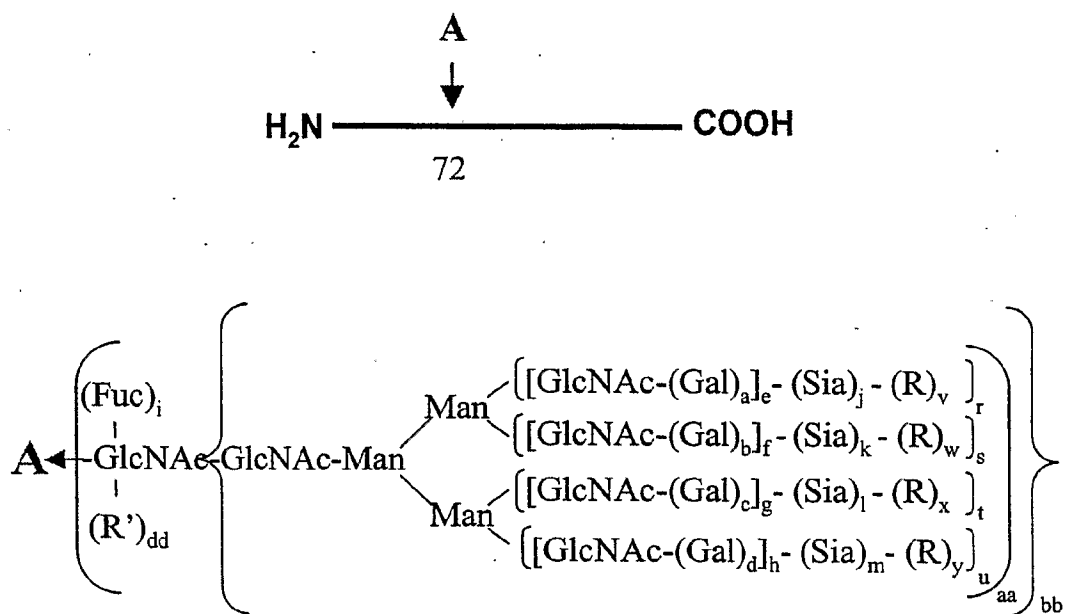


FIG. 29G

64/498



a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 30A

65/498

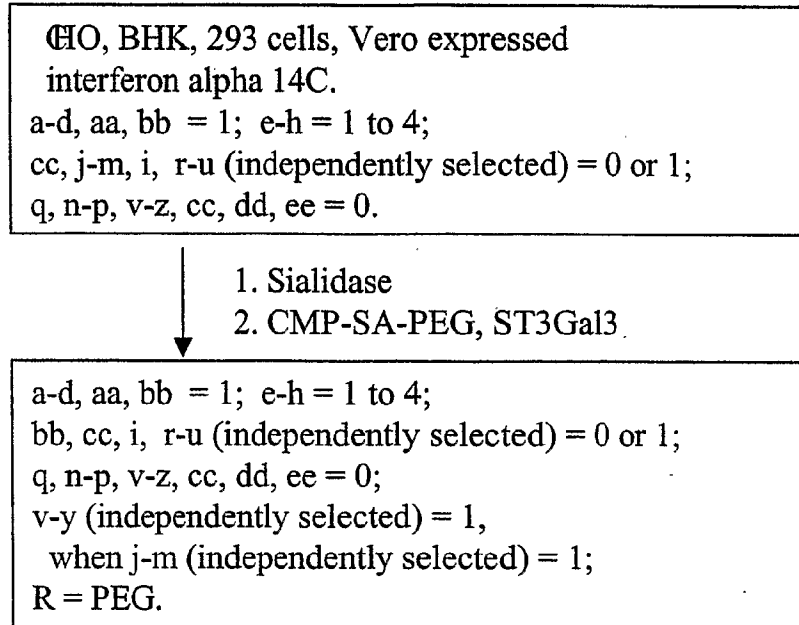


FIG. 30B

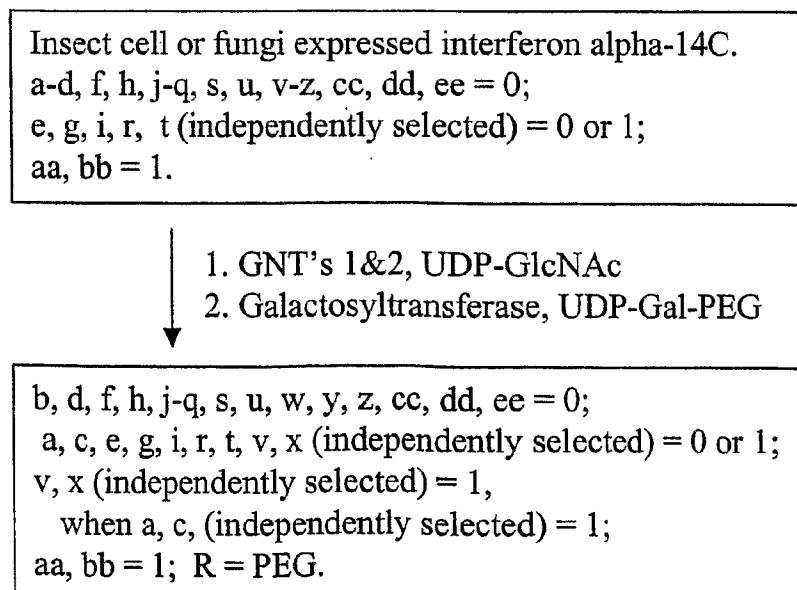


FIG. 30C

66/498

Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

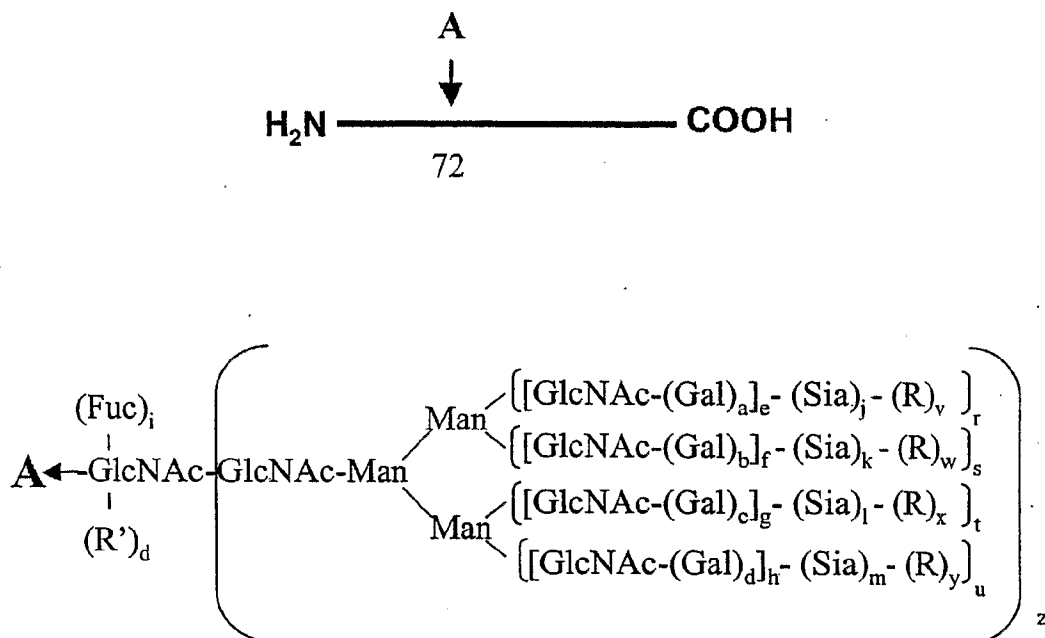
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 30D

67/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 30E

68/498

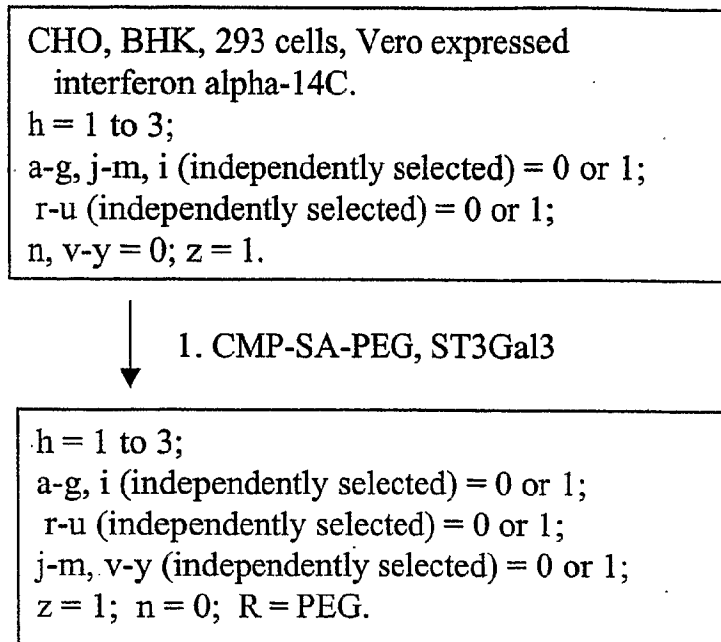


FIG. 30F

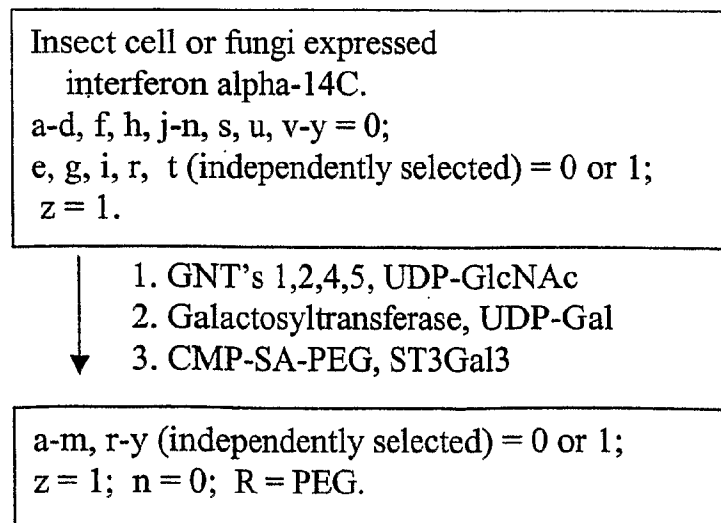


FIG. 30G



69/498

Yeast expressed interferon alpha-14C.  
 a-n = 0; r-y (independently selected) = 0 to 1;  
 z = 1; R (branched or linear) = Man,  
 oligomannose.

1. mannosidases
2. GNT's 1,2,4,5, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal
- ▼ 4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
 z = 1; n = 0; R = PEG.

FIG. 30H

NSO expressed interferon alpha 14C.  
 a-i, r-u (independently selected) = 0 or 1;  
 j-m, n, v-y = 0; z = 1.

1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
- ▼ 2. H<sub>4</sub>N<sub>2</sub>-PEG

a-i, j-m, r-y (independently selected) = 0 or 1;  
 n = 0; z = 1; R = PEG.

FIG. 30I

70/498

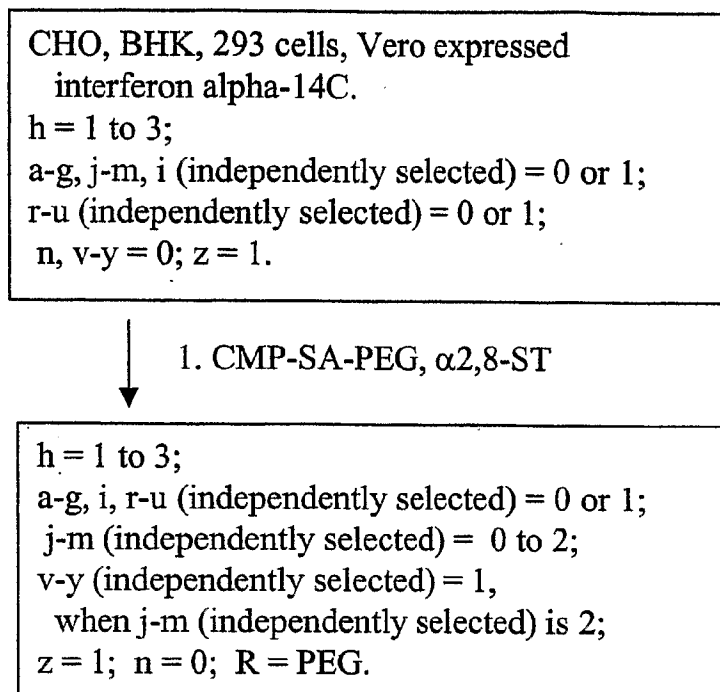


FIG. 30J

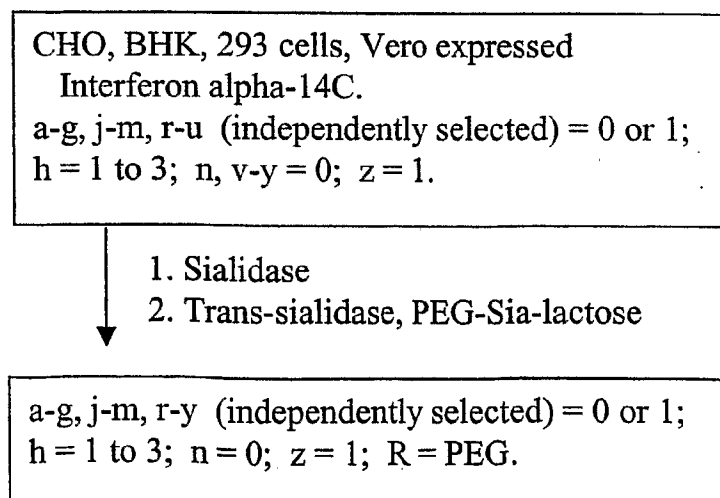


FIG. 30K

71/498

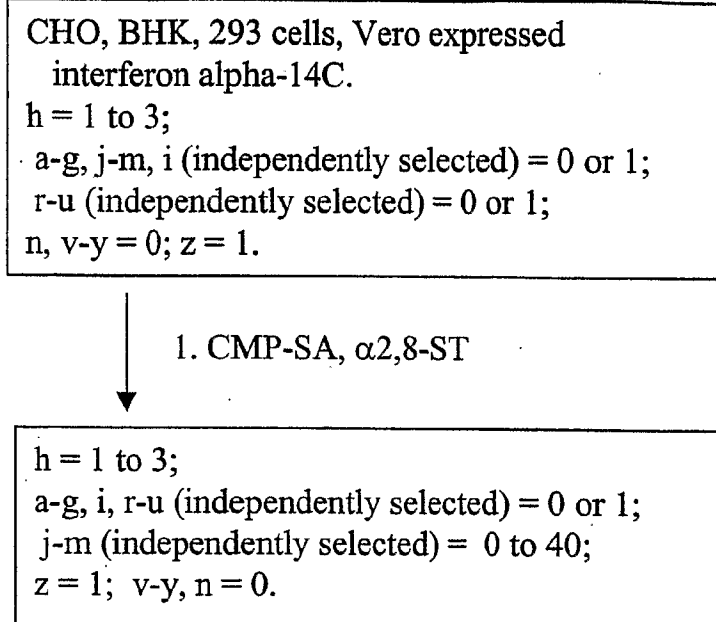


FIG. 30L

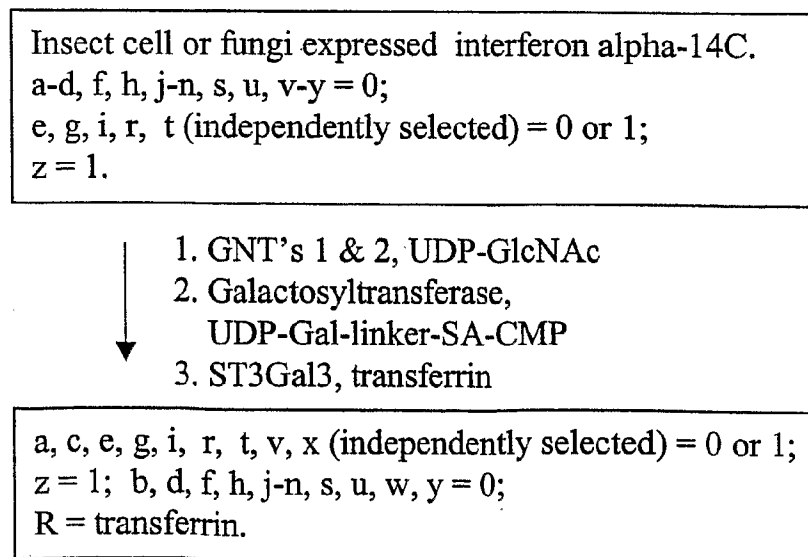


FIG. 30M

72/498

Insect cell or fungi expressed interferon alpha-14C.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
  2. Galactosyltransferase,  
UDP-Gal-linker-SA-CMP
  3. ST3Gal3, transferrin

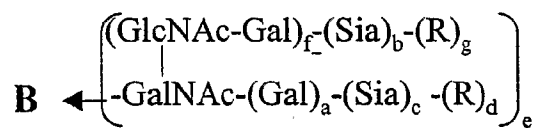
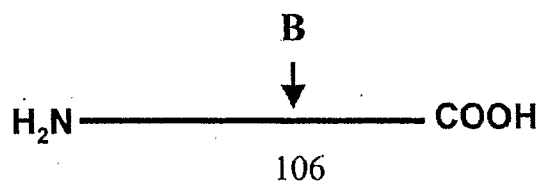
i (independently selected) = 0 or 1;

a-h, j-m, r-z = 0;

n = 1; R' = -Gal-linker-transferrin.

FIG. 30N

73/498



a-c, e, f (independently selected) = 0 or 1;  
 d, g = 0; R = polymer, glycoconjugate.

FIG. 300

74/498

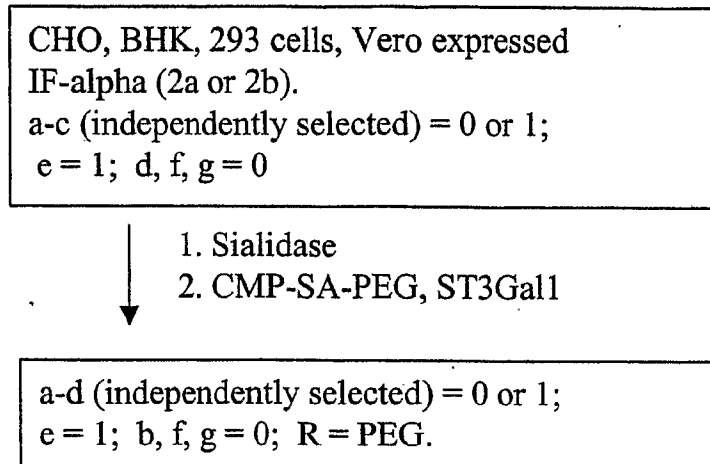


FIG. 30P

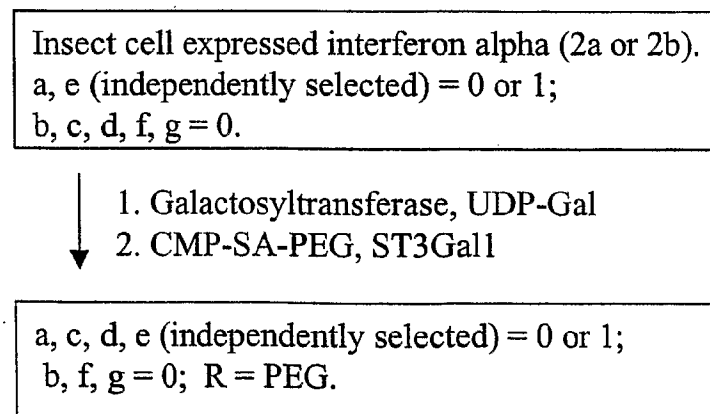


FIG. 30Q

75/498

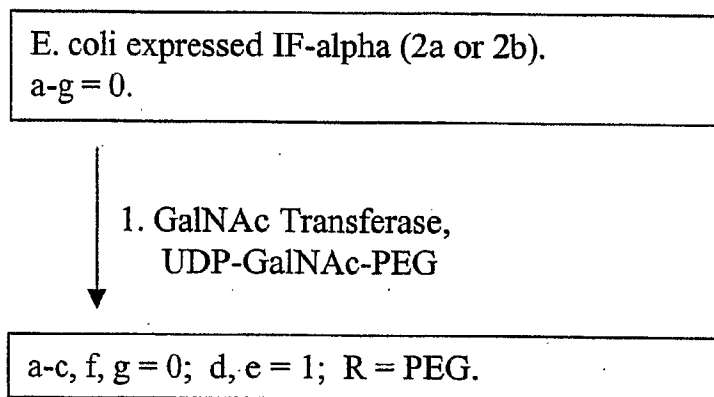


FIG. 30R

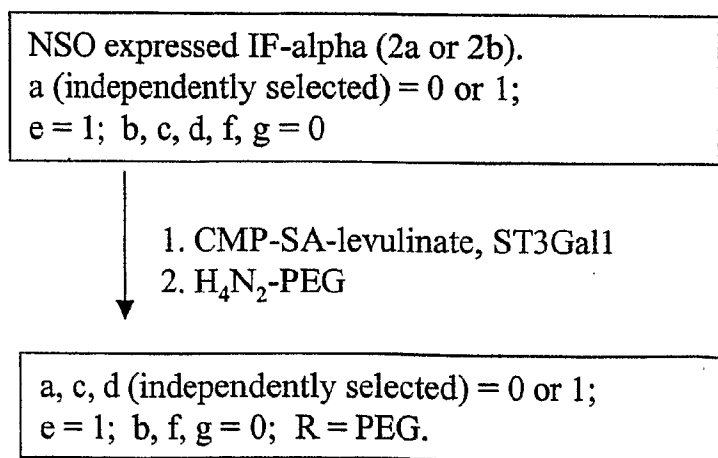


FIG. 30S

76/498

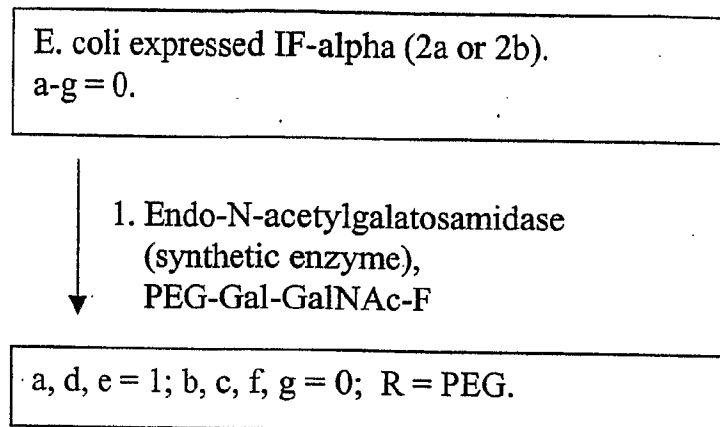


FIG. 30T

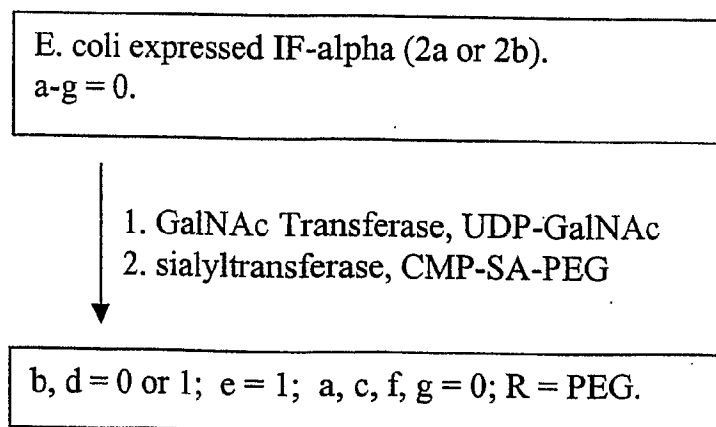


FIG. 30U



77/498

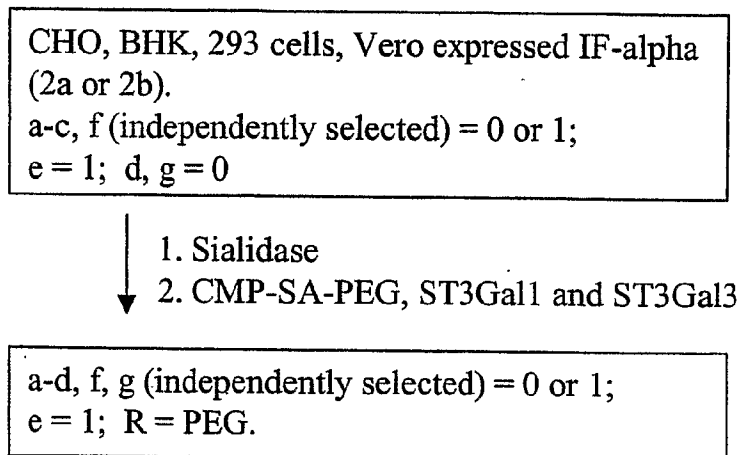


FIG. 30V

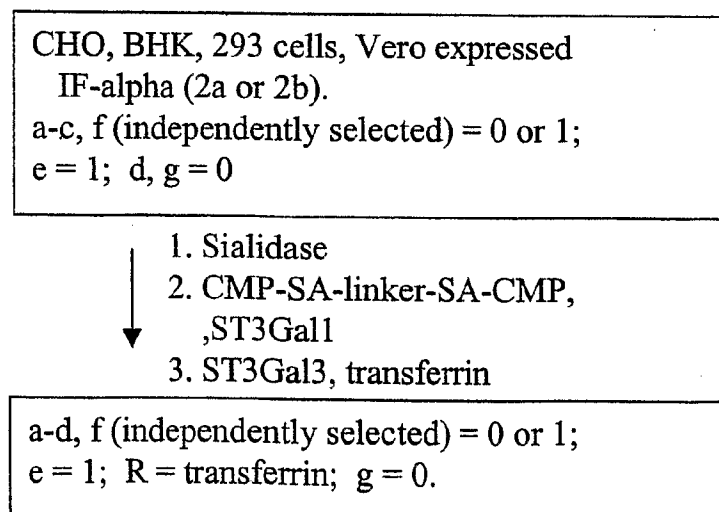
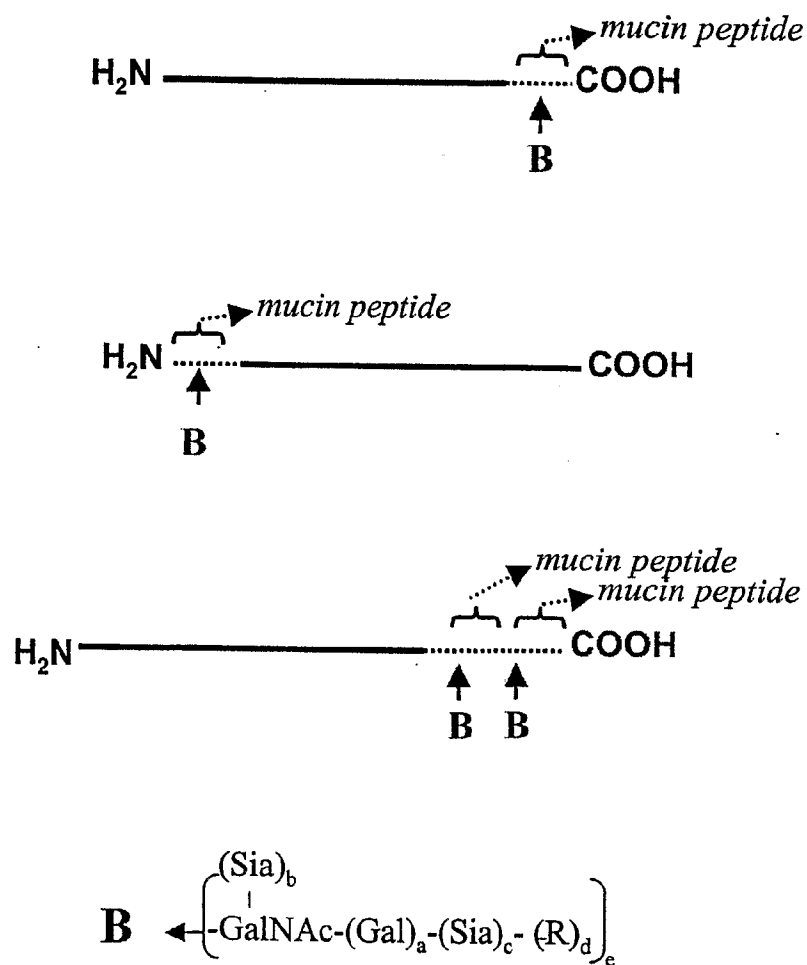


FIG. 30W

78/498



a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer, glycoconjugate.

FIG. 30X

79/498

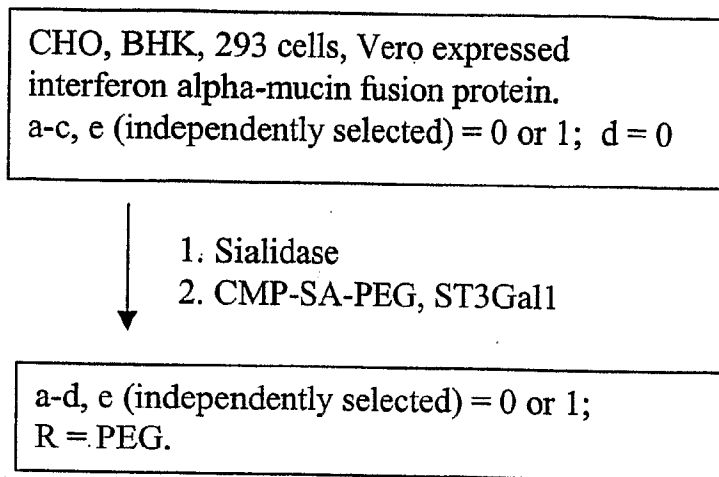


FIG. 30Y

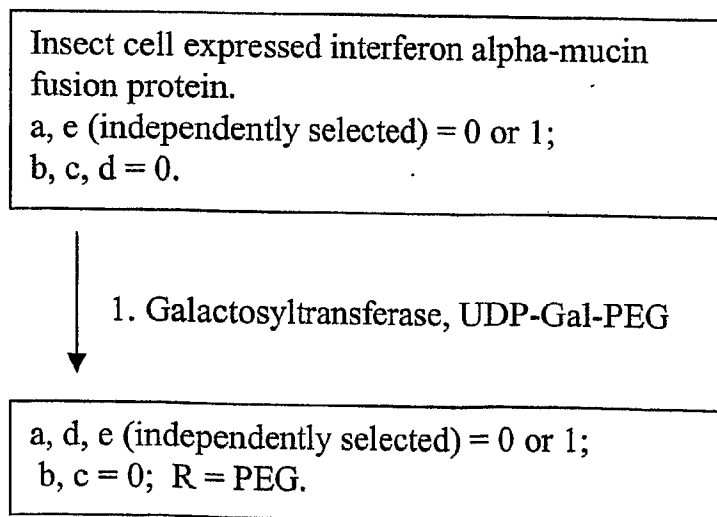


FIG. 30Z

80/498

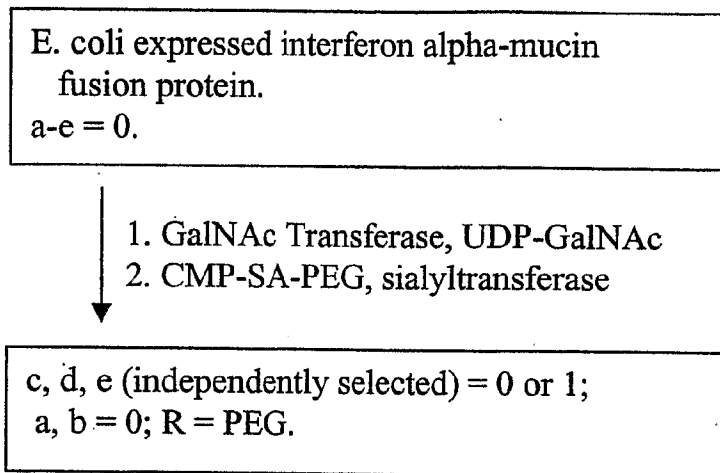
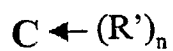
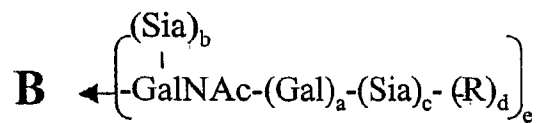
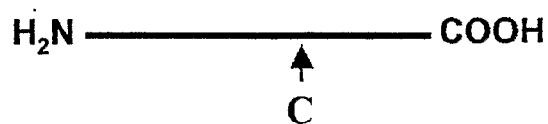
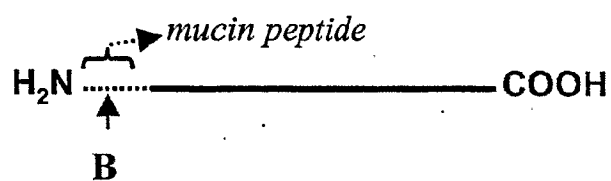
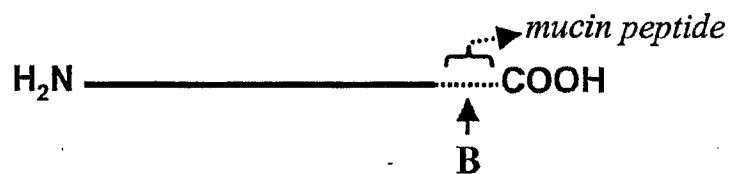


FIG. 30AA

81/498



a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer, linker.

FIG. 30BB

82/498

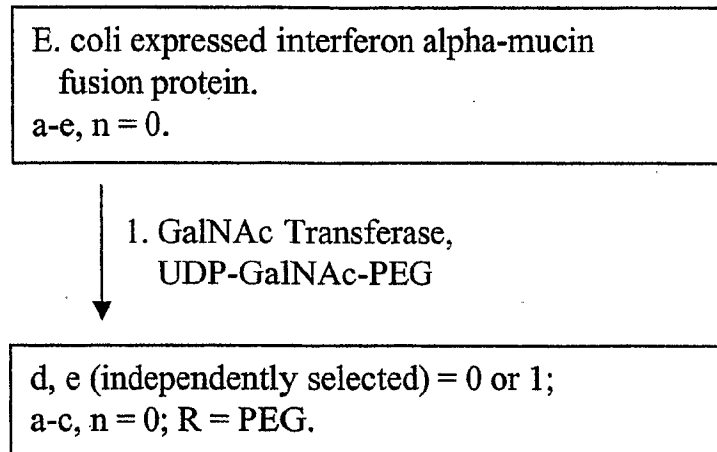


FIG. 30CC

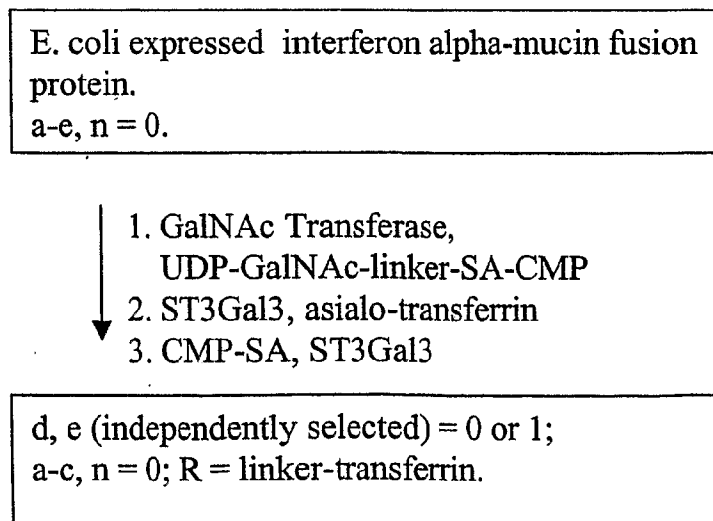


FIG. 30DD

83/498

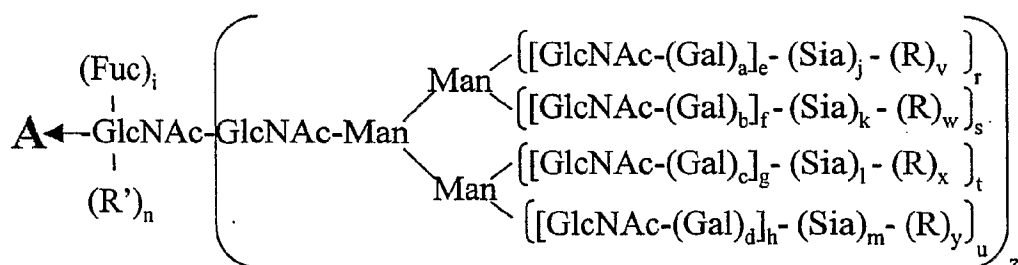
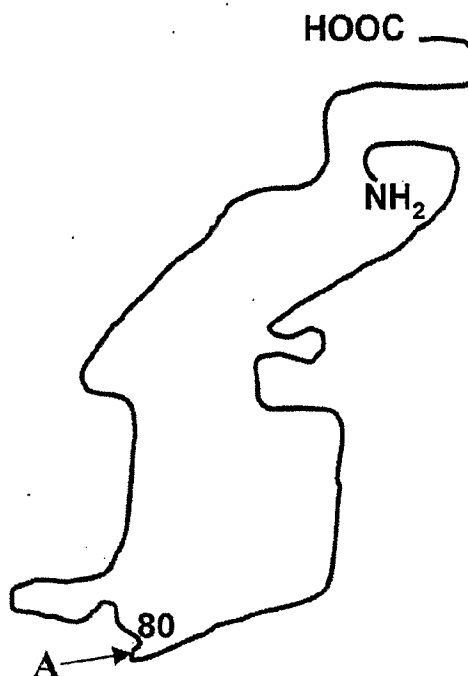
E. coli expressed Interferon alpha (no fusion).  
a-e, n = 0.

- ↓  
1. NHS-CO-linker-SA-CMP  
2. ST3Gal3, transferrin

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 30EE

84/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 31A



85/498

CHO, BHK, 293 cells, Vero expressed IF-beta  
 h = 1 to 3;  
 a-g, j-m, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 n, v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;  
 a-g, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 j-m, v-y (independently selected) = 0 or 1;  
 z = 1; n = 0; R = PEG.

FIG. 31B

Insect cell expressed IF-beta  
 a-d, f, h, j-n, s, u, v-y = 0;  
 e, g, i, r, t (independently selected) = 0 or 1;  
 z = 1.



1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
2. CMP-SA-PEG, ST3Gal3,  
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;  
 a, c, e, g, i, r, t (independently selected) = 0 or 1;  
 j, l, v, x (independently selected) = 0 or 1;  
 z = 1; R = PEG.

FIG. 31C

86/498

Yeast expressed IF-beta

a-n = 0; z = 1;

r-y (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed IF-beta

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

- ↓
1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 31E

87/498

Insect cell expressed IF-beta  
 a-d, f, h, j-n, s, u, v-y = 0; e, g, i, r, t  
 (independently selected) = 0 or 1; z = 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
 z = 1; n = 0; R = PEG.

FIG. 31F

Yeast expressed IF-beta  
 a-n = 0; z = 1;  
 r-y (independently selected) = 0 to 1;  
 R (branched or linear) = Man, oligomannose.

- ↓
1. mannosidases
  2. GNT's 1,2,4,5, UDP-GlcNAc
  3. Galactosyltransferase, UDP-Gal
  4. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
 z = 1; n = 0; R = PEG.

FIG. 31G

88/498

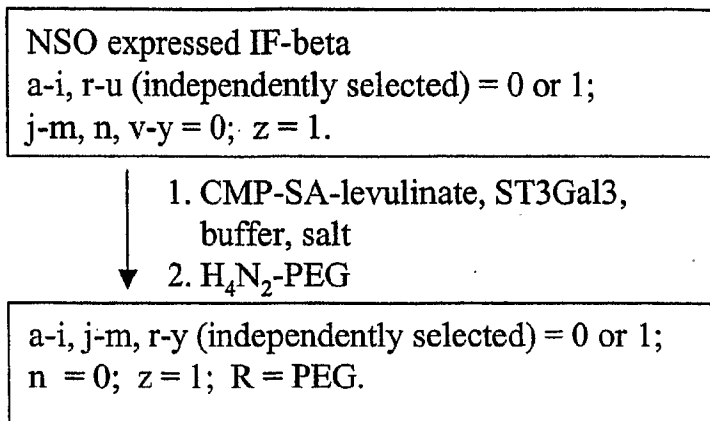


FIG. 31H

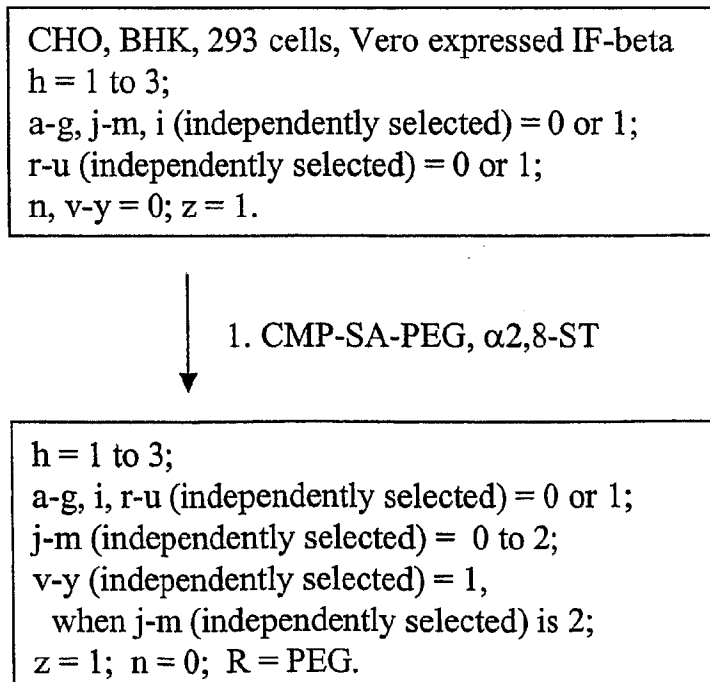


FIG. 31I

89/498

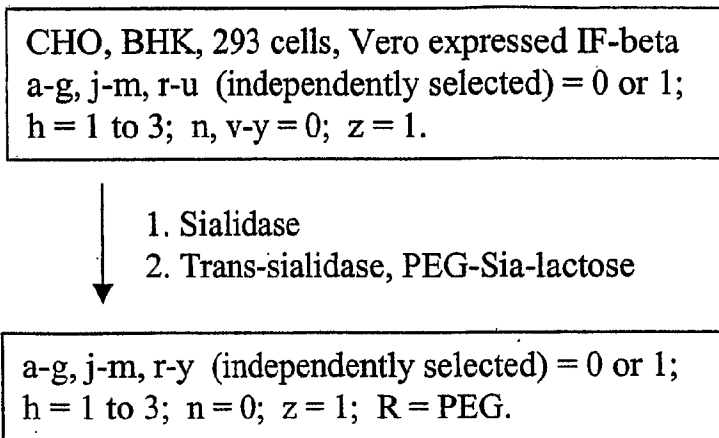


FIG. 31J

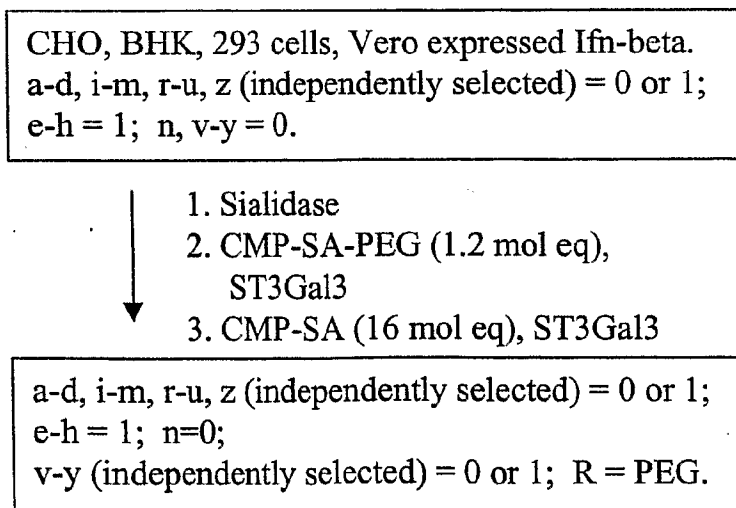


FIG. 31K

90/498

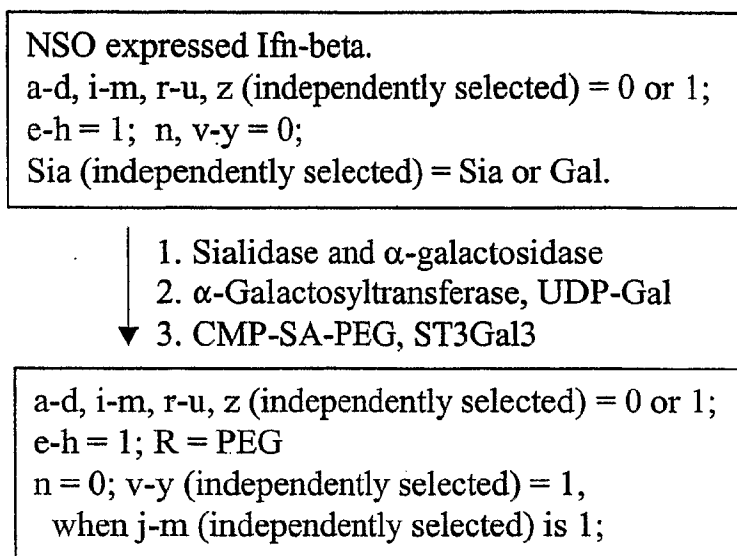


FIG. 31L

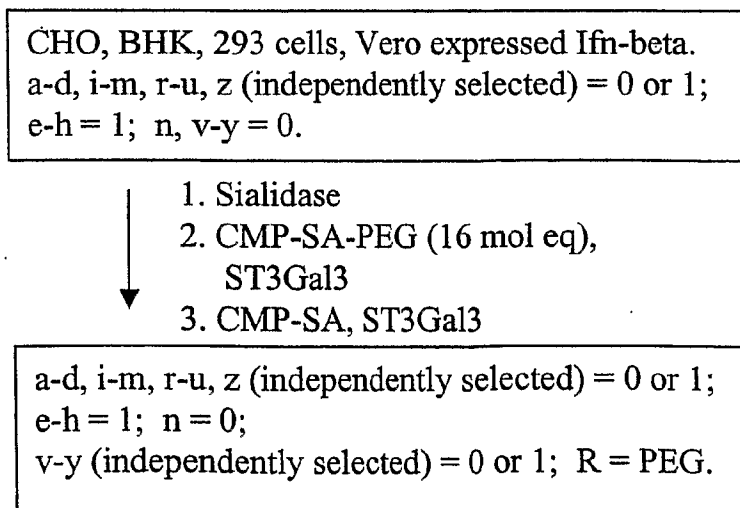


FIG. 31M

91/498

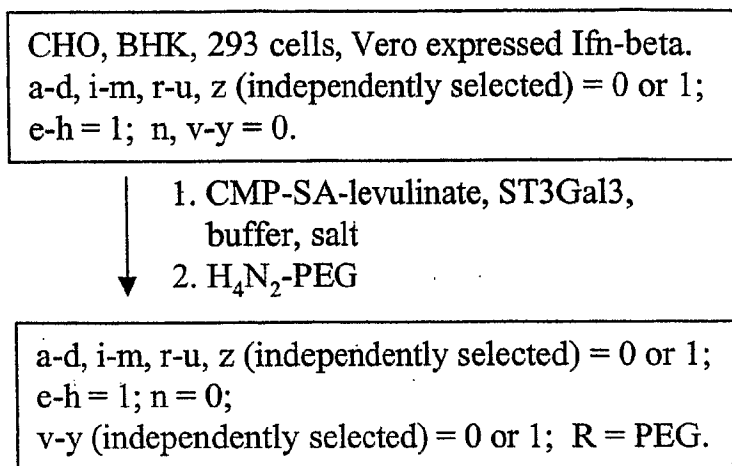


FIG. 31N

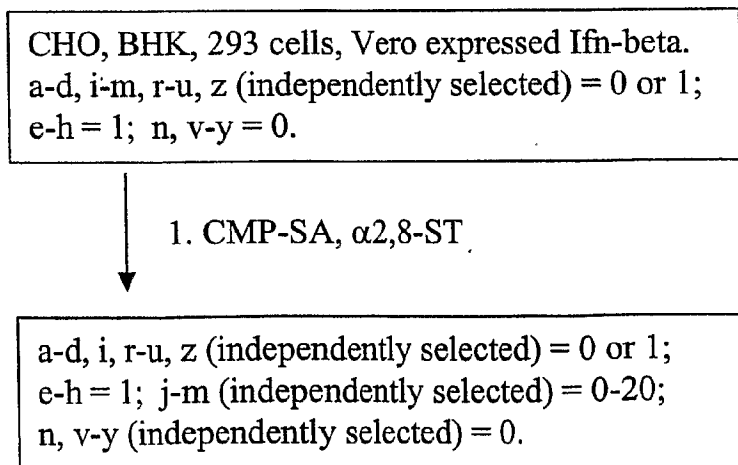
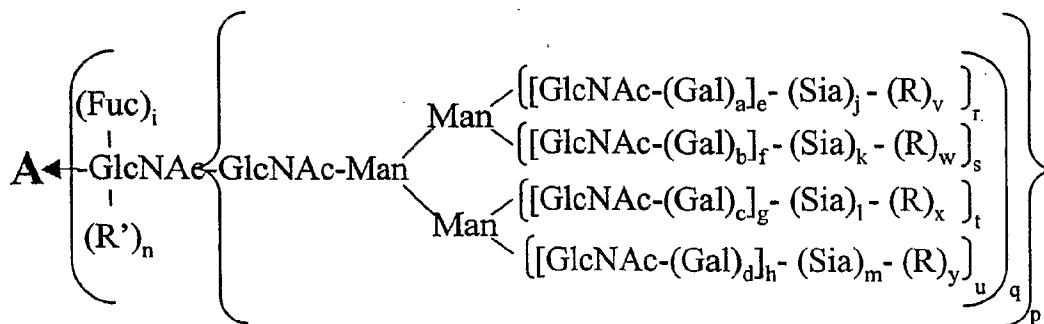
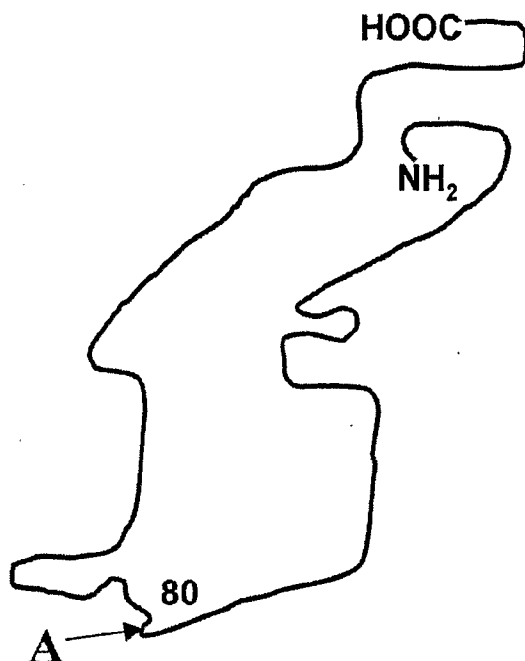


FIG. 31O

92/498



a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group;

R' = H, glycosyl group, modifying group,  
glycoconjugate.

FIG. 31P



93/498

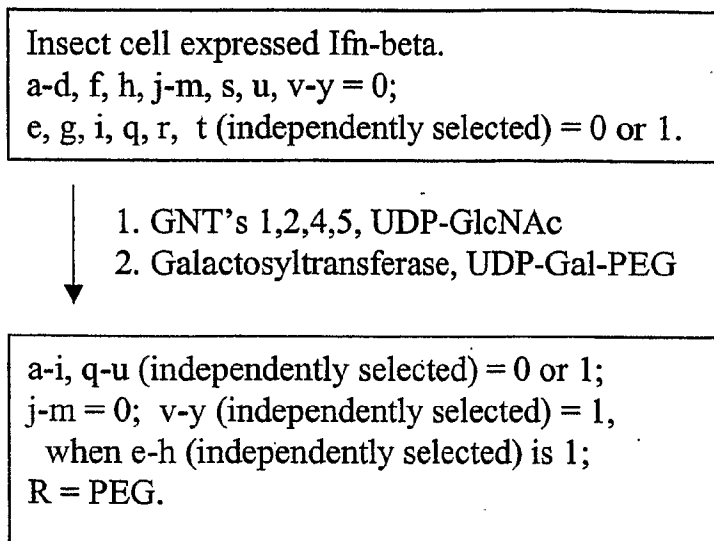


FIG. 31Q

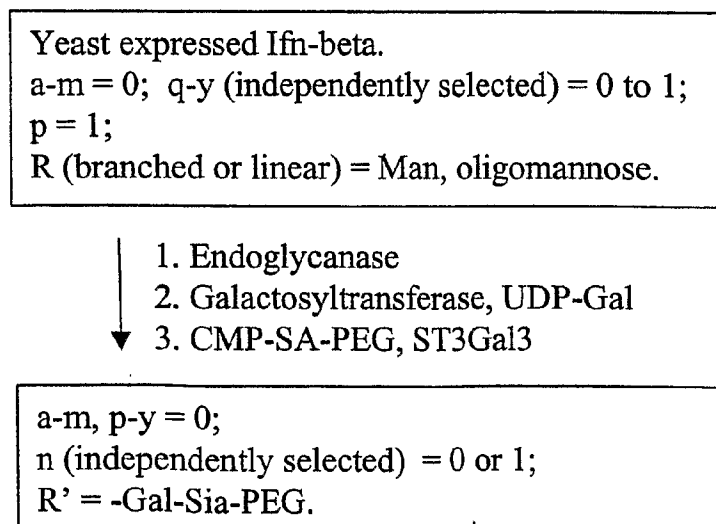


FIG. 31R

94/498

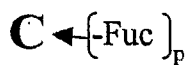
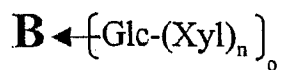
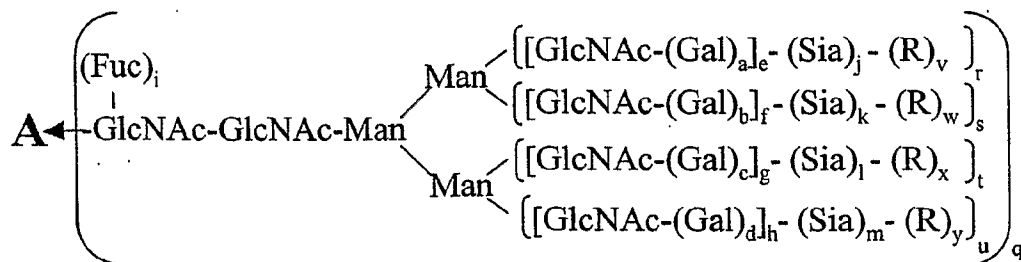
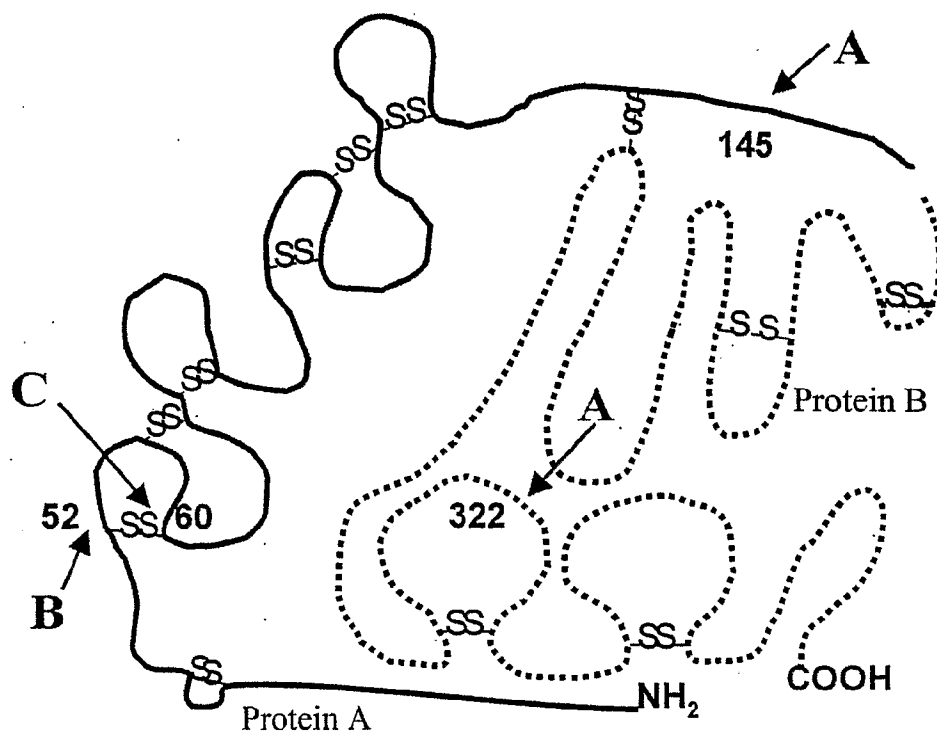
CHO, BHK, 293 cells, Vero expressed Ifn-beta.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,  
ST3Gal3
  2. ST3Gal3, desialylated transferrin.
  3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 31S

95/498



a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A..

FIG. 32A

96/498

BHK expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;  
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mole eq),  
ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;  
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;  
v, x, (independently selected) = 1,  
when j, l (respectively, independently selected) is 1;  
R = PEG.

FIG. 32B

CHO, BHK, 293 cells, Vero expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;  
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mole eq),  
ST3Gal3
  3. CMP-SA (8 mol eq), ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;  
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;  
v or x, (independently selected) = 1,  
when j or l, (respectively, independently selected) is 1;  
R = PEG.

FIG. 32C

97/498

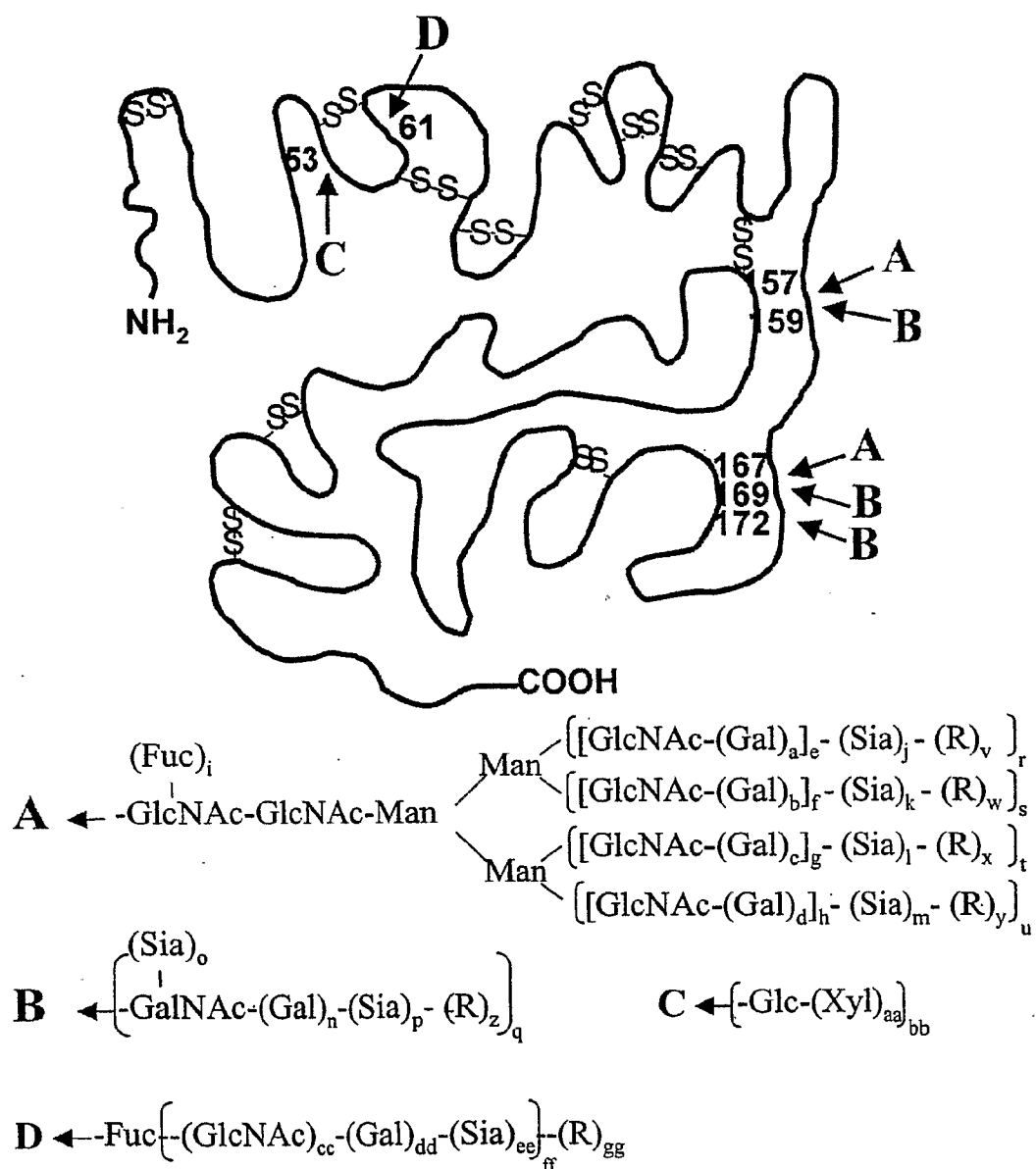
NSO expressed Factor VII or VIIa  
a--u (independently selected) = 0 or 1;  
v-y = 0; n = 0-4;  
Sia (independently selected) = Sia or Gal.

- ↓  
1. Sialidase and  $\alpha$ -galactosidase  
2. Galactosyltransferase, UDP-Gal  
▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;  
n = 0-4; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
Sia = Sia; R = PEG.

FIG. 32D

98/498



a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 33A

99/498

CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1;  
 o, p, z = 0;  
 j-m, ee, v-y, gg (independently selected) = 0 or 1;  
 R = PEG.

FIG. 33B

CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, n, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3
3. ST3Gal1, CMP-SA

a-d, n, p, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =  
 0 or 1;  
 j-m, ee, v-y, gg (independently selected) = 0 or 1;  
 o, z = 0; R = PEG.

FIG. 33C

100/498

CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,  
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

- ↓
1. sialidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA, ST3Gal3
  - ↓
  4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =  
 0 or 1; R = PEG;  
 o, v-y, gg = 0;  
 j-m, p, ee (independently selected) = 0 or 1, but when  
 p = 1, z = 1.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

↓ CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1; R = PEG;  
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =  
 0 or 1.

FIG. 33E



101/498

CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1;  
 o, p, z = 0; R = PEG;  
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 33F

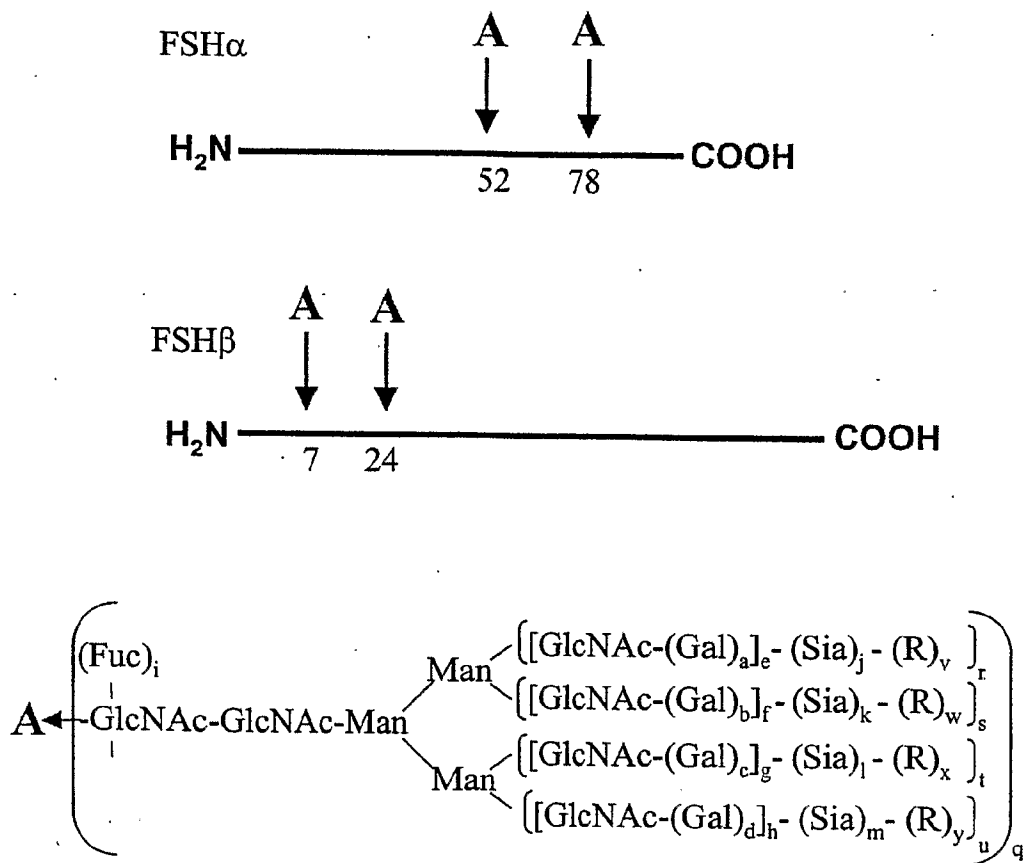
CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, n, q, bb, cc, dd, ff = 1;  
 e-h, aa = 1 to 4;  
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG,  $\alpha$ 2,8-ST

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1;  
 o, p, z = 0; R = PEG;  
 j-m, ee (independently selected) = 0 to 2;  
 v-y, gg (independently selected) = 1, when j-m  
 (independently selected) is 2;

FIG. 33G

102/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 34A

103/498

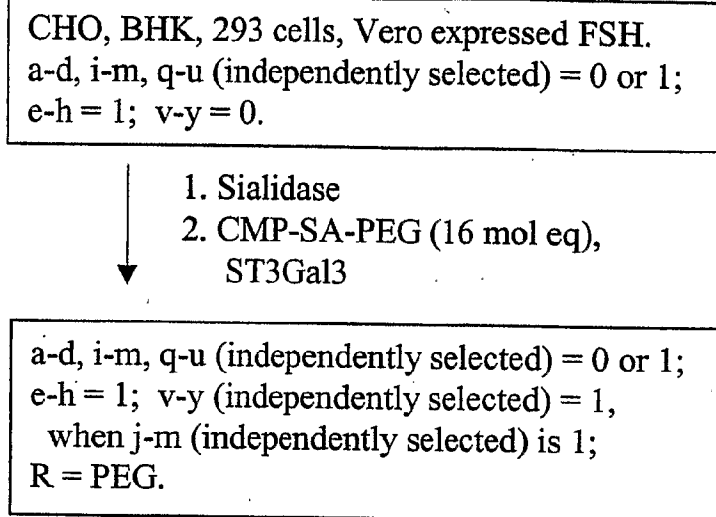


FIG. 34B

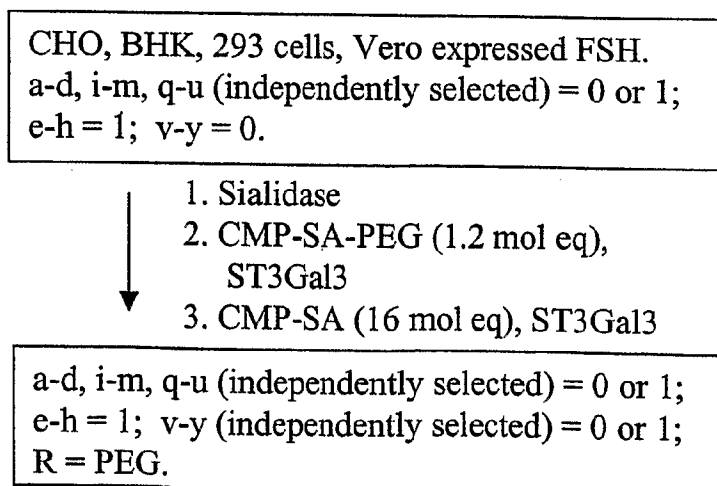


FIG. 34C

104/498

NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  - ↓ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 34D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  - ↓ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 34E

105/498

CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 34F

CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 34G

106/498

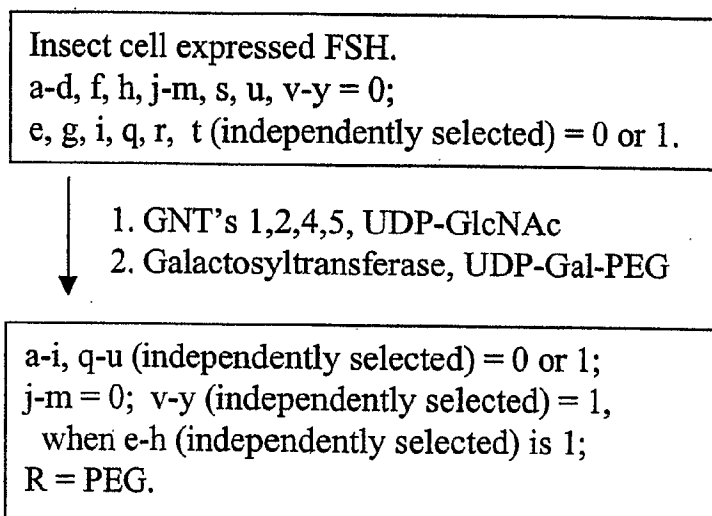


FIG. 34H

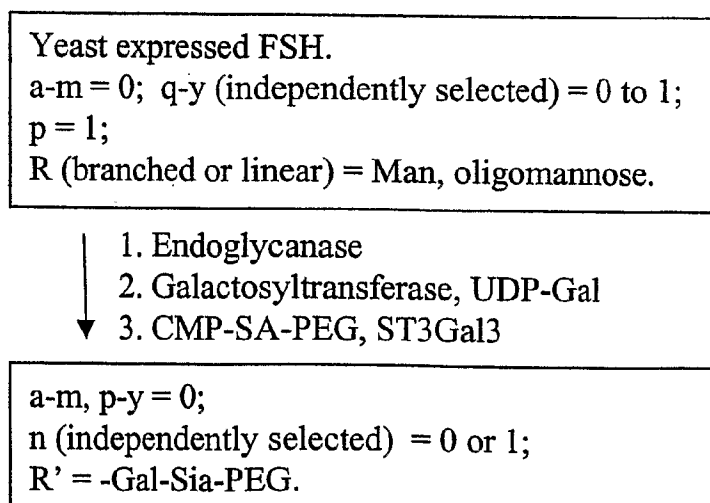


FIG. 34I

107/498

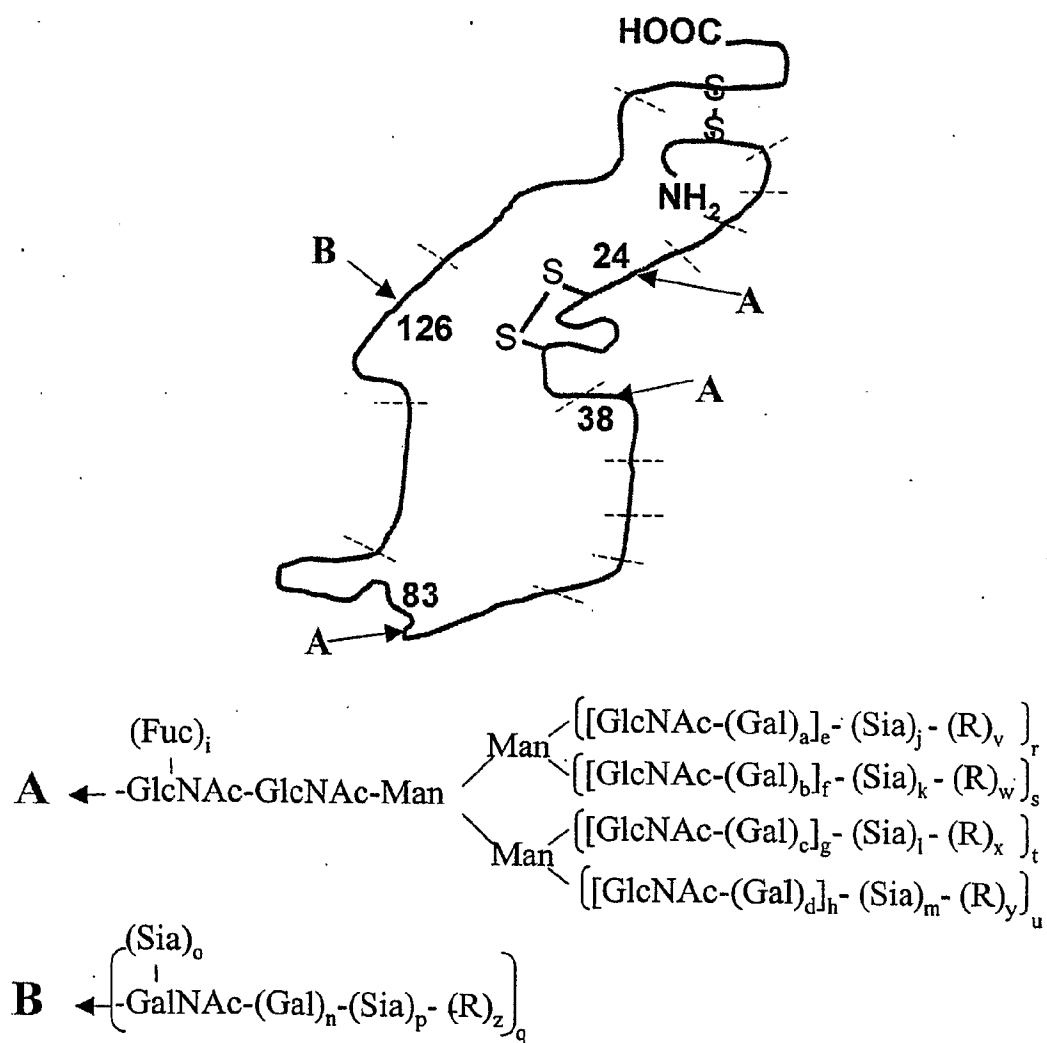
CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated chorionic gonadotrophin (CG) produced in CHO.
  3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-CG.

FIG. 34J

108/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35A



109/498

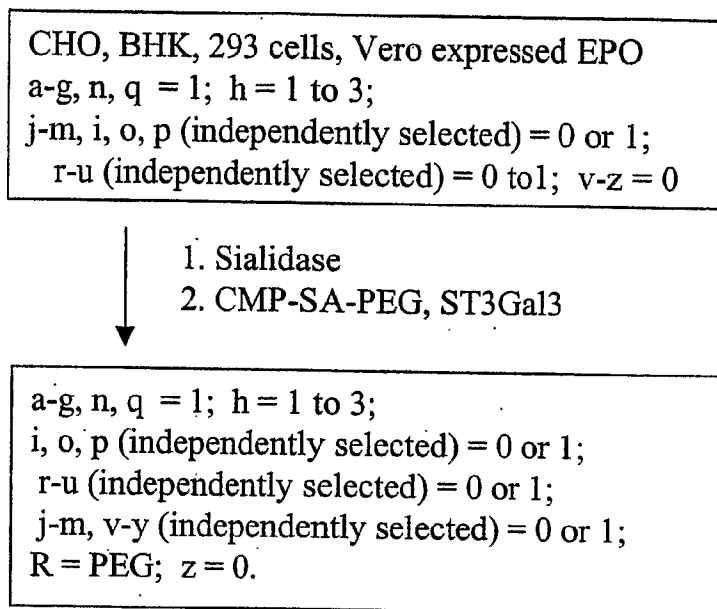


FIG. 35B

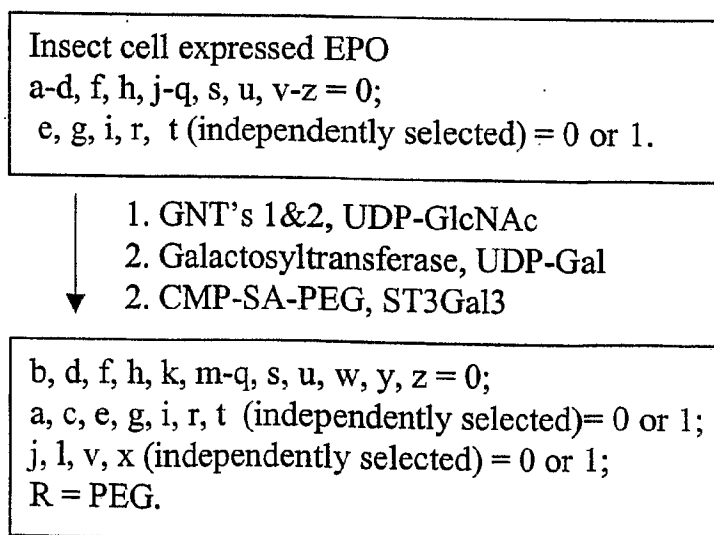


FIG. 35C

110/498

CHO, BHK, 293 cells, Vero expressed EPO  
 a-q, r-u (independently selected) = 0 or 1;  
 v-z = 0.

- ↓
1. sialidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA, ST3Gal3
  4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;  
 i-m, o, r-u (independently selected) = 0 or 1;  
 v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed EPO  
 a-g, n, q = 1; h = 1 to 3;  
 j-m, i, o, p (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 v-z = 0

- ↓
1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;  
 i, o, p (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 to 1;  
 j-m, v-y (independently selected) = 0 or 1;  
 R = PEG; z = 0.

FIG. 35E

111/498

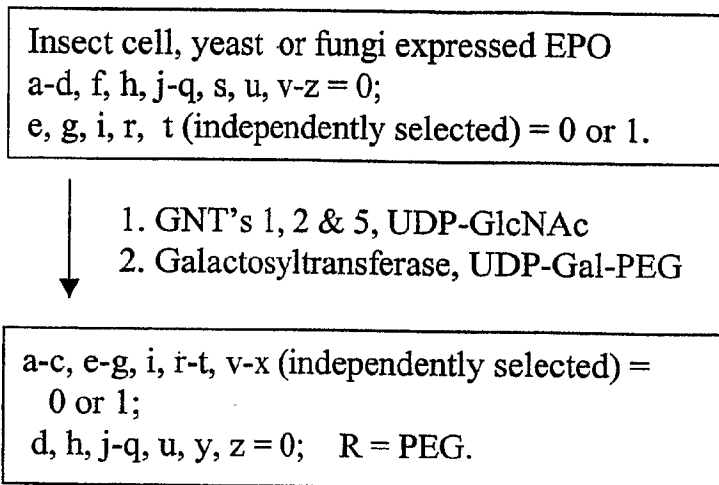


FIG. 35F

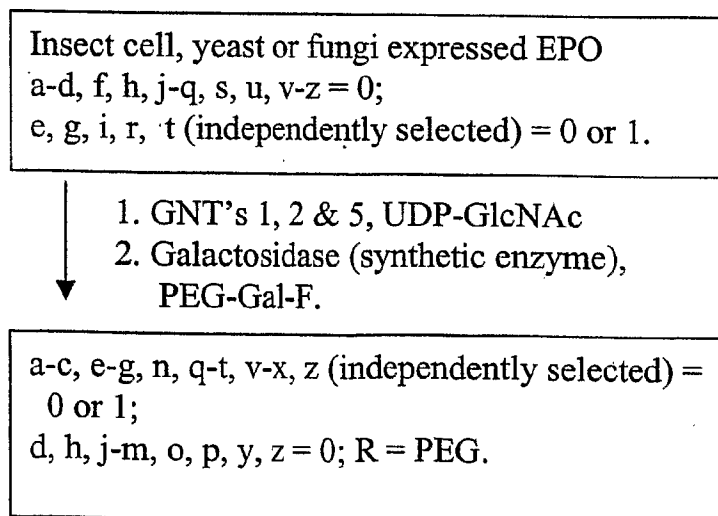


FIG. 35G

112/498

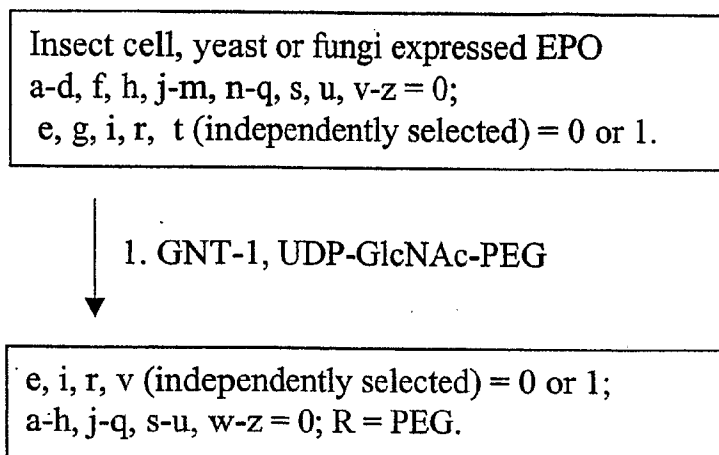


FIG. 35H

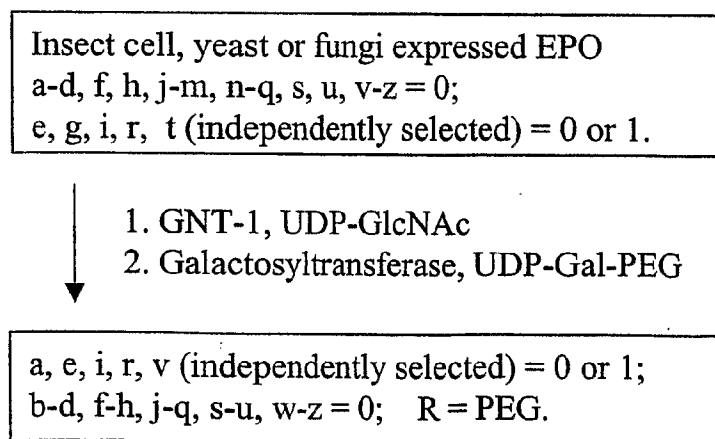


FIG. 35I

113/498

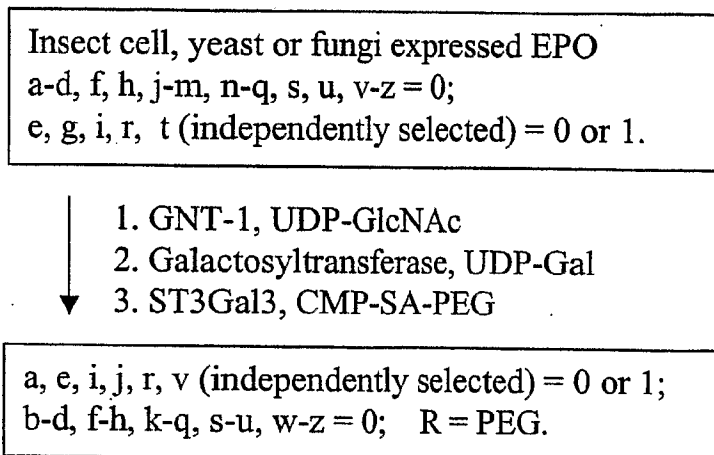


FIG. 35J

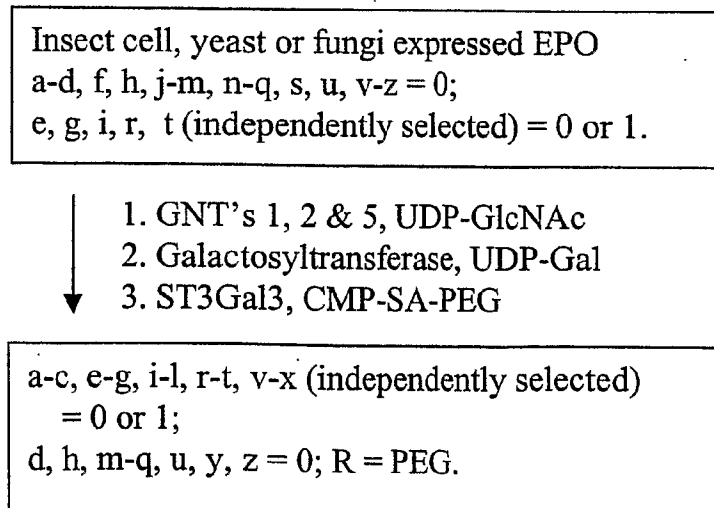


FIG. 35K

114/498

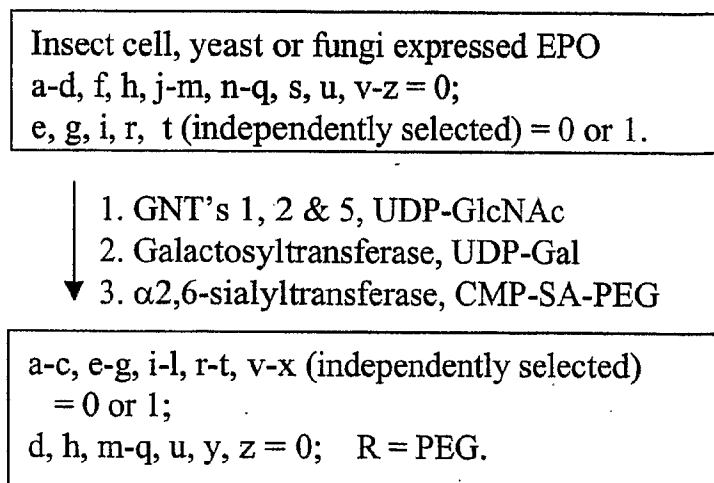


FIG. 35L

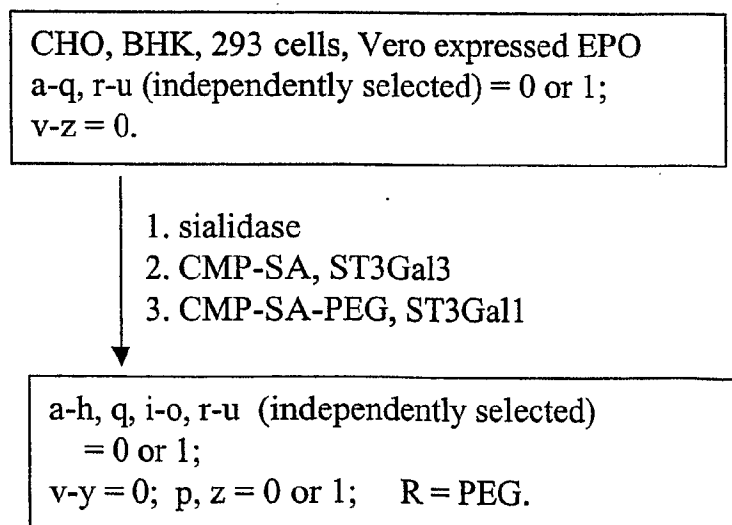


FIG. 35M

115/498

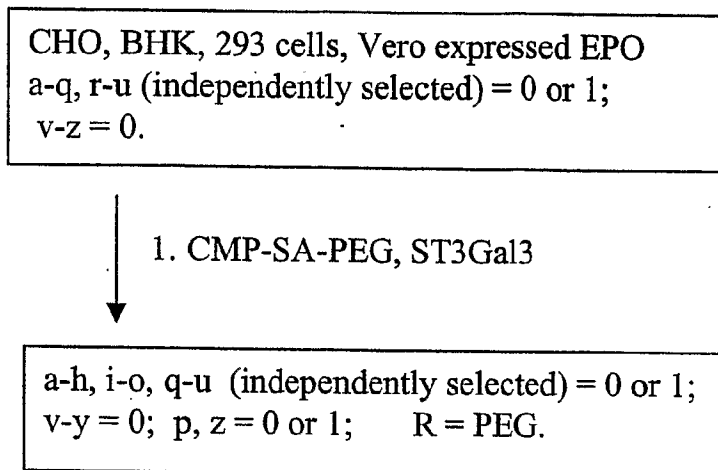


FIG. 35N

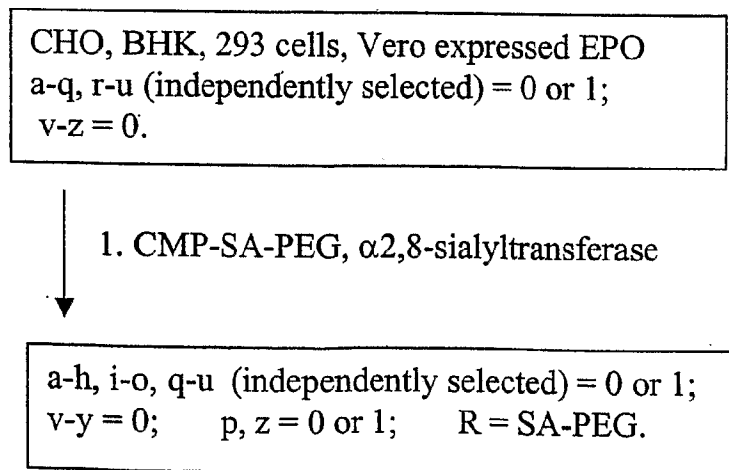


FIG. 35O

116/498

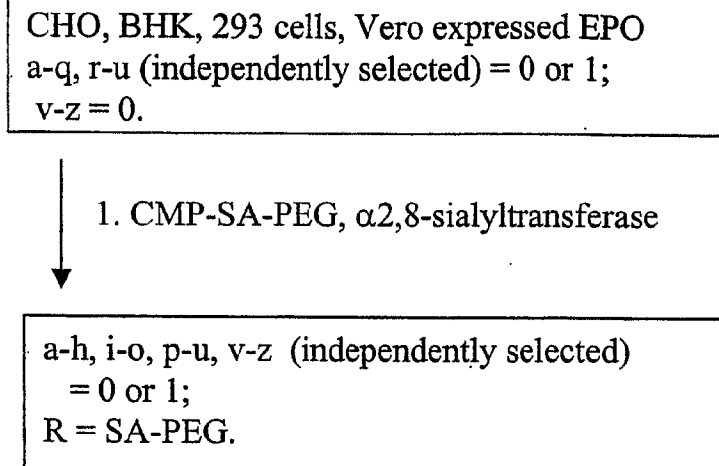


FIG. 35P

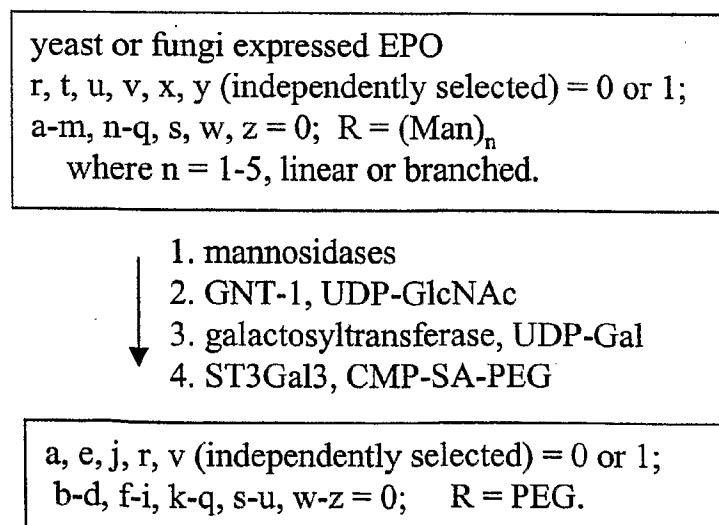


FIG. 35Q



117/498

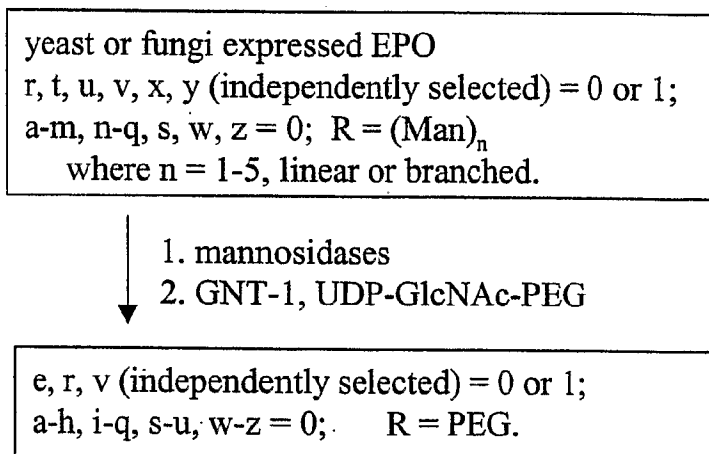


FIG. 35R

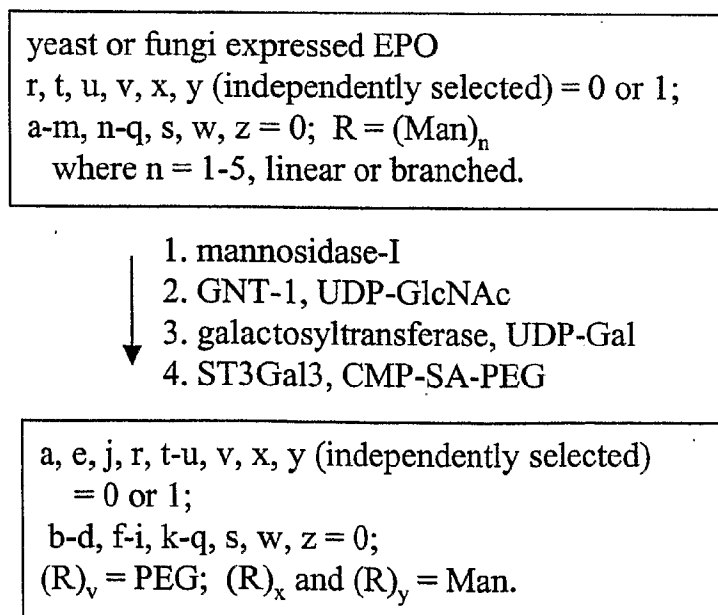


FIG. 35S

118/498

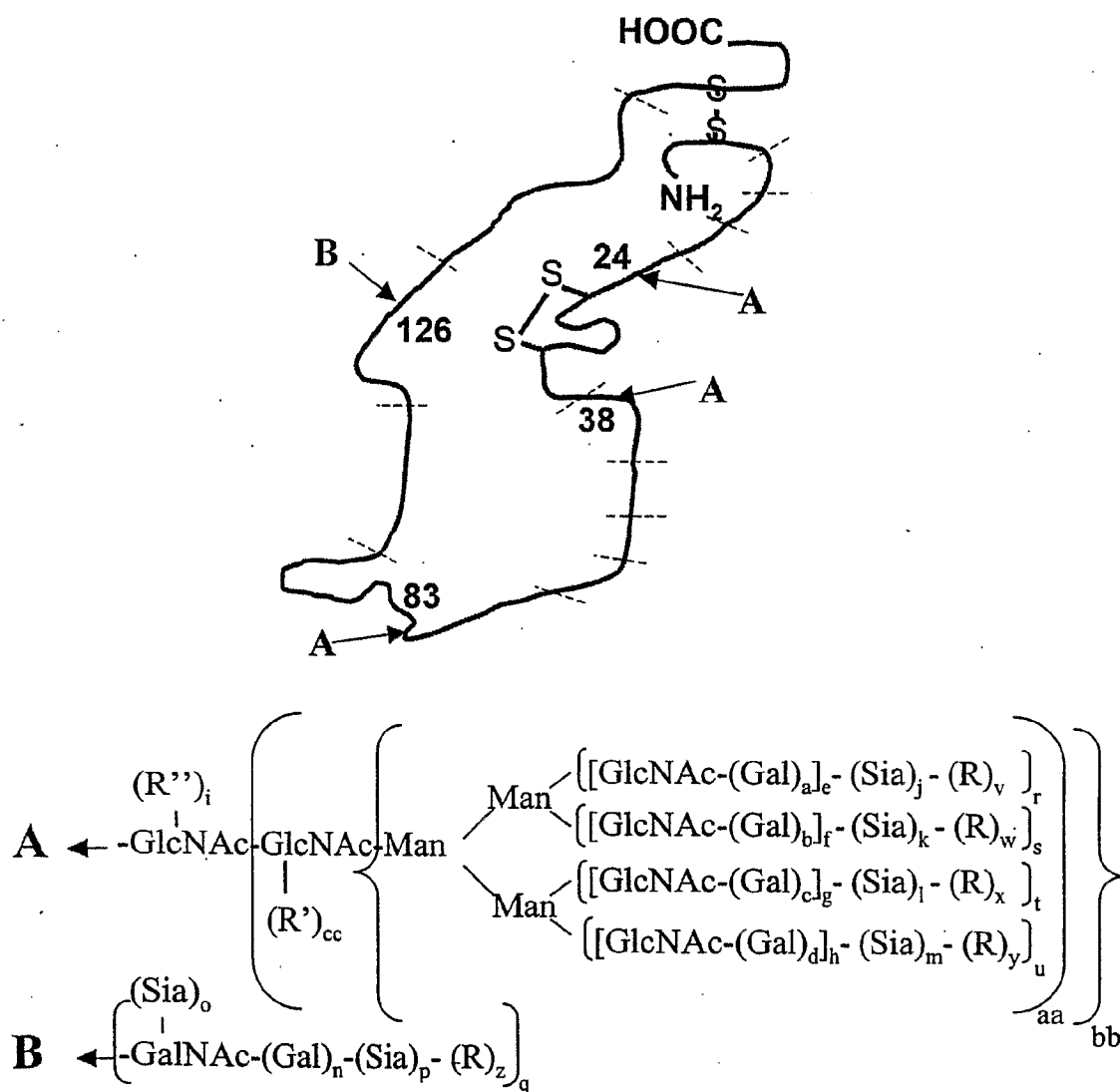


FIG. 35T

119/498

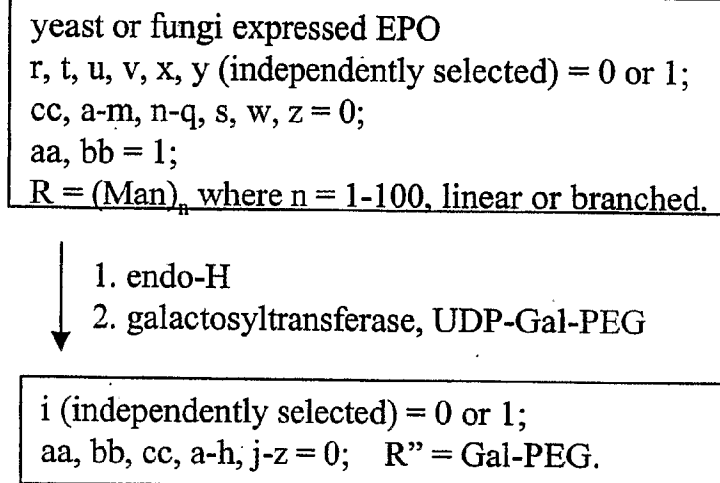


FIG. 35U

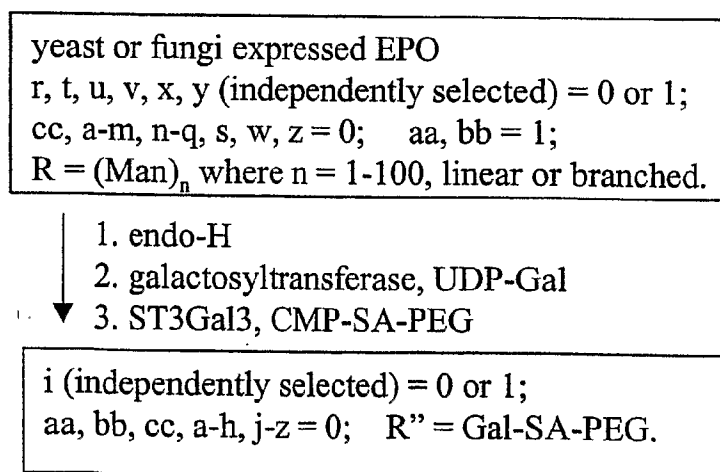


FIG. 35V

120/498

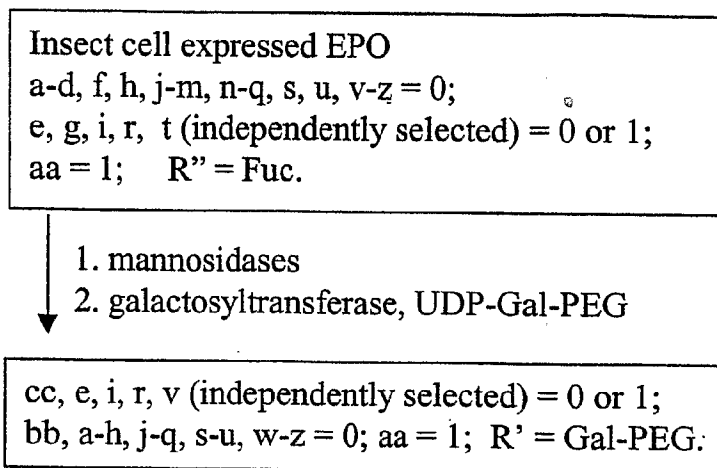


FIG. 35W

121/498

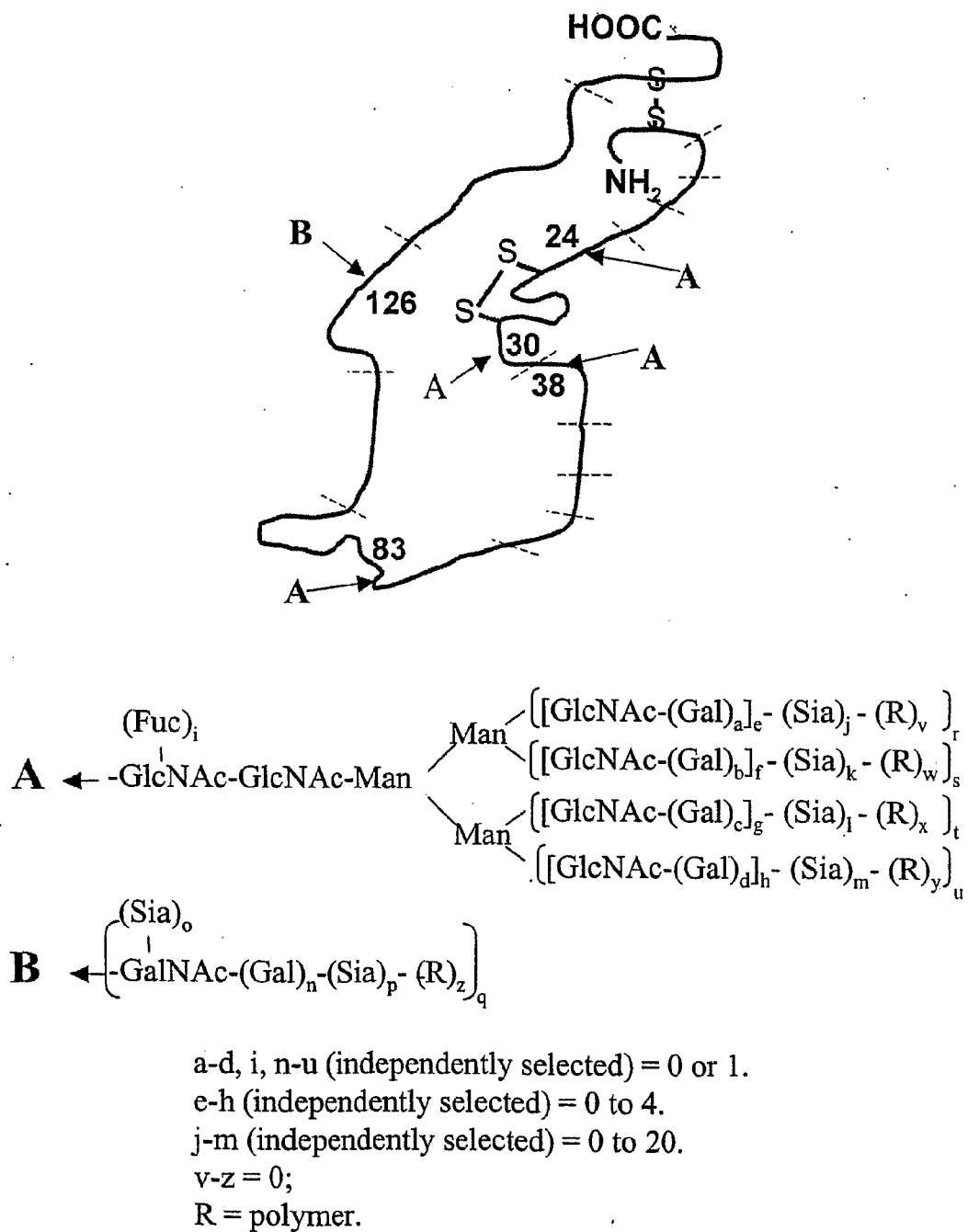


FIG. 35X

122/498

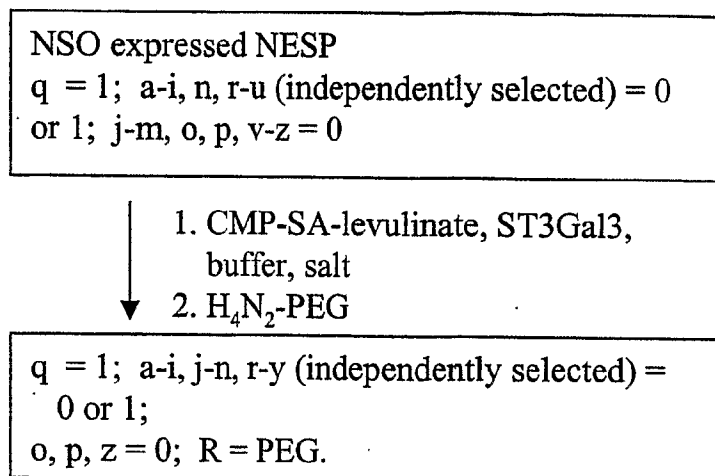


FIG. 35Y

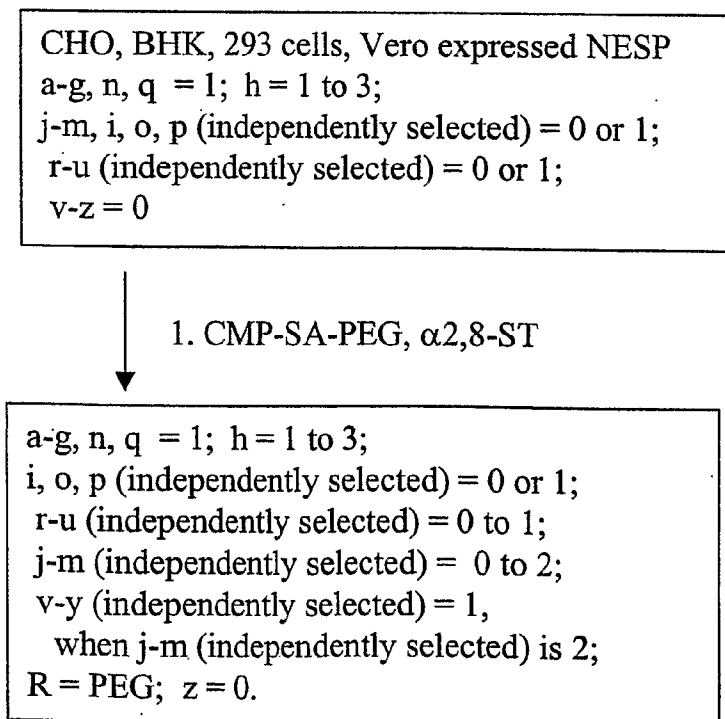


FIG. 35Z

123/498

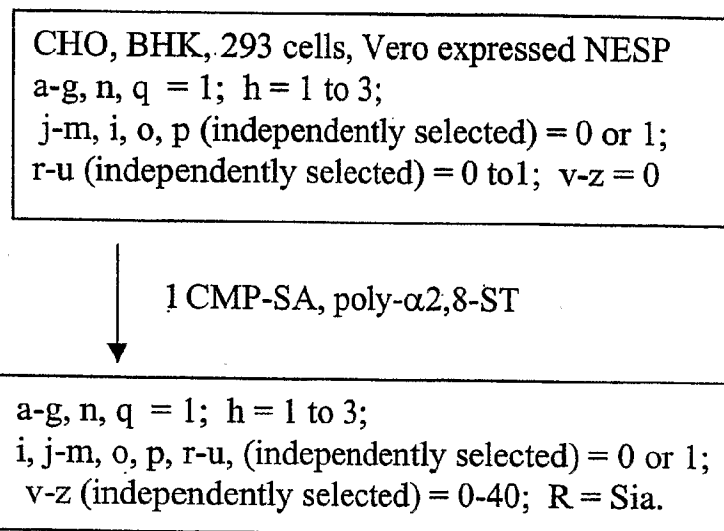
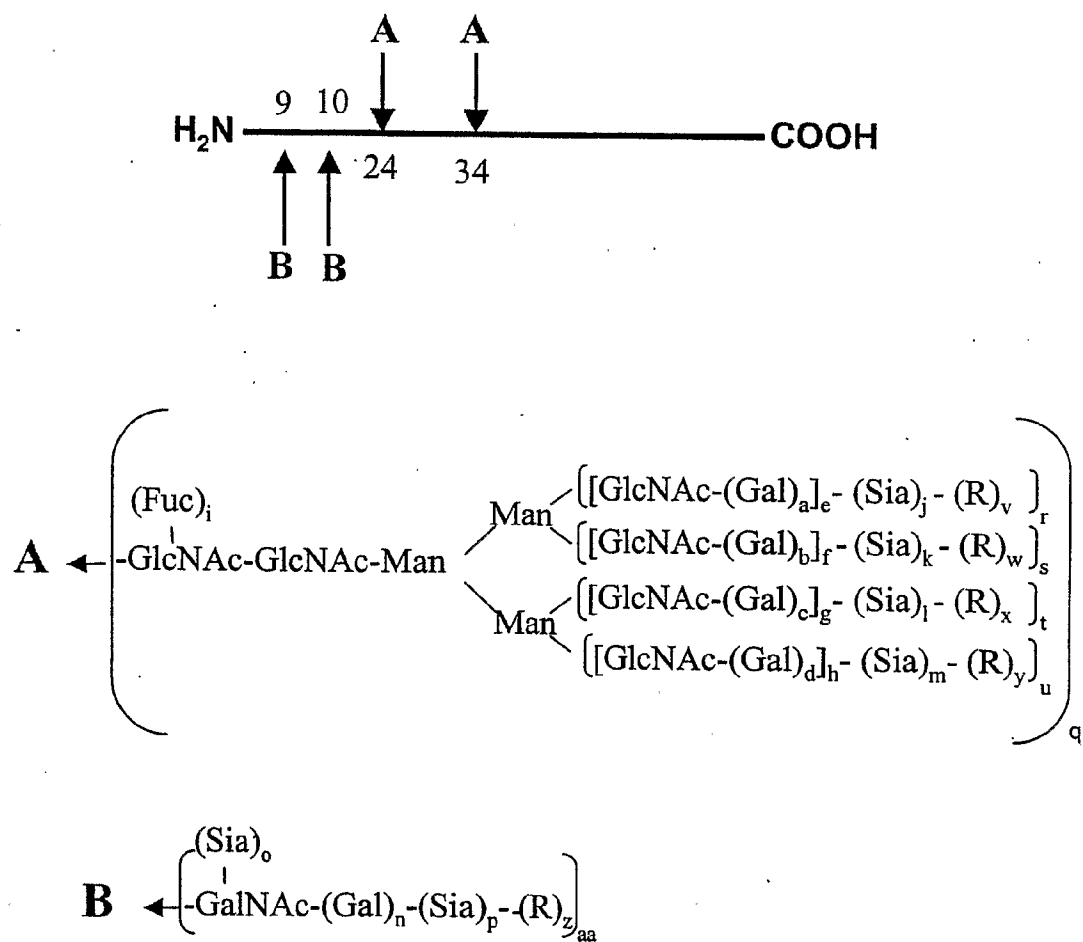


FIG. 35AA

124/498



a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 36A



125/498

CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;  
o, p, z = 0; n, e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 36B

CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3 &  
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;  
o, z = 0; n, e-h = 1;  
v-y (independently selected) = 0 or 1; R = PEG.

FIG. 36C

126/498

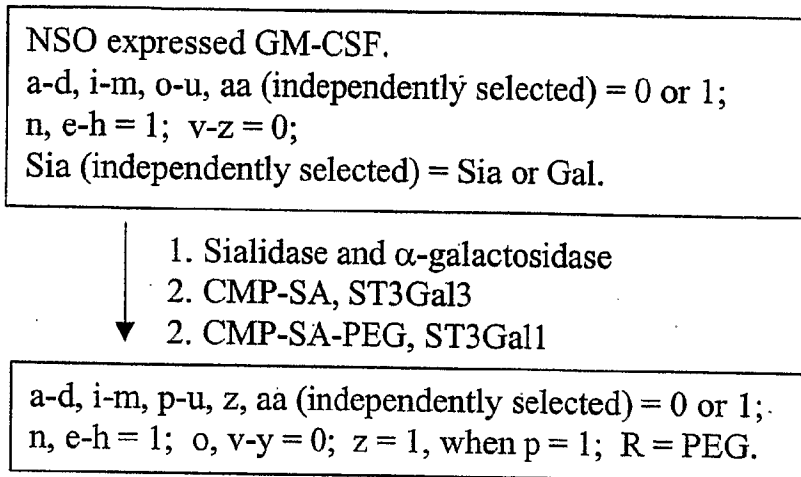


FIG. 36D

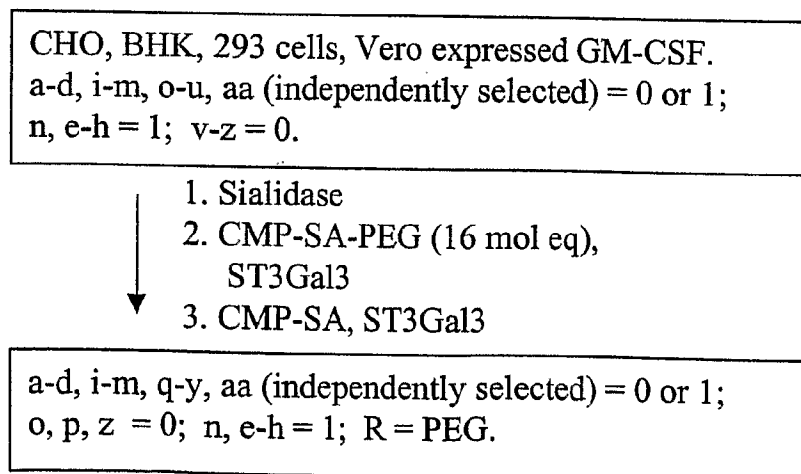


FIG. 36E

127/498

CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt  
2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;  
z = 0; n, e-h = 1; R = PEG.

FIG. 36F

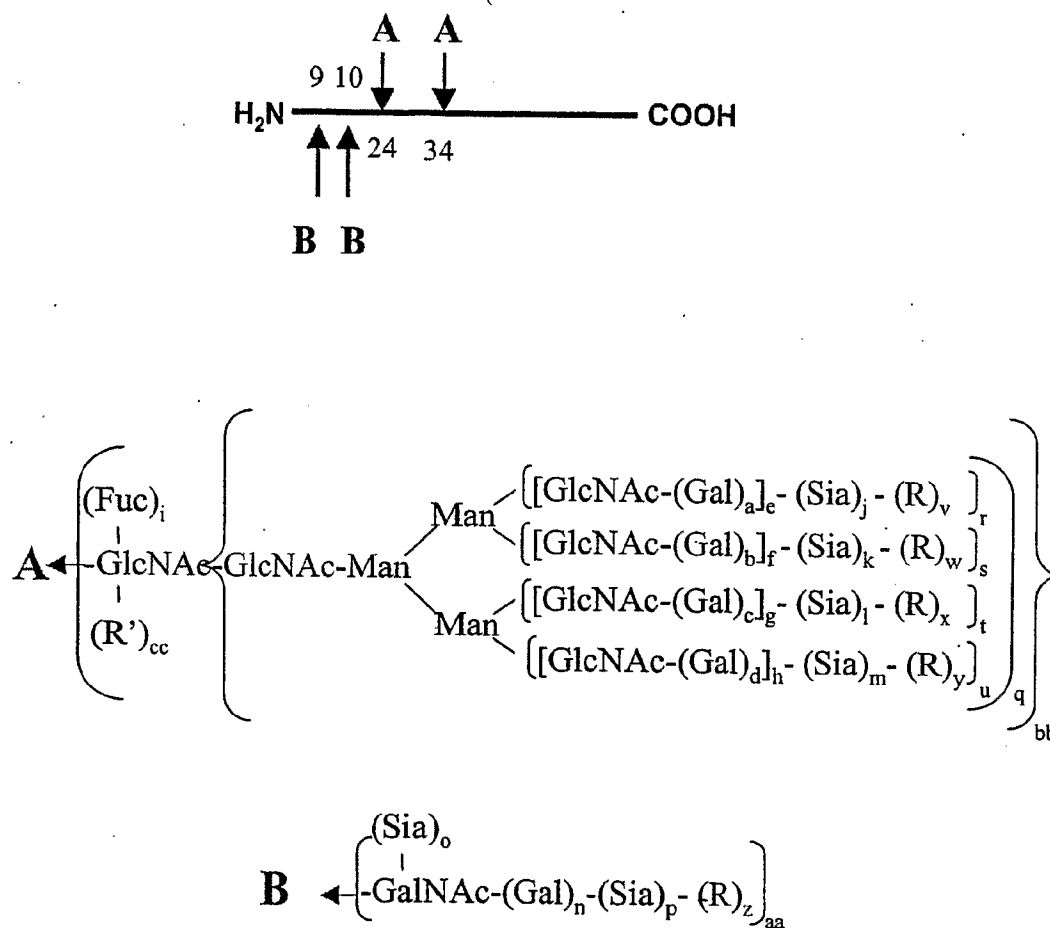
CHO, BHK, 293 cells, Vero expressed GMCSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; j-m (independently selected) = 0-20;  
v-z (independently selected) = 0.

FIG. 36G

128/498



a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

**v-y = 0; R = modifying group, mannose, oligo-mannose.**

R' = H, glycosyl residue, modifying group. glycoconjugate.

FIG. 36H

129/498

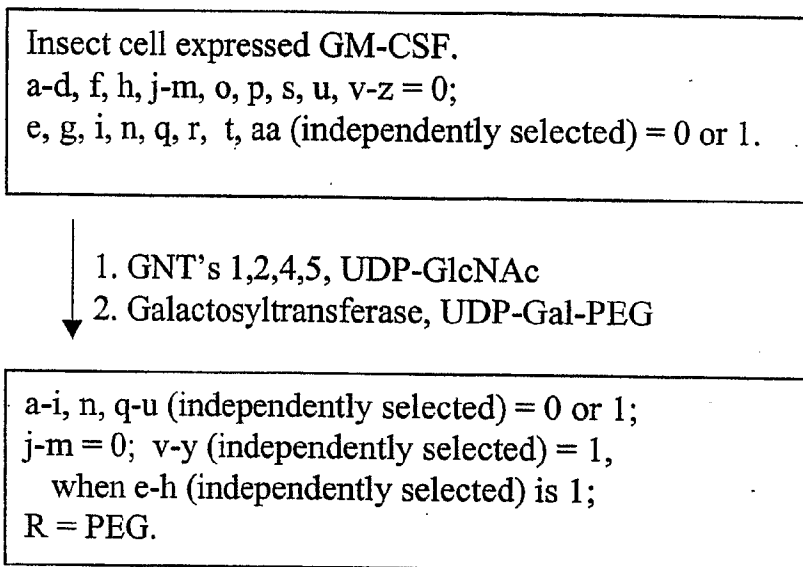


FIG. 36I

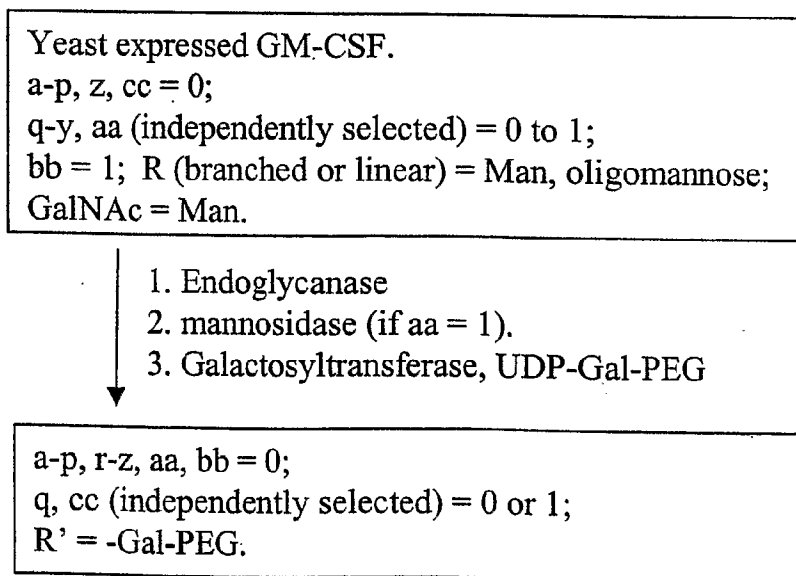


FIG. 36J

130/498

CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a--m, o-u, aa, bb (independently selected) = 0 or 1;  
n, v-z, cc = 0.

- ↓
1. sialidase
  2. CMP-SA, ST3Gal3
  2. CMP-SA-linker-SA-CMP, ST3Gal1
  3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;  
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 36K



132/498

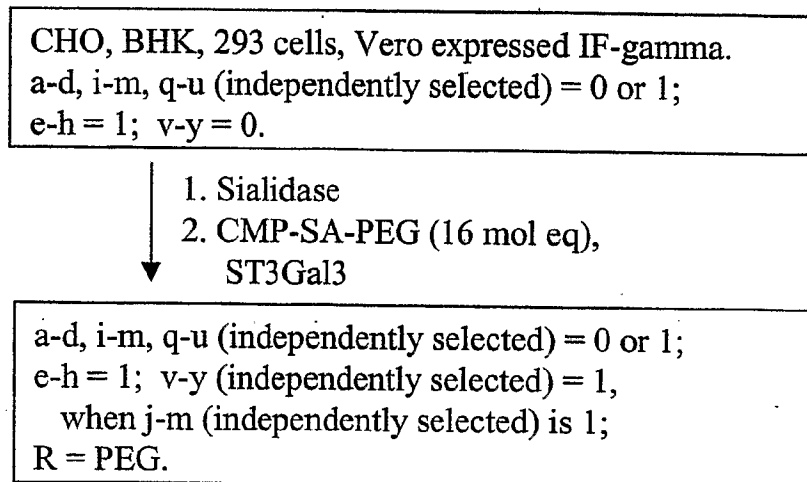


FIG. 37B

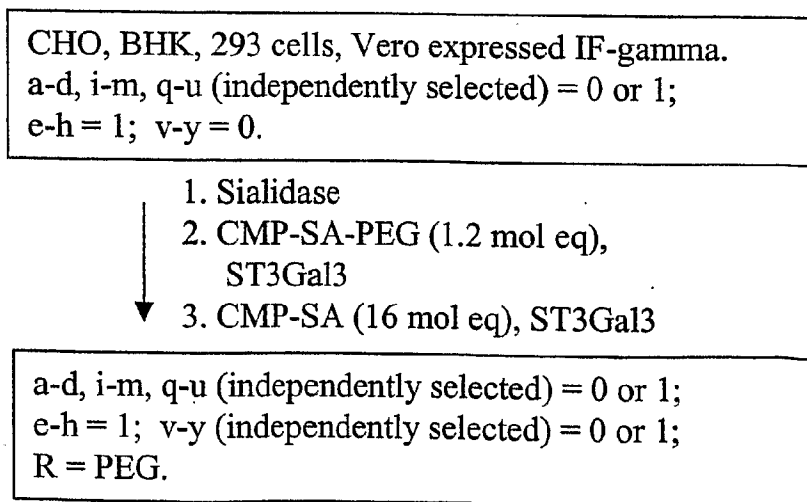


FIG. 37C



133/498

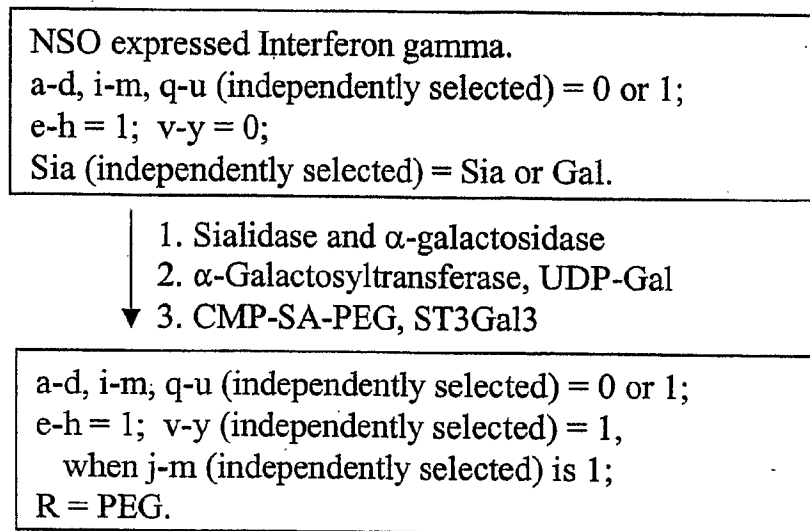


FIG. 37D

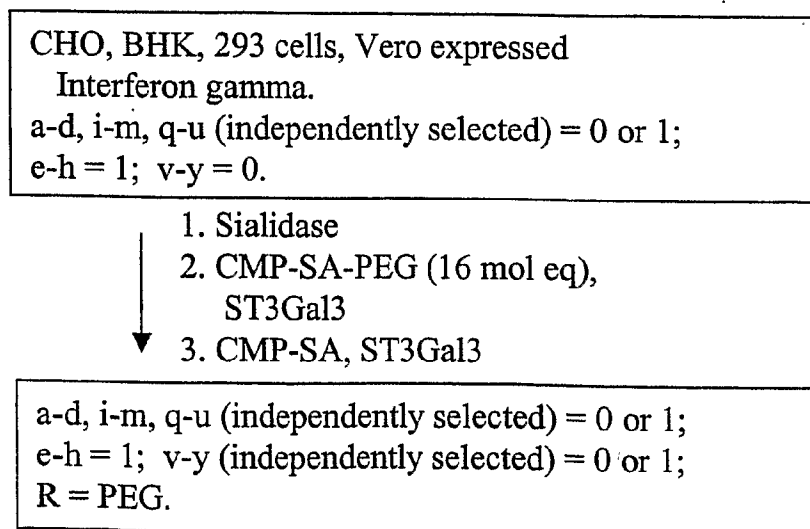


FIG. 37E

134/498

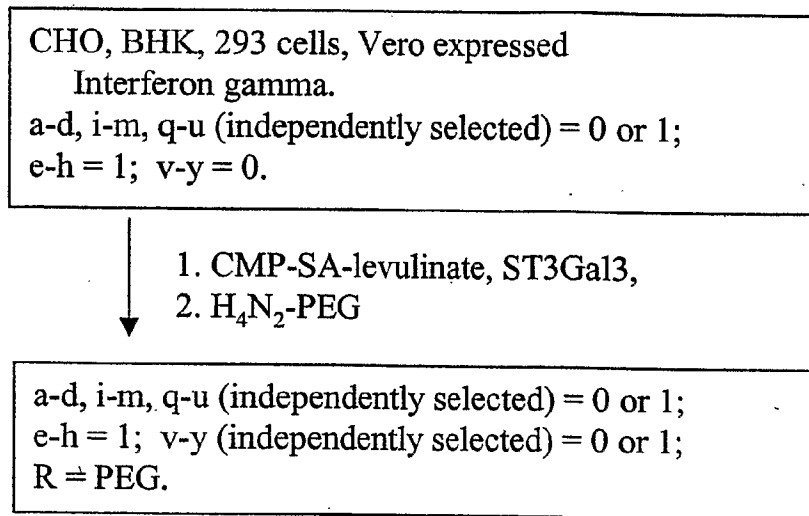


FIG. 37F

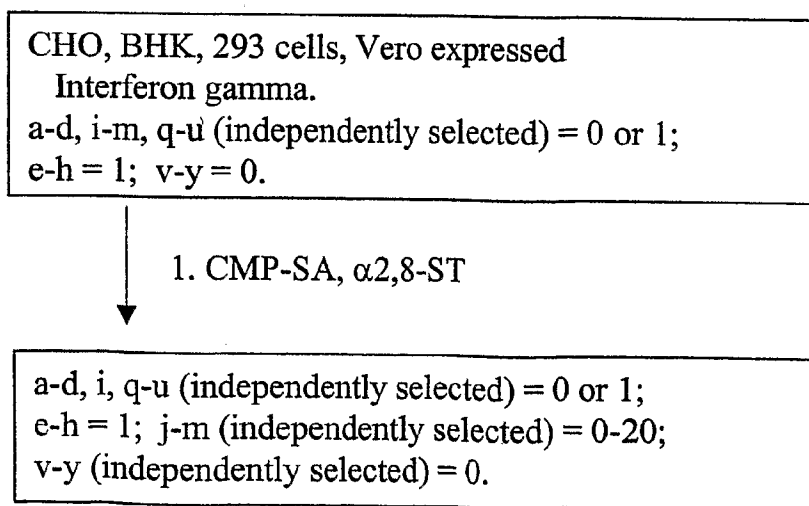
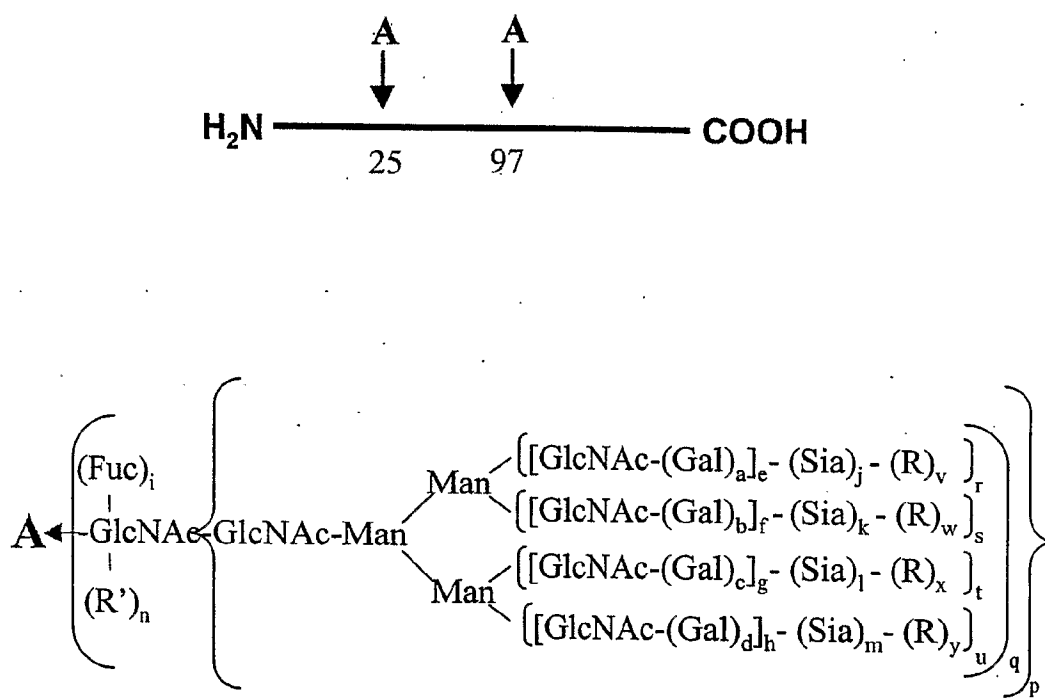


FIG. 37G

135/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 37H

136/498

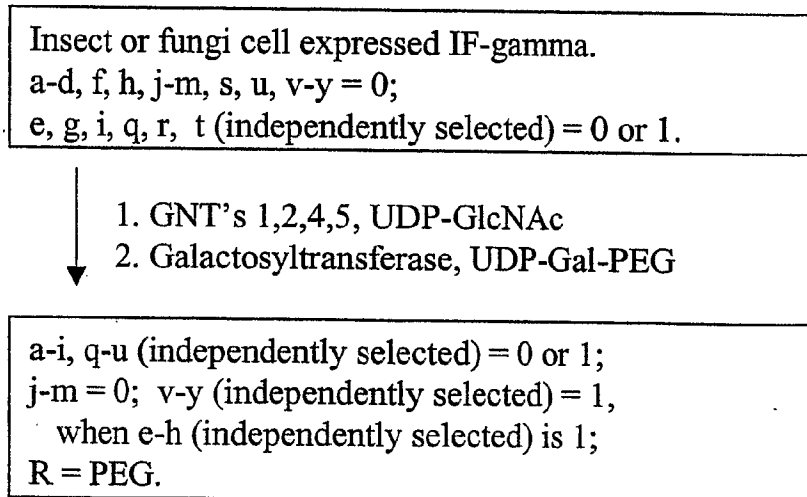


FIG. 37I

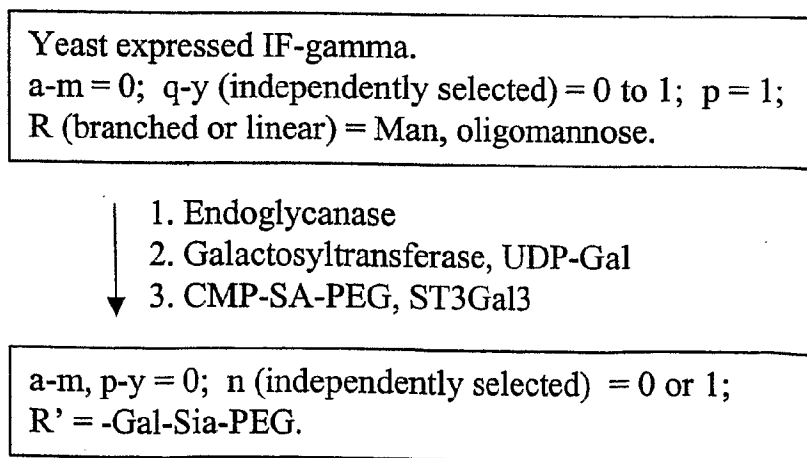


FIG. 37J

137/498

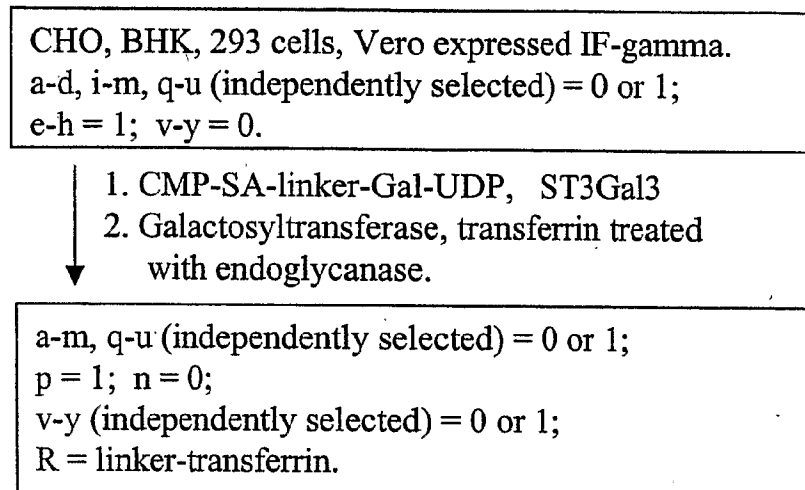


FIG. 37K

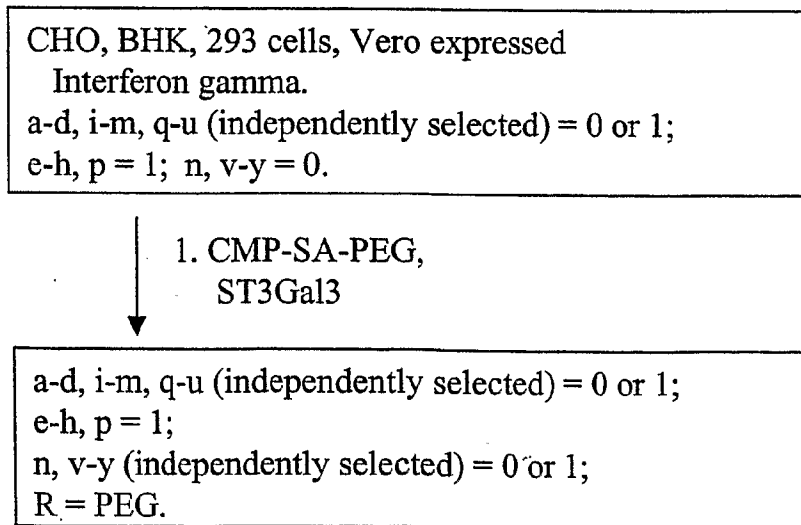


FIG. 37L

138/498

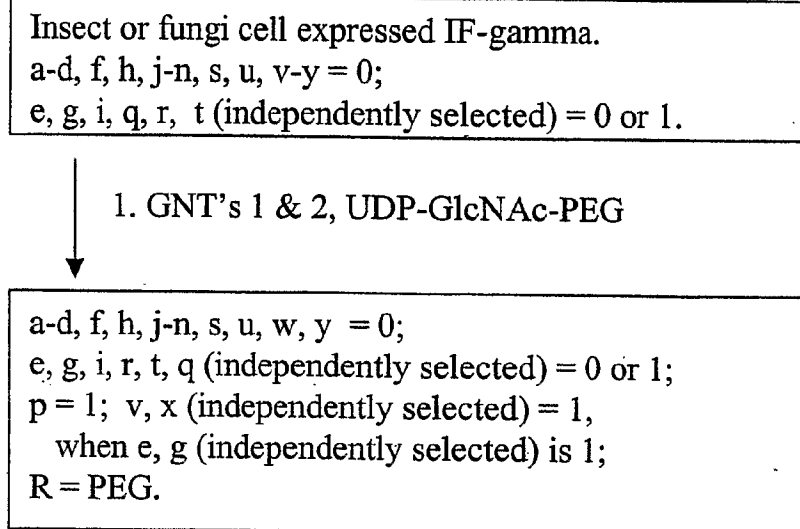


FIG. 37M

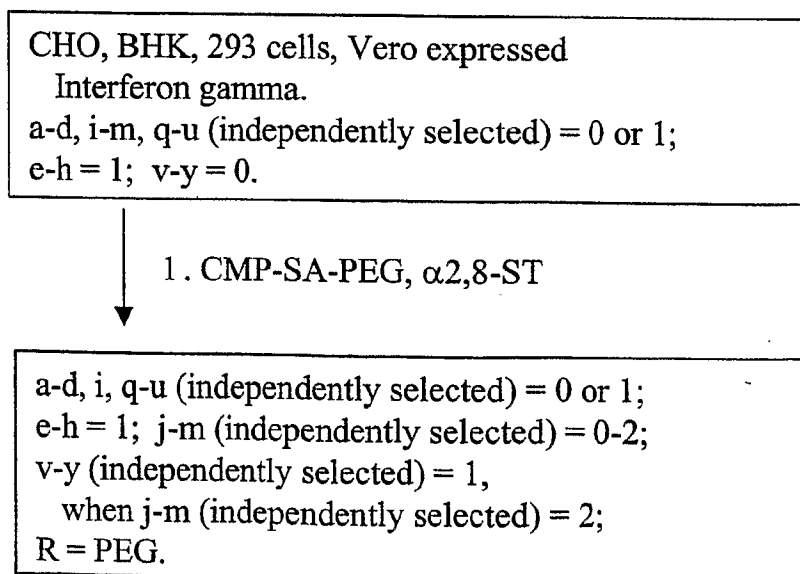
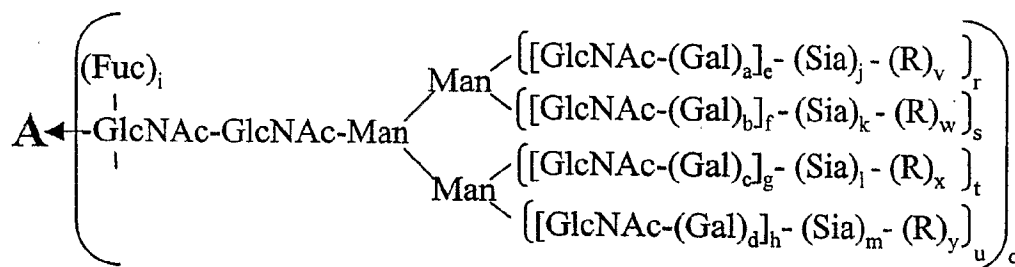
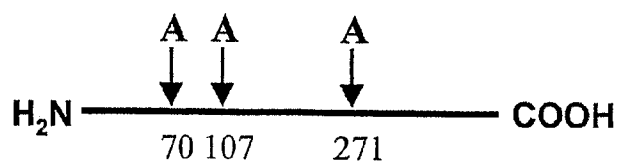


FIG. 37N

139/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 38A

140/498

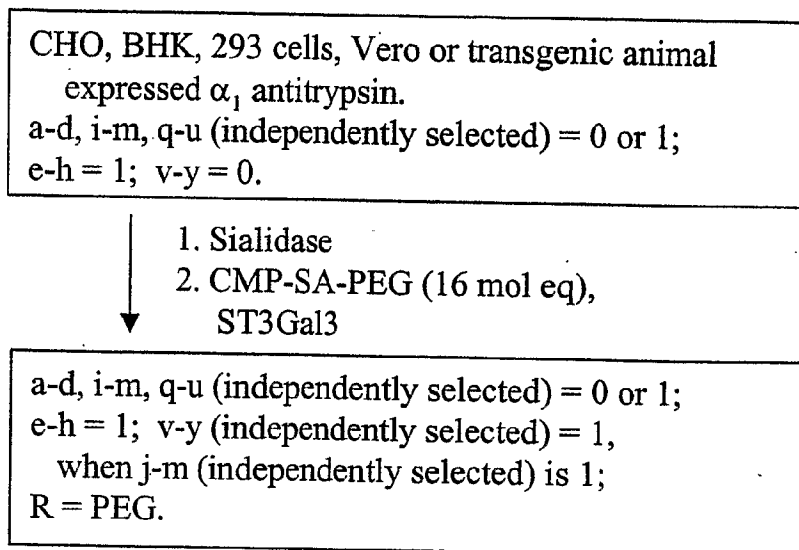


FIG. 38B

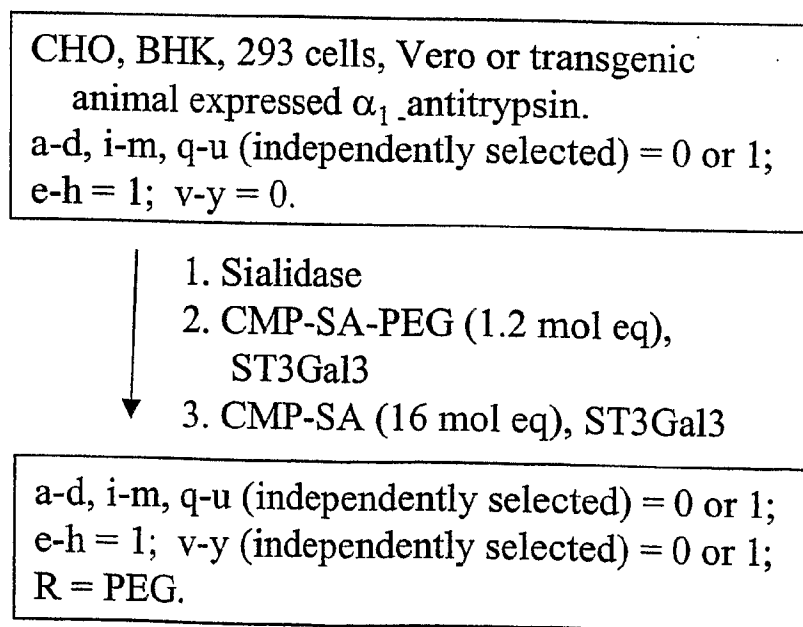


FIG. 38C



141/498

CHO, BHK, 293 cells, Vero or transgenic animal  
expressed alpha-1 antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 38D

CHO, BHK, 293 cells, Vero or transgenic animal  
expressed  $\alpha_1$ -antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  - ▼ 2.  $H_4N_2$ -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 38E

142/498

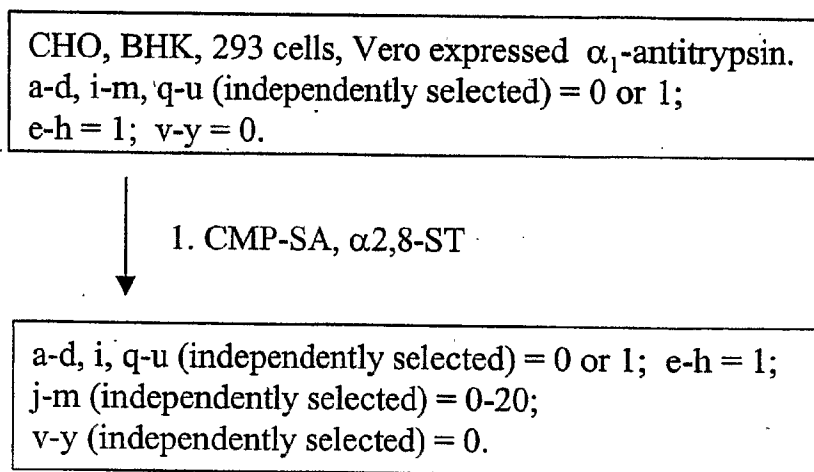
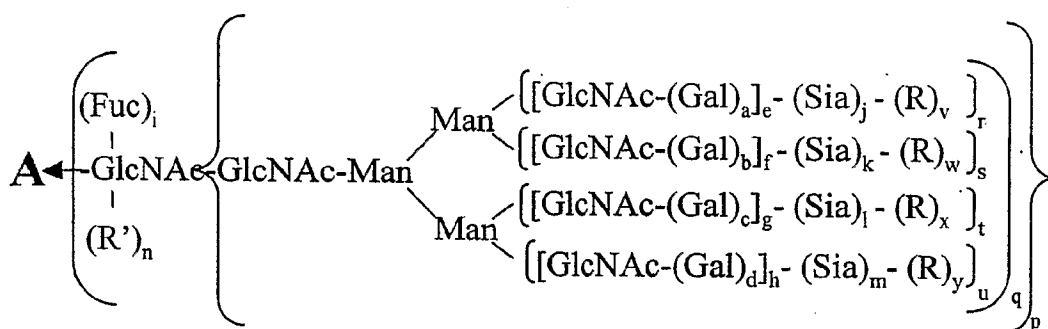
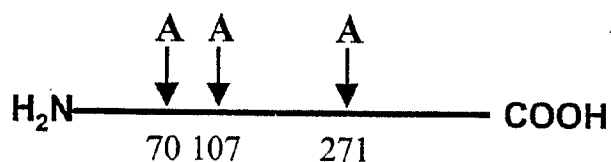


FIG. 38F

143/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

$$v-y=0;$$

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

**FIG. 38G**

144/498

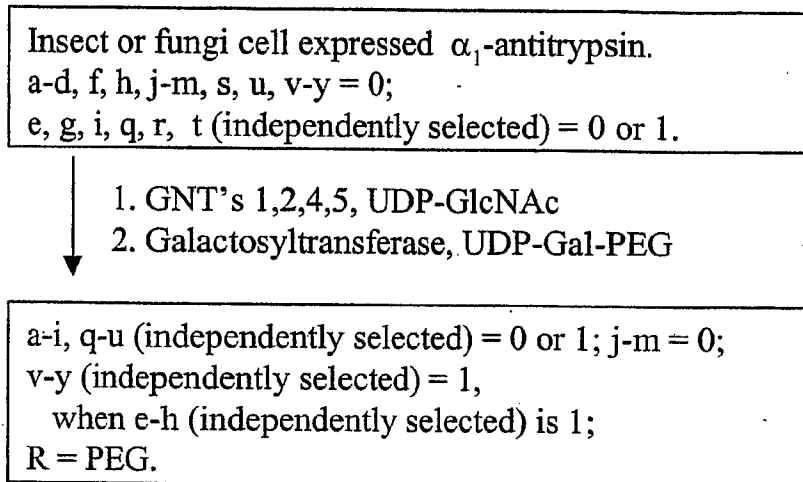


FIG. 38H

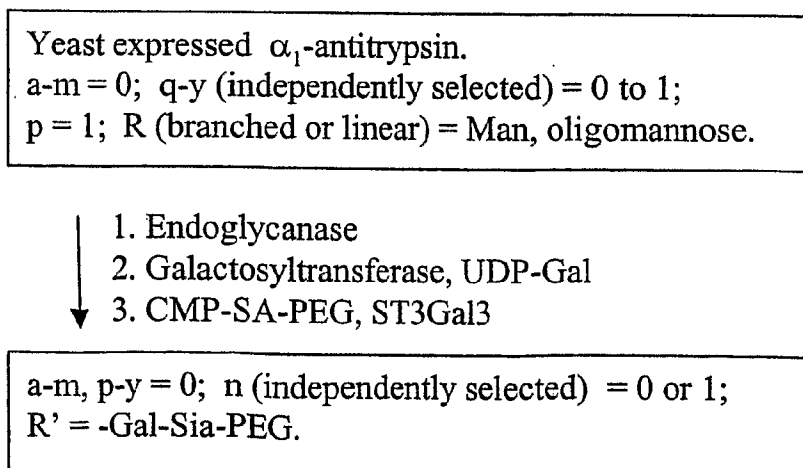


FIG. 38I

145/498

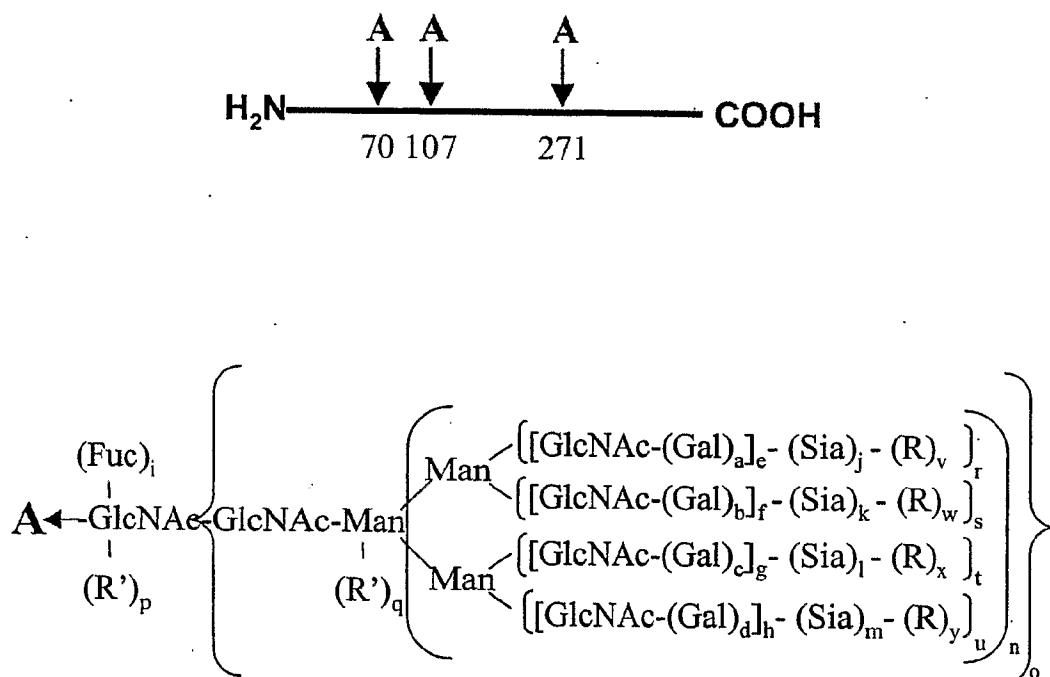
CHO, BHK, 293 cells, Vero expressed  $\alpha_1$ -antitrypsin.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, transferrin treated  
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 38J

146/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 38K

147/498

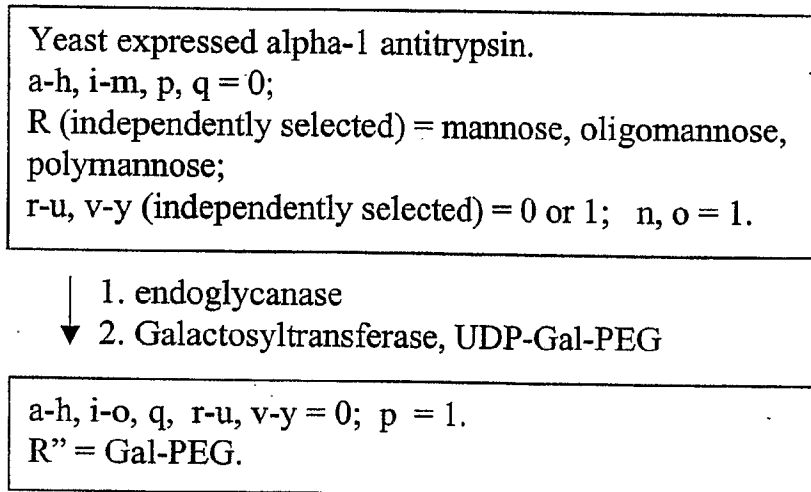


FIG. 38L

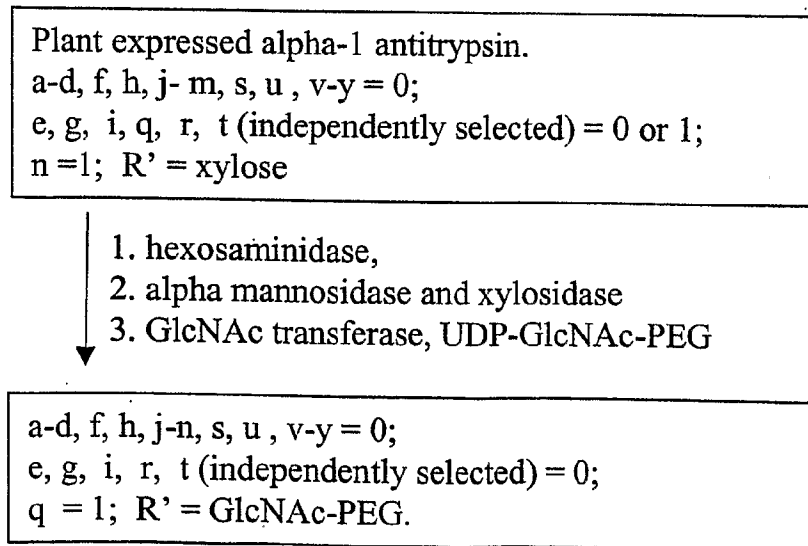


FIG. 38M

148/498

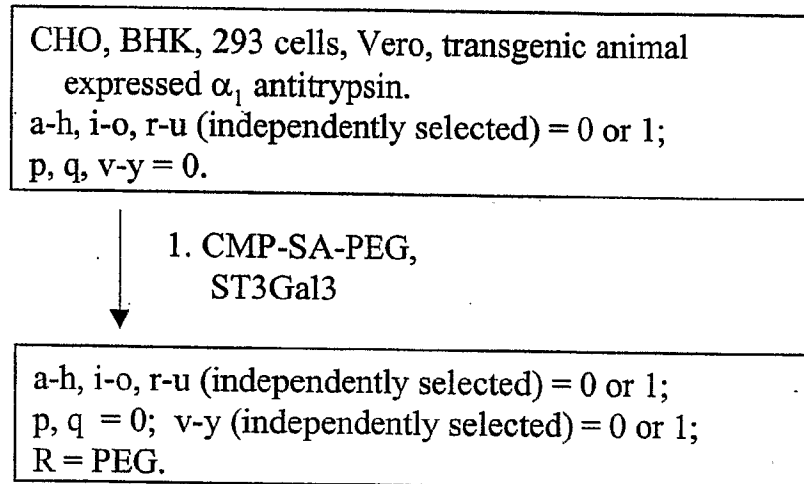
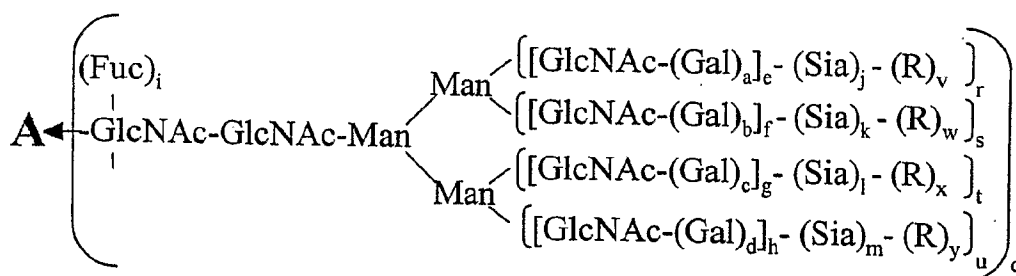
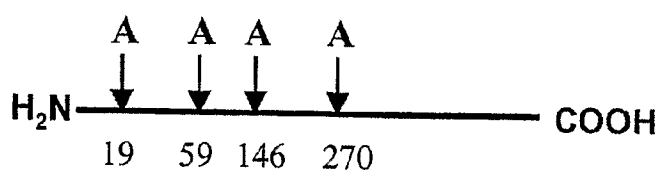


FIG. 38N



149/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 39A

150/498

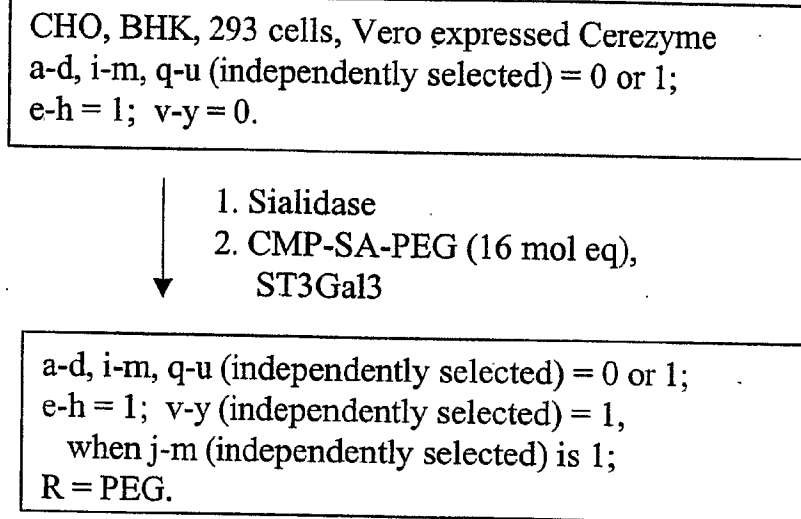


FIG. 39B

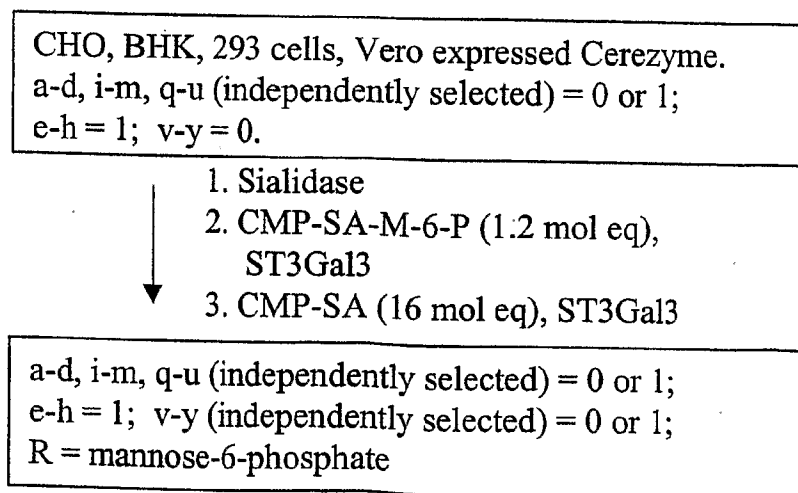


FIG. 39C

151/498

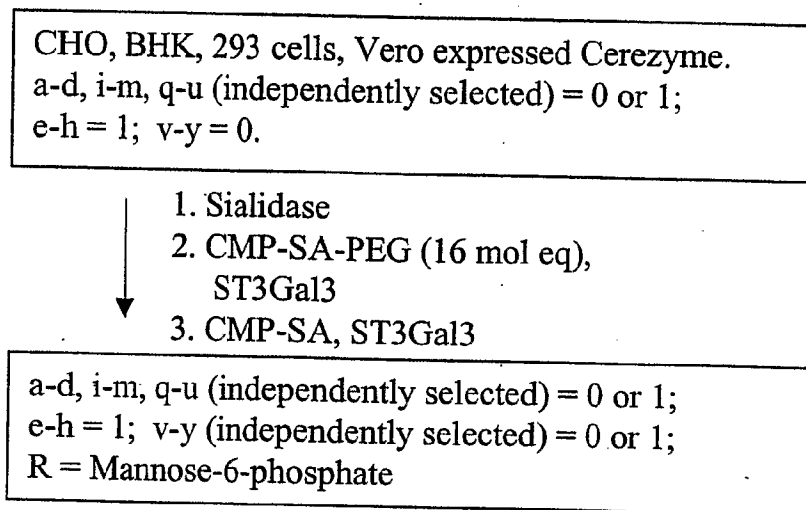


FIG. 39D

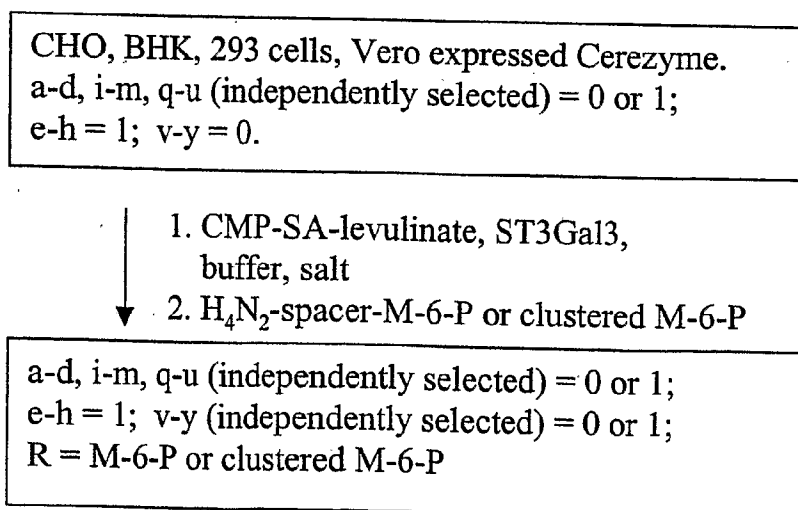


FIG. 39E

152/498

CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 39F

153/498

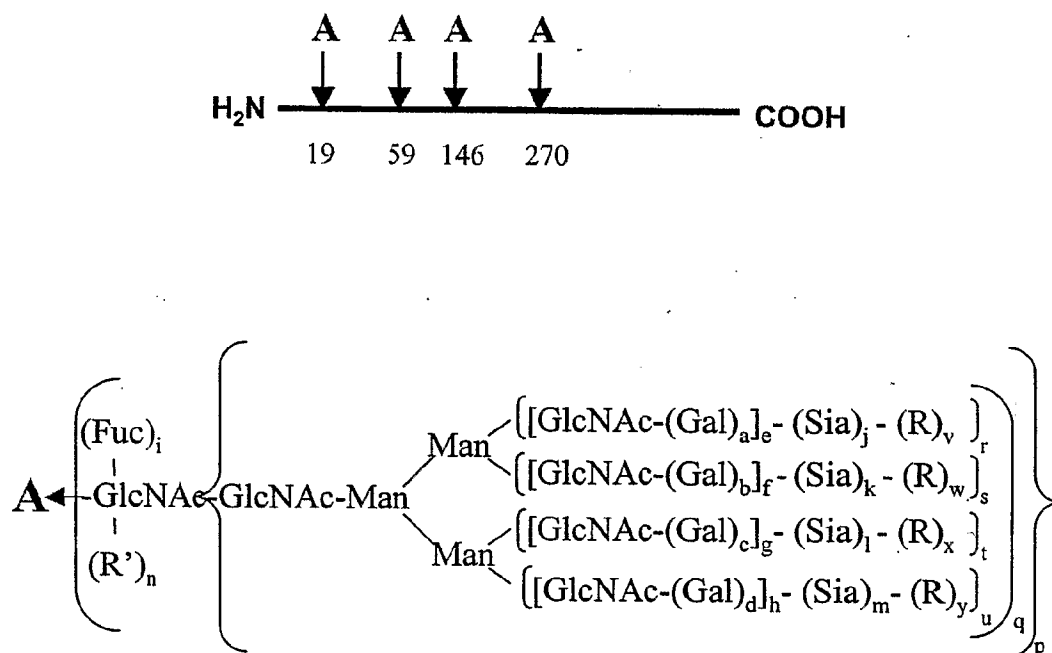


FIG. 39G

154/498

Insect cell expressed Cerezyme.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 39H

Yeast expressed Cerezyme.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3


a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 39I

155/498

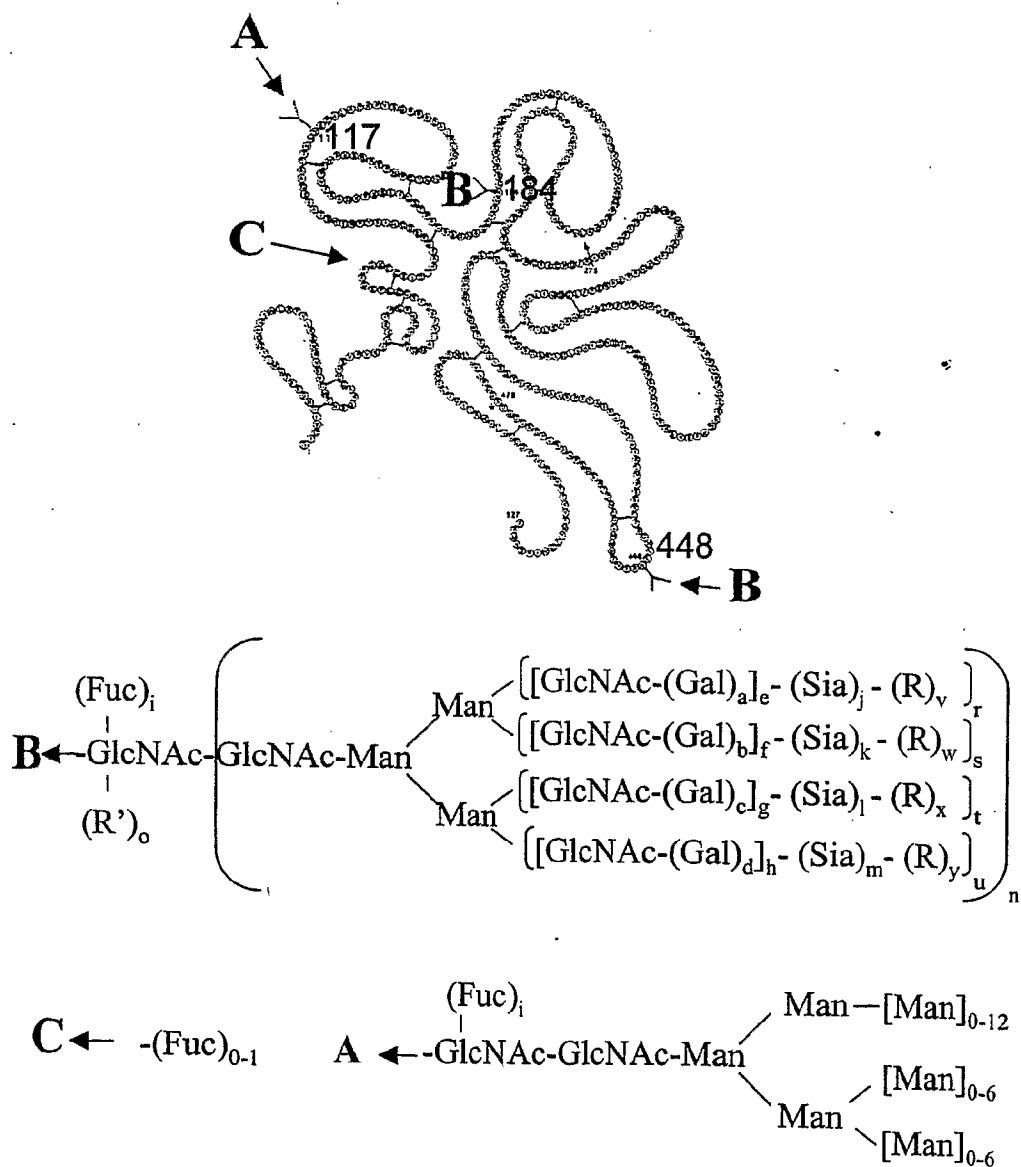
CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- 
1. CMP-SA-linker-SA-CMP,  
ST3Gal3
  2. ST3Gal3, desialylated transferrin.
  3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0; v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 39J

156/498



a-d, i, n-u (independently selected) = 0 or 1.  
e-h (independently selected) = 0 to 4.  
j-m (independently selected) = 0 to 20.  
R = polymer; R' = sugar, glycoconjugate.

**FIG. 40A**



157/498

CHO, BHK, 293 cells, Vero expressed tPA  
 a-g, n = 1; h = 1 to 3;  
 j-m, i, (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;  
 i, r-u (independently selected) = 0 or 1;  
 o = 0; j-m, v-y (independently selected) = 0 or 1;  
 R = PEG

FIG. 40B

Insect or fungi cell expressed tPA  
 A = B; a-d, f, h, j-o, s, u, v-y = 0;  
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;  
 a, c, e, g, i, r, t (independently selected) = 0 or 1;  
 n = 1; j, l, v, x (independently selected) = 0 or 1;  
 R = PEG.

FIG. 40C

158/498

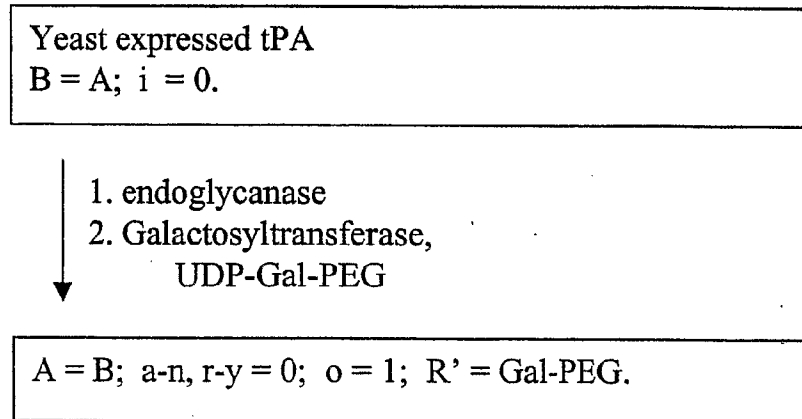


FIG. 40D

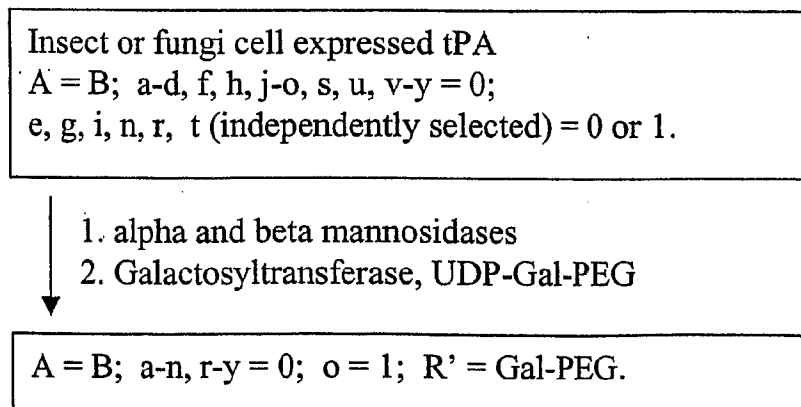


FIG. 40E

159/498

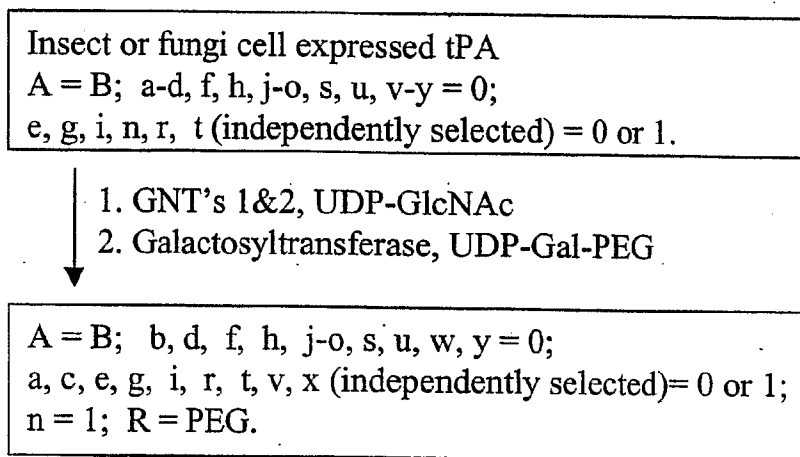


FIG. 40F

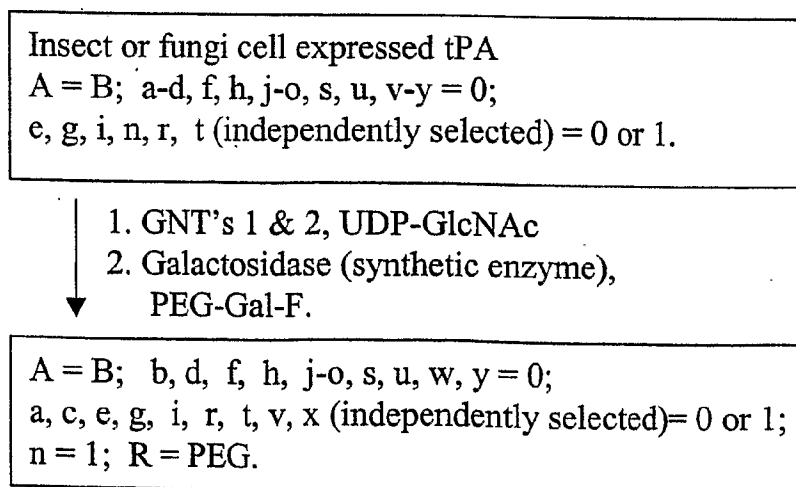
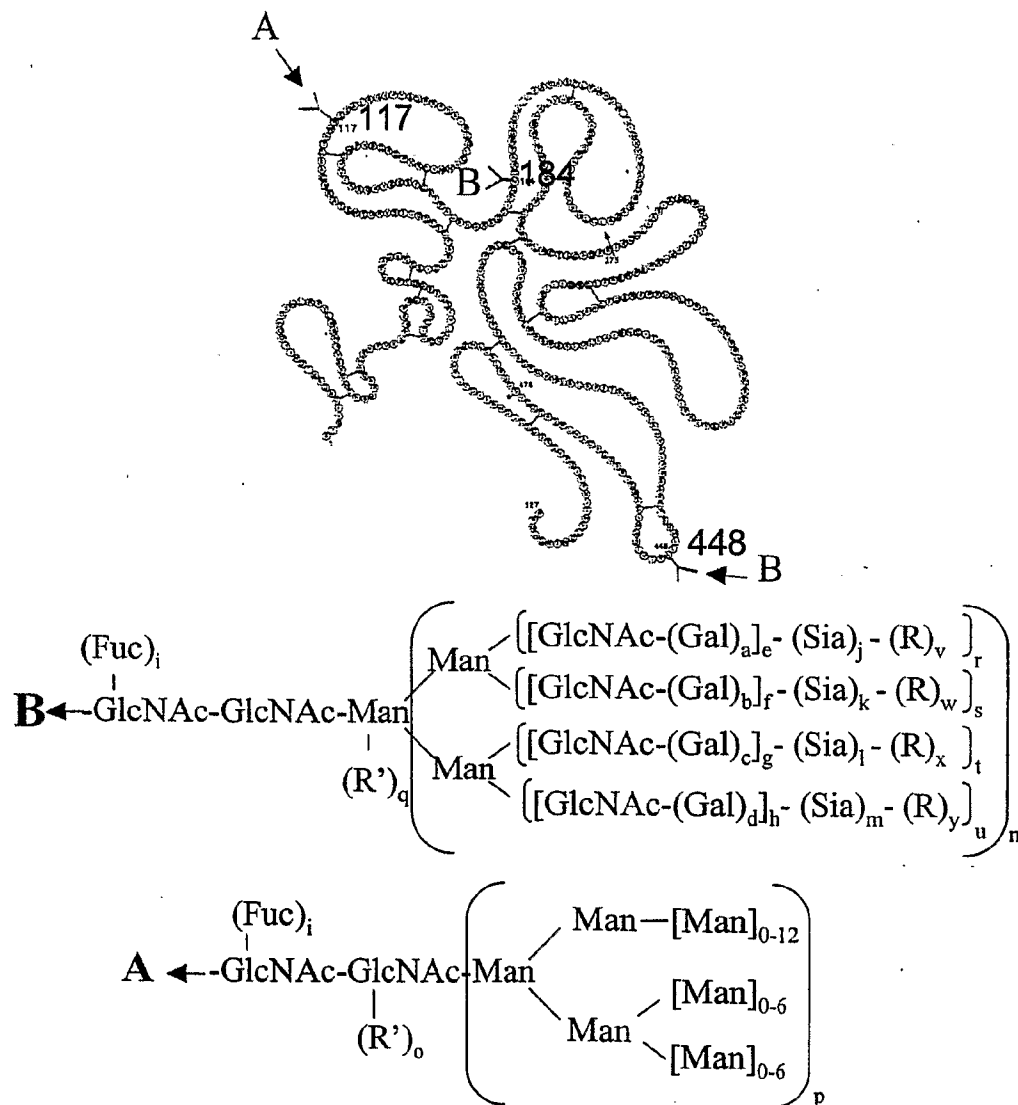


FIG. 40G

160/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40H

161/498

NSO expressed tPA

A = B; a-m, r-u (independently selected) = 0 or 1;  
n = 1; o, p, q, v-y = 0

1. sialidase, alpha-galactosidase
2. CMP-SA-levulinate, ST3Gal3,
3. H<sub>4</sub>N<sub>2</sub>-PEG

A = B; a-m, r-y (independently selected) = 0 or 1;  
n = 1; o, p, q = 0;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 40I

CHO, BHK, 293 cells, Vero expressed tPA

a-g, n, p = 1; h = 1 to 3;  
j-m, i, (independently selected) = 0 or 1;  
r-u (independently selected) = 0 to 1; q, o, v-y = 0.

1. alpha and beta Mannosidases
2. CMP-SA, ST3Gal3
3. Galactosyltransferase, UDP-Gal-PEG

a-g, n = 1; h = 1 to 3;  
i, r-u (independently selected) = 0 or 1; o = 1;  
q, p, v-y = 0; j-m (independently selected) = 0 or 1;  
R' = Gal-PEG

FIG. 40J

162/498

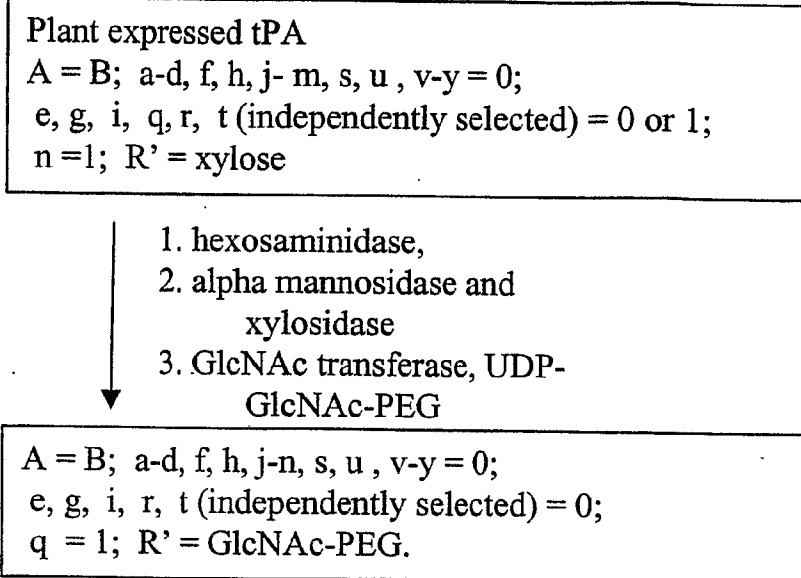
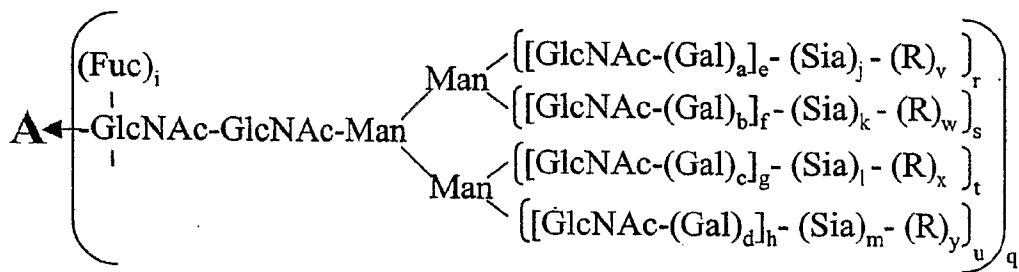
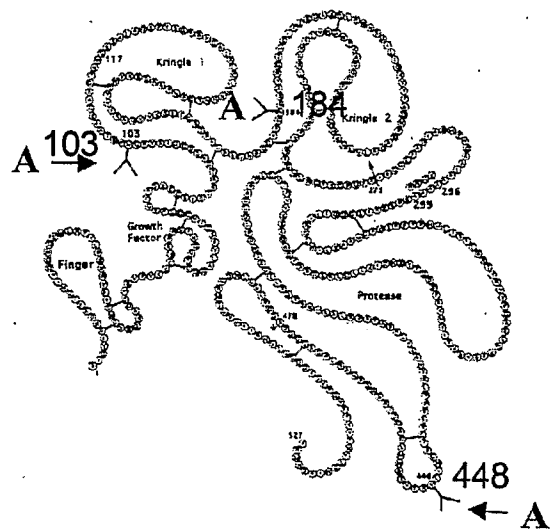


FIG. 40K

163/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40L

164/498

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 40M

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40N



165/498

NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 400



167/498

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40Q

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40R

168/498

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

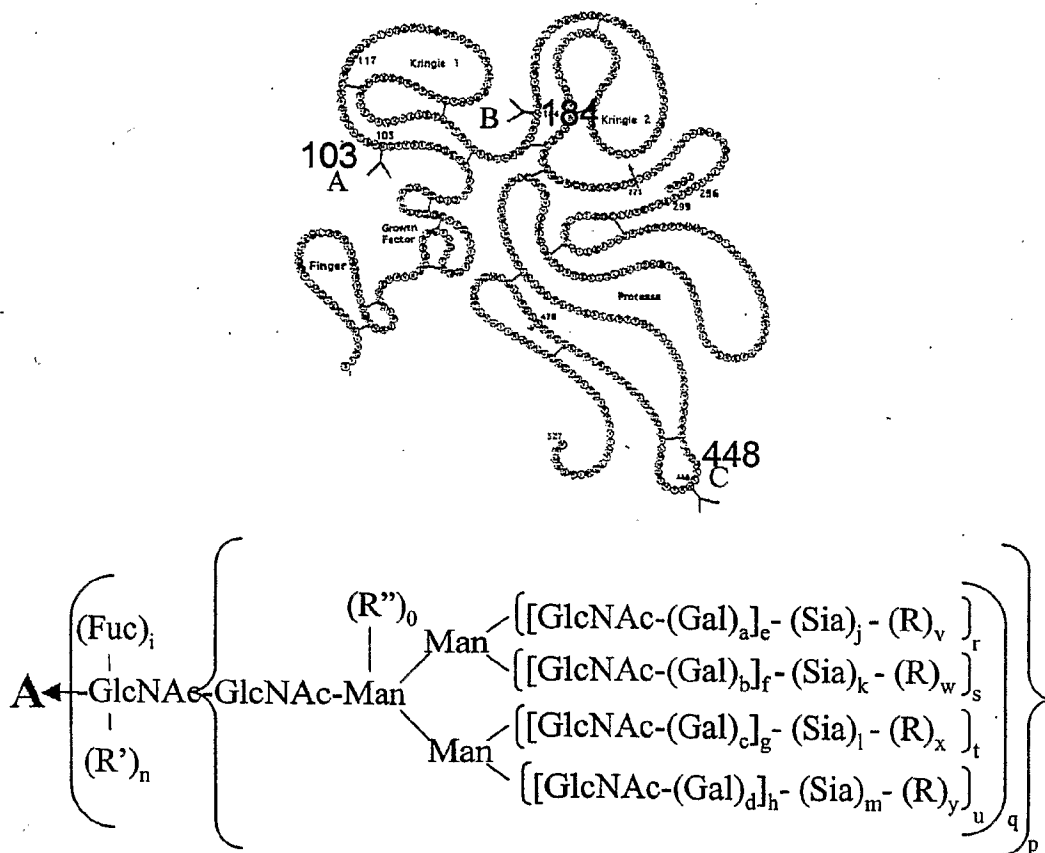


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 40S

169/498



a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 40T

170/498

Insect cell expressed TNK tPA

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 40U

Yeast expressed TNK tPA

a-m = 0; q-y (independently selected) = 0 to 1; p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal-PEG

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 40V

171/498

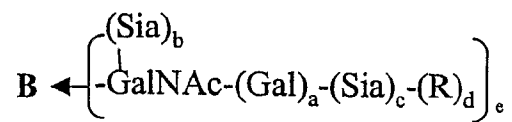
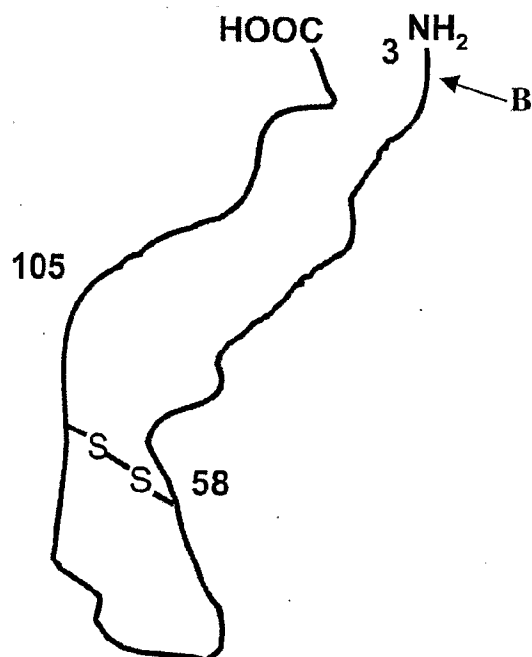
CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, anti-TNF  
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;  
n = 0; v-y (independently selected) = 0 or 1;  
R = linker-anti-TNF IG chimera protein.

FIG. 40W

172/498



a-c, e (independently selected) = 0 or 1;  
d = 0;

R = modifying group, mannose, oligo-  
mannose.

FIG. 41A



173/498

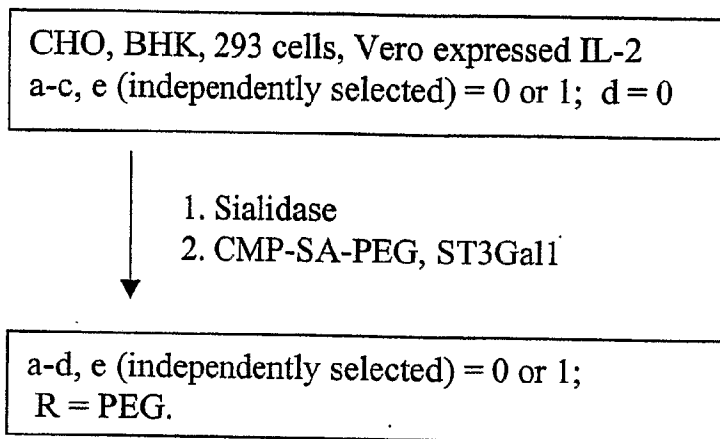


FIG. 41B

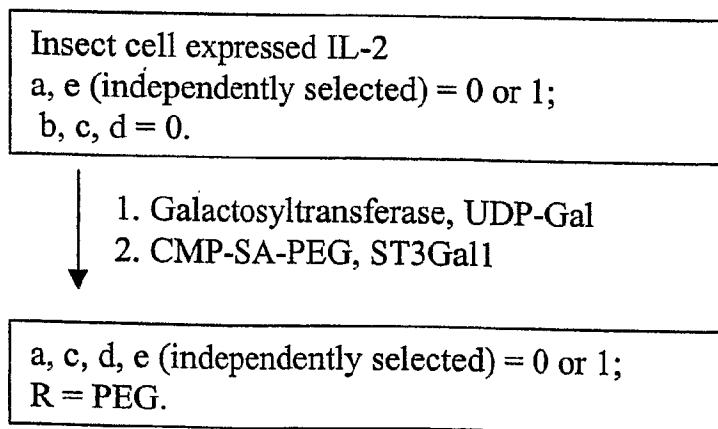


FIG. 41C

174/498

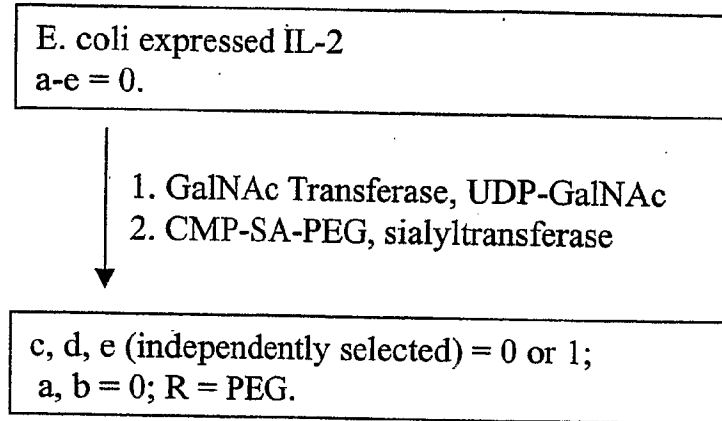


FIG. 41D

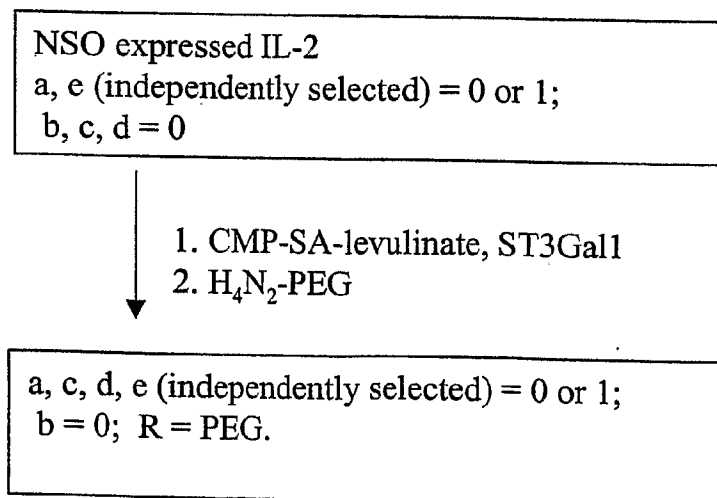


FIG. 41E

175/498

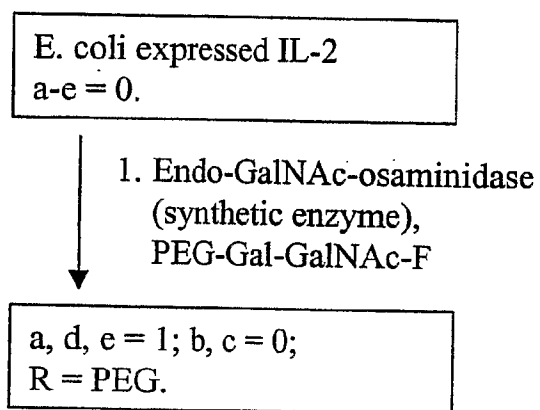


FIG. 41F

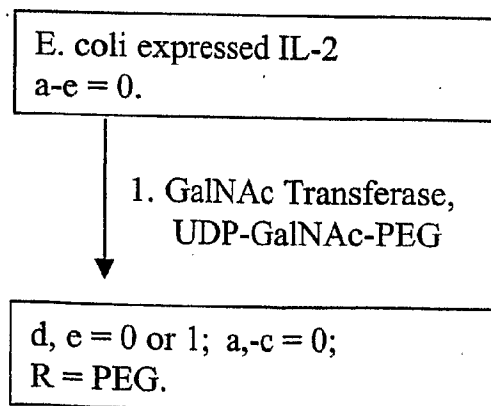
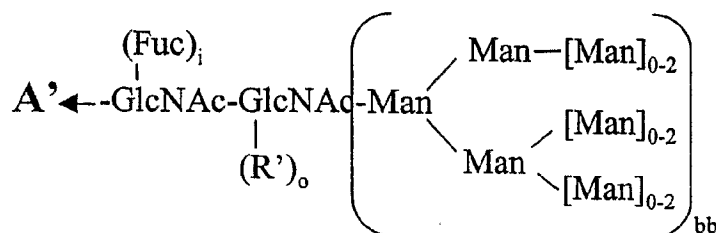
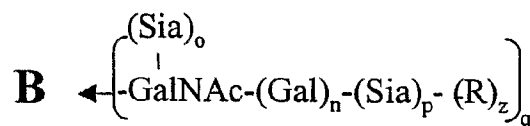
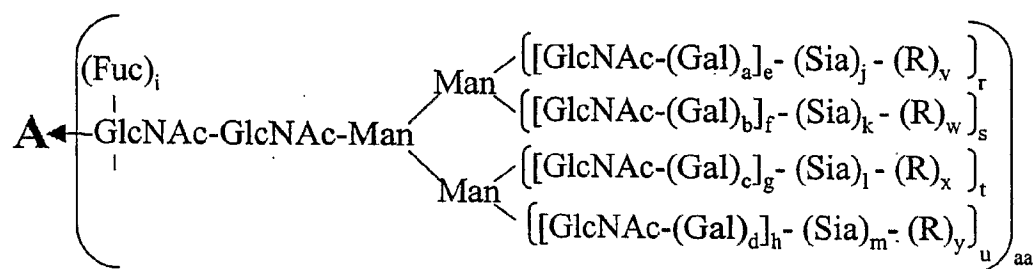


FIG. 41G

176/498

2 peptides  
 A and A' - N-linked sites  
 B - O-linked sites



Alternate structure  
 for some N-linked  
 structures of A.

a-d, i, n-u (independently selected) = 0 or 1.  
 aa, bb (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 6.  
 j-m (independently selected) = 0 to 20.  
 v-z = 0; R = polymer, glycoconjugate.

FIG. 42A

177/498

CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed  
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓  
1. Sialidase  
2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓  
1. Sialidase  
2. CMP-SA-PEG, ST3Gal3  
3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42C

178/498

CHO, BHK, 293s cells, Vero, MDCK, HEKC  
expressed Factor VIII.  
e-h = 1 to 4;  
aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;  
v-z = 0.

↓  
1. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;  
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;  
z = 0; j-m, v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 42D

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.  
e-h = 1 to 4;  
aa, bb, a-d, j-m, i, n-u (independently selected) 0 or 1;  
v-z = 0.

↓  
1. CMP-SA-PEG, ST3Gal1

e-h = 1 to 4;  
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;  
z = 0; j-m, v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 42E

179/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.



1. CMP-SA-PEG,  $\alpha$ 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

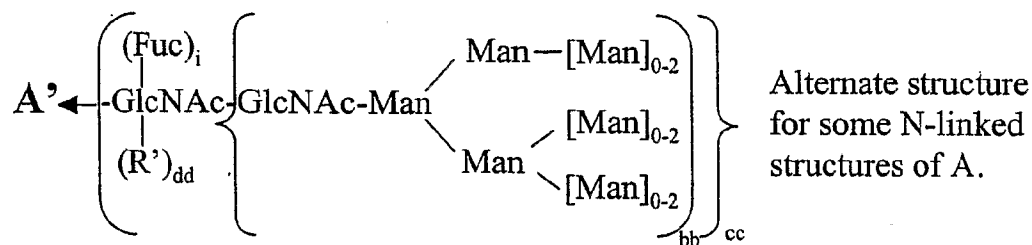
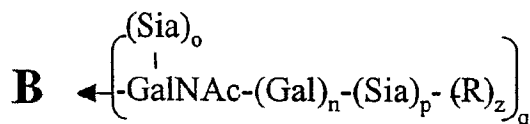
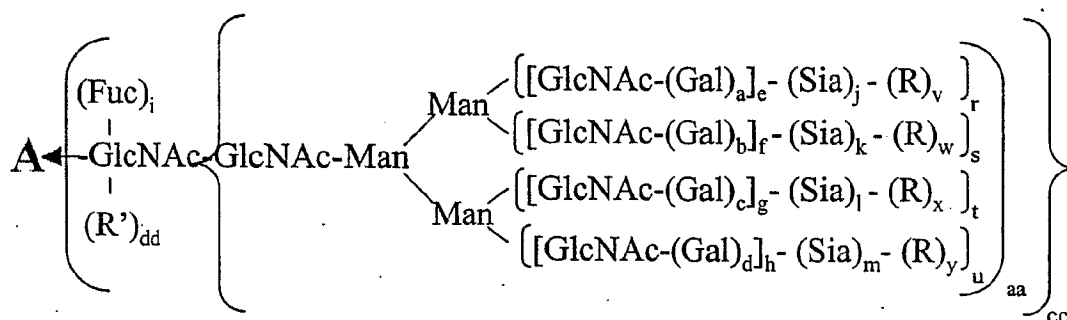
when j-m (independently selected) is 2;

R = PEG.

FIG. 42F

180/498

2 peptides

**A or A'** - N-linked sites**B** - O-linked sites

a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 42G



181/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓  
1. CMP-SA-levulinate, ST3Gal3,  
2. H<sub>4</sub>N<sub>2</sub>-PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;

dd, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42H

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓  
1. endo-H  
2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 42I

182/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC

expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
  2. endo-H
  3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 42J

CHO, BHK, 293S cells, Vero, MDCK, HEKC

expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
  2. GNT 1 & 2, UDP-GlcNAc
  3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0; R = PEG.

FIG. 42K

183/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

1. mannosidases
- ↓ 2. GNT-1, 2, 4 & 5; UDP-GlcNAc
- ↓ 3. galactosyltransferase, UDP-Gal
4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;

dd, v-z = 0.

FIG. 42L

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓ 1. mannosidases
- ↓ 2. GNT-1, UDP-GlcNAc-PEG

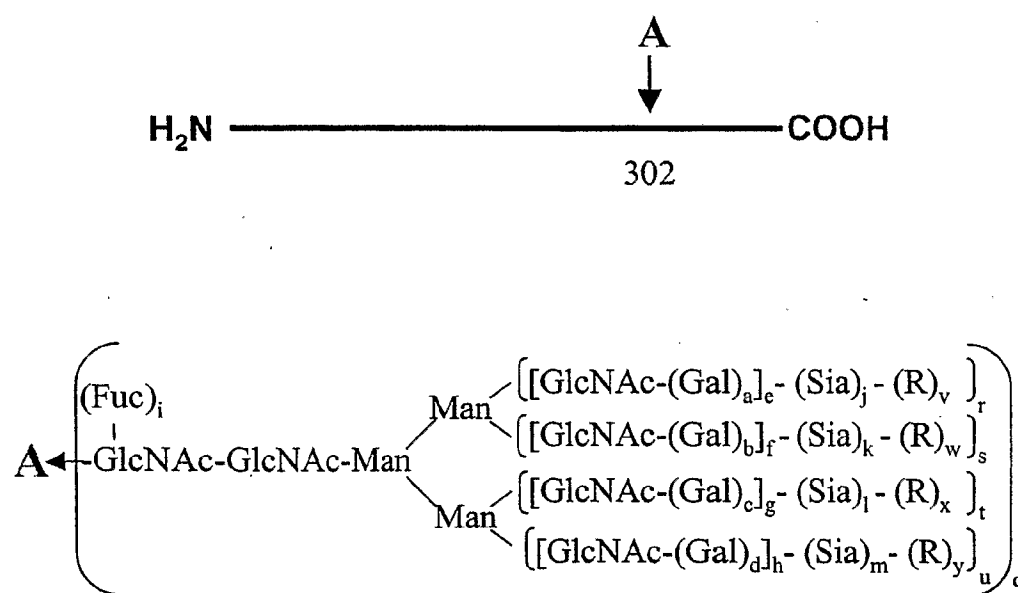
e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0.

FIG. 42M

184/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 43A

185/498

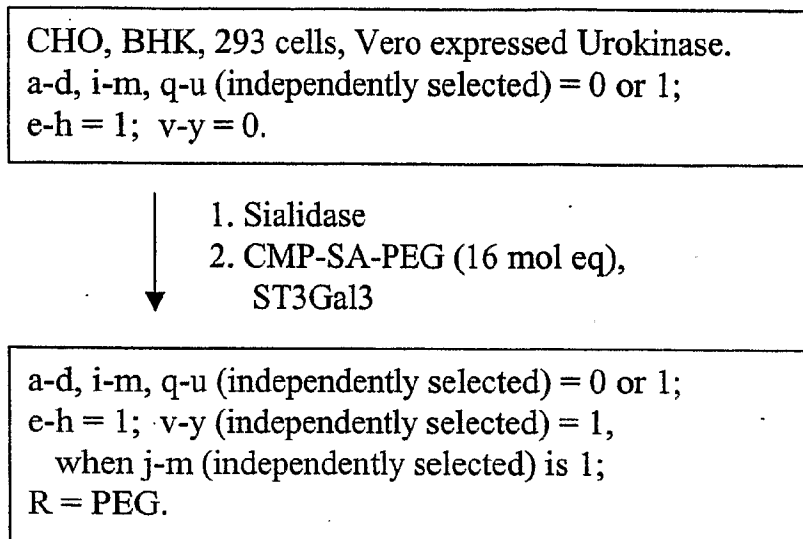


FIG. 43B

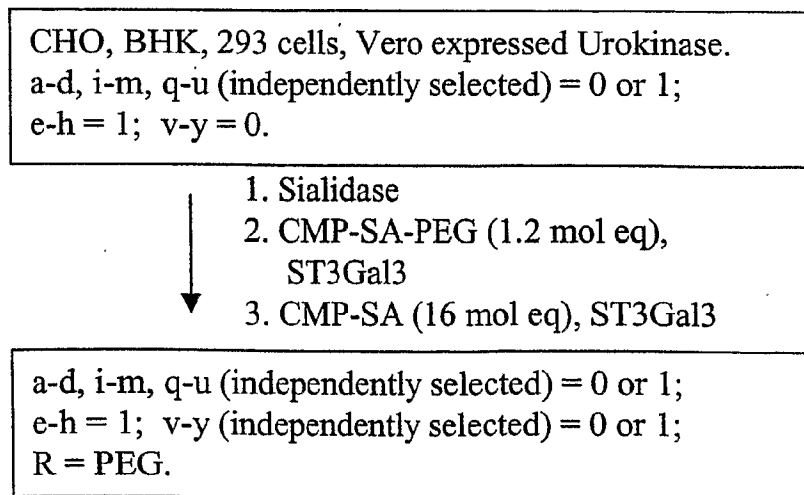


FIG. 43C

186/498

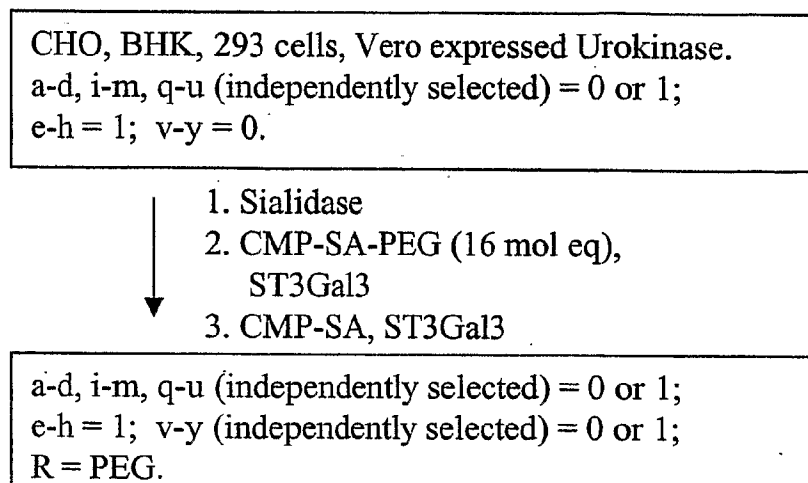


FIG. 43D

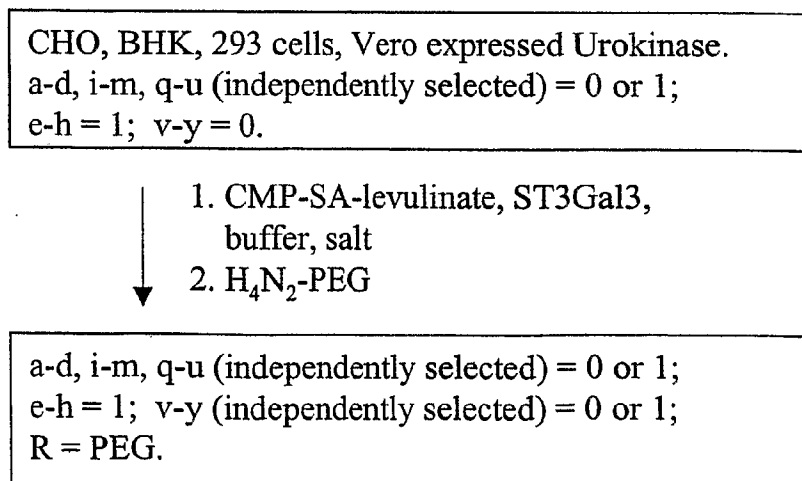


FIG. 43E

187/498

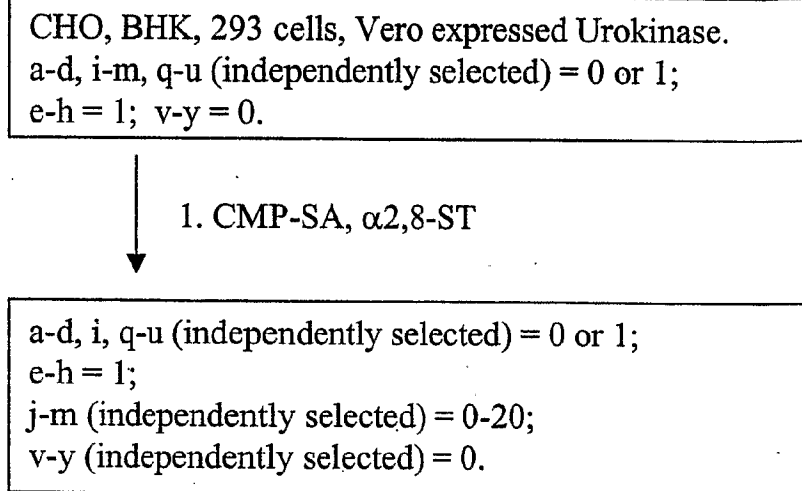
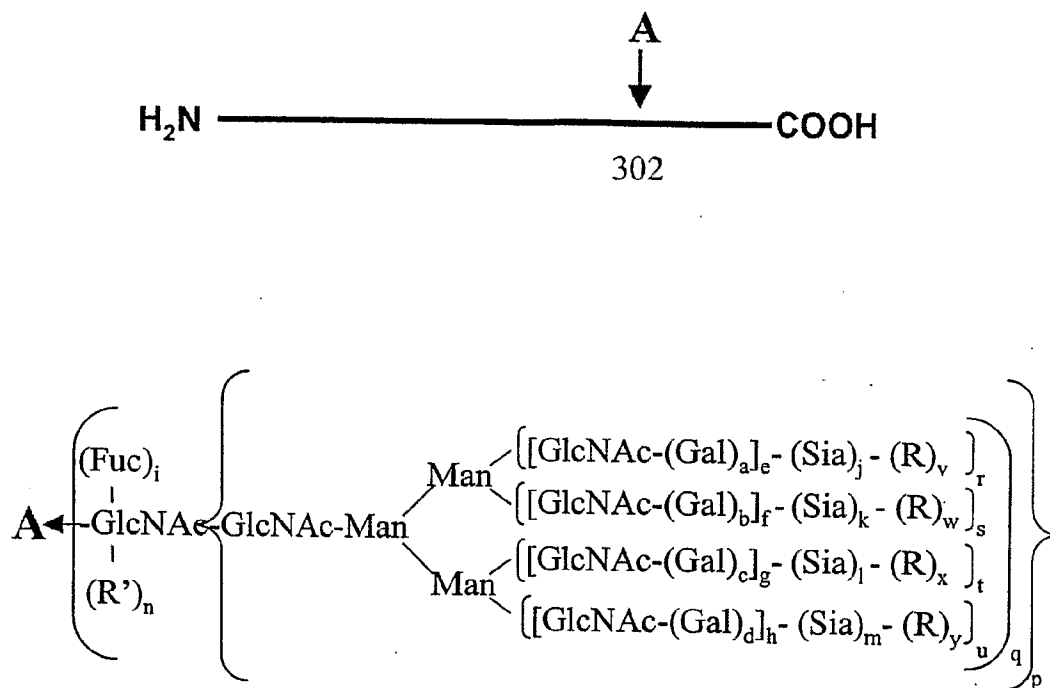


FIG. 43F

188/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 43G



189/498

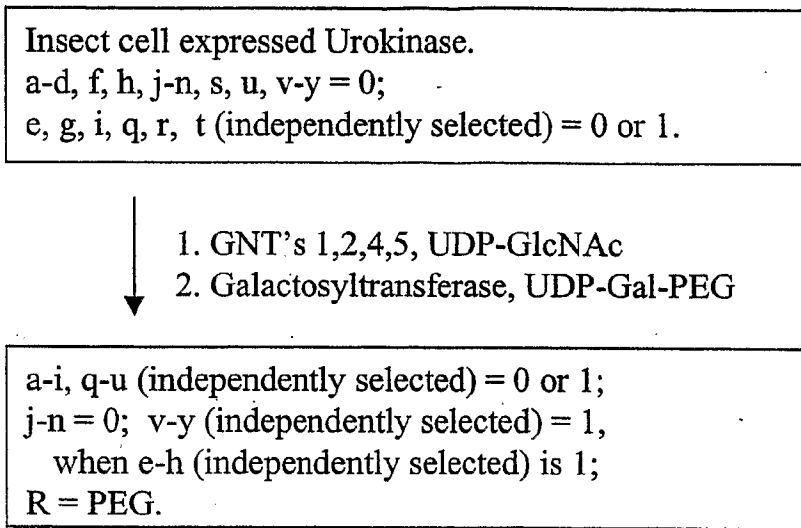


FIG. 43H

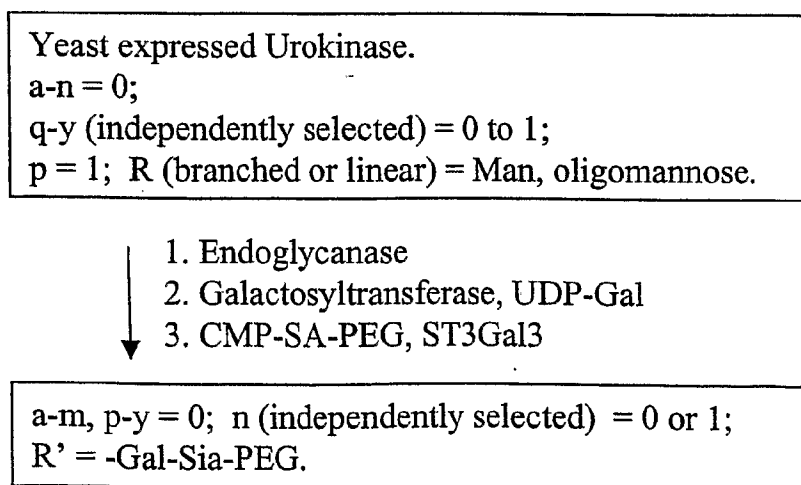


FIG. 43I

190/498

CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated Urokinase produced in CHO.
  - ↓ 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;

p = 1; n = 0;

v-y (independently selected) = 0 or 1;

R = linker-Urokinase.

FIG. 43J

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0; n = 0;

Sia (independently selected) = Sia or SO<sub>4</sub>;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase
  2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

n = 0; e-h = 1; Sia = Sia;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 43K

191/498

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO<sub>4</sub>;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.



1. sulfohydrolase, hexosaminidase

2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

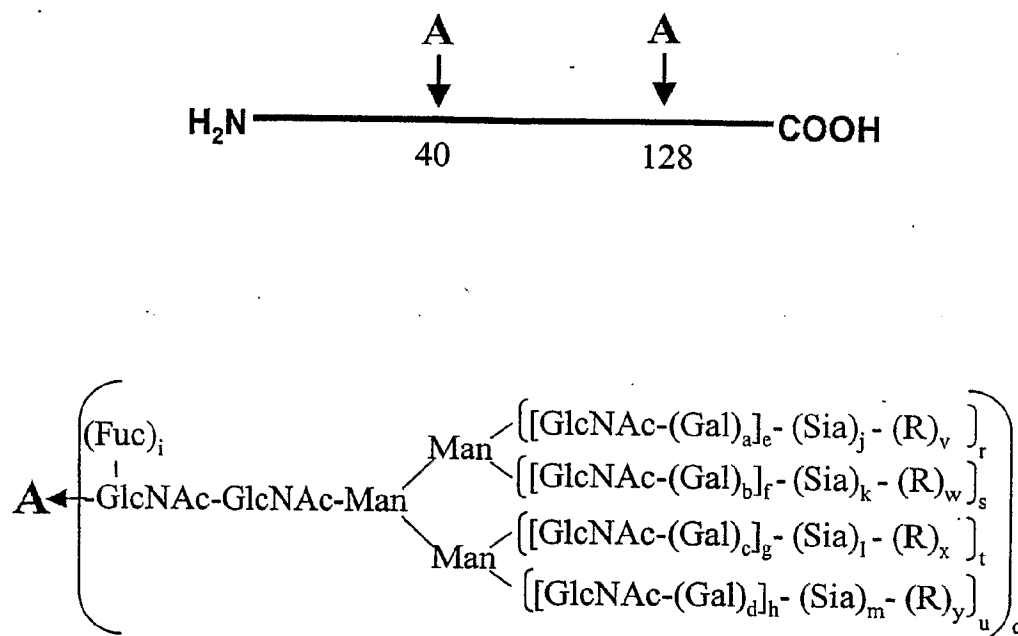
e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 43L

192/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

193/498

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 44C

194/498

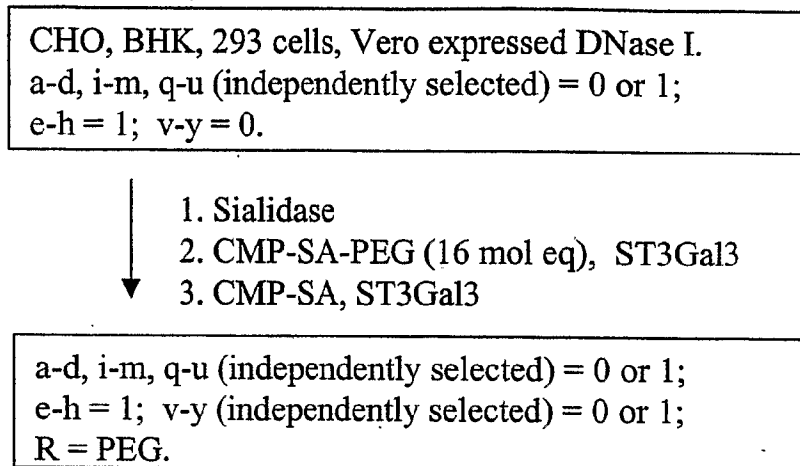


FIG. 44D

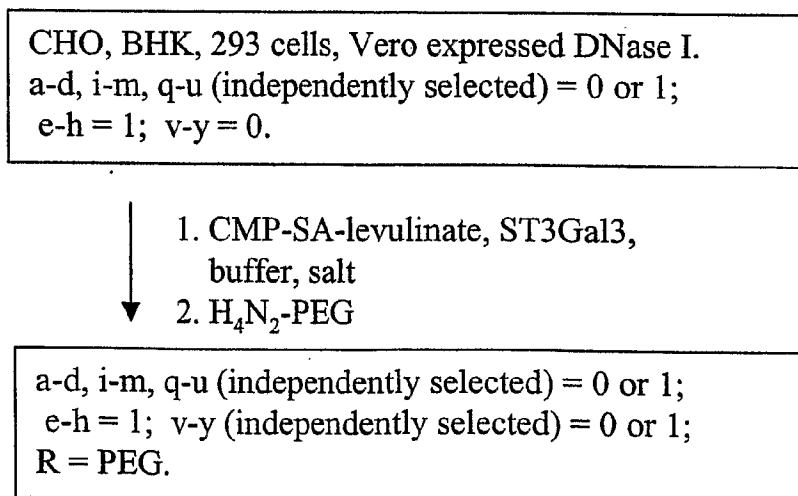


FIG. 44E

195/498

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

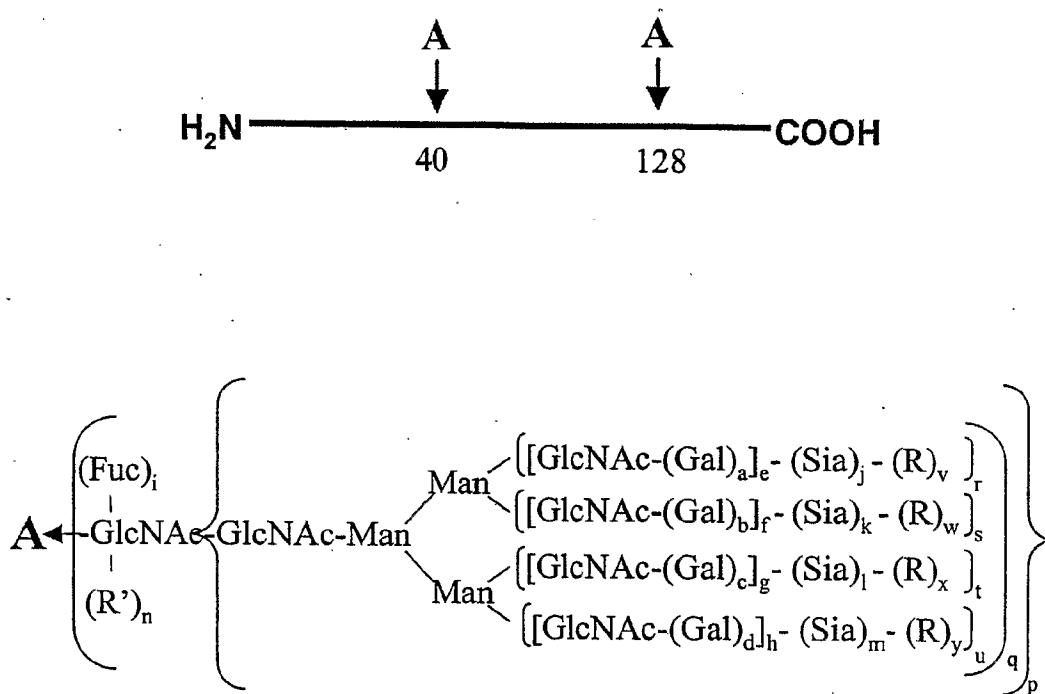


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1;  
j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 44F

196/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 44G



197/498

Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 44H

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 44I

198/498

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
  3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker- alpha-1-Proteinase inhibitor.

FIG. 44J



200/498

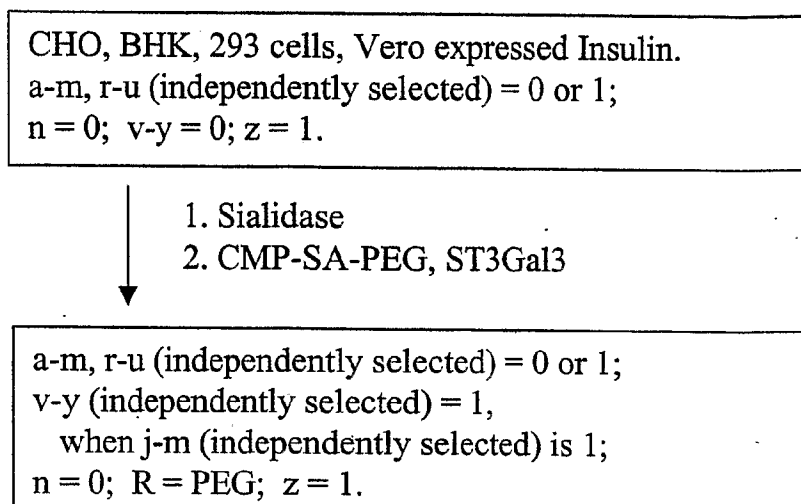


FIG. 45B

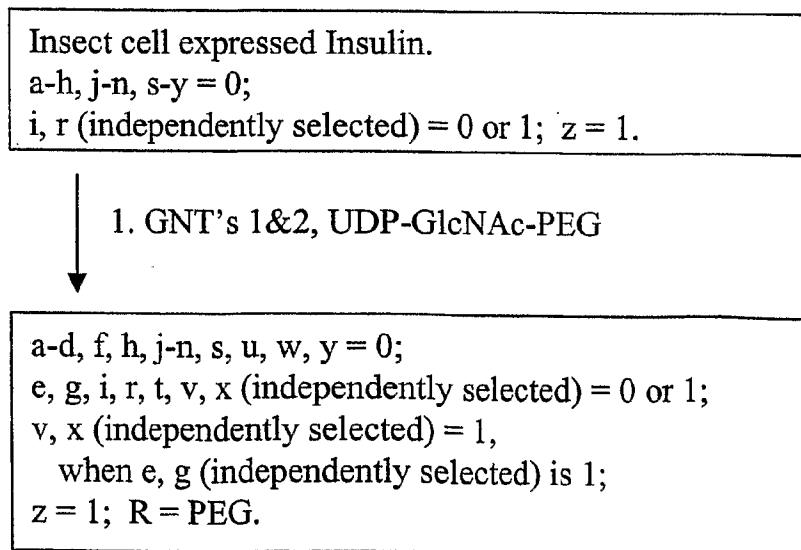


FIG. 45C

201/498

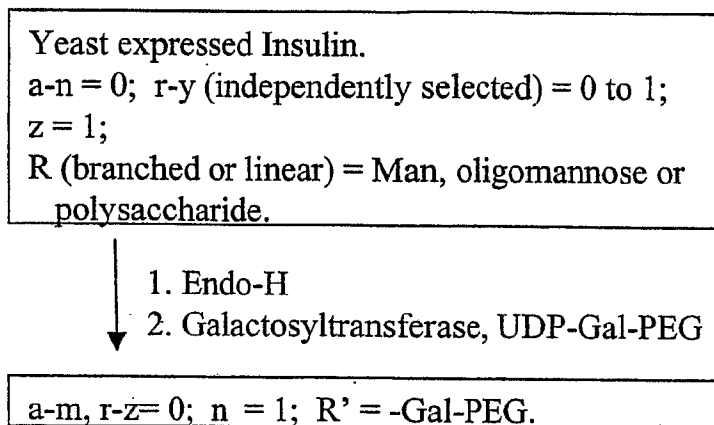
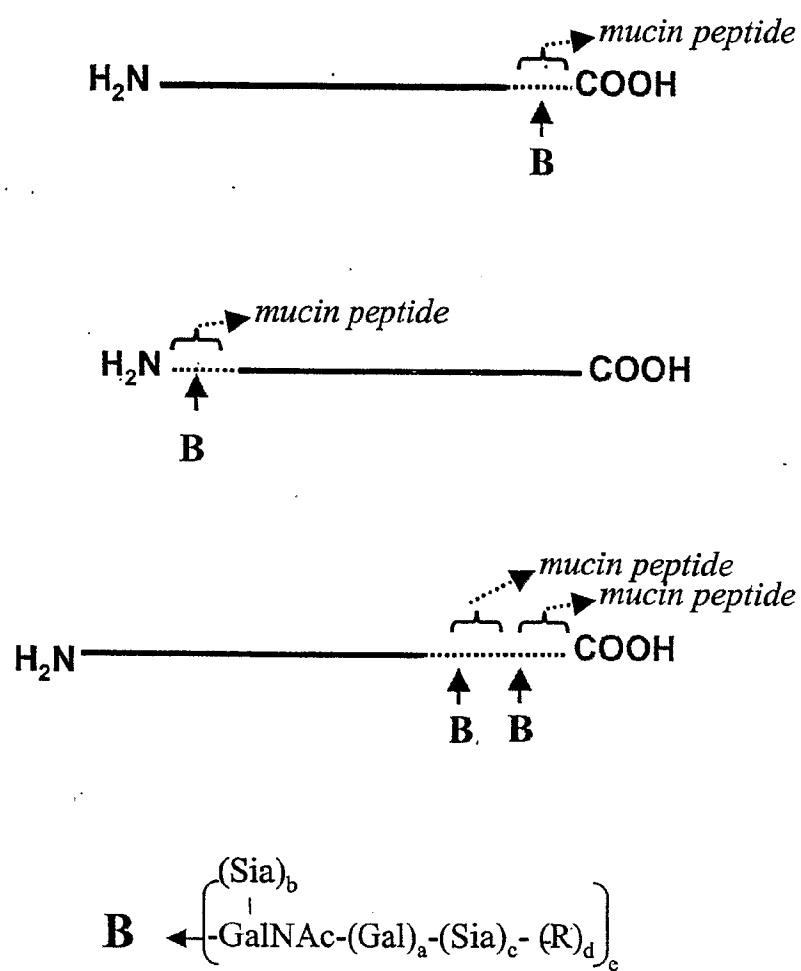


FIG. 45D

202/498



a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer

FIG. 45E

203/498

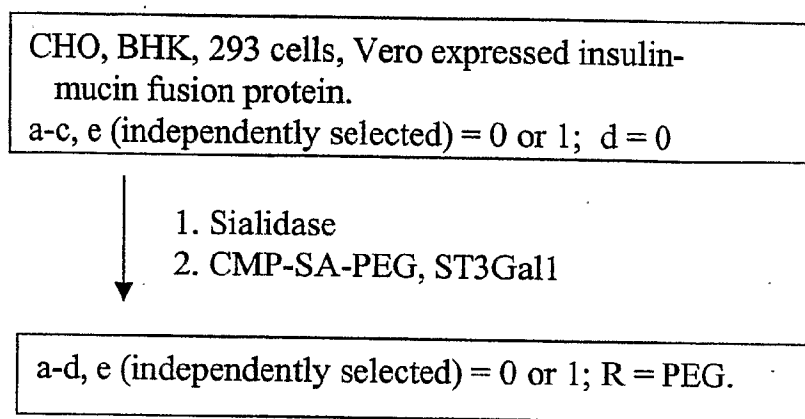


FIG. 45F

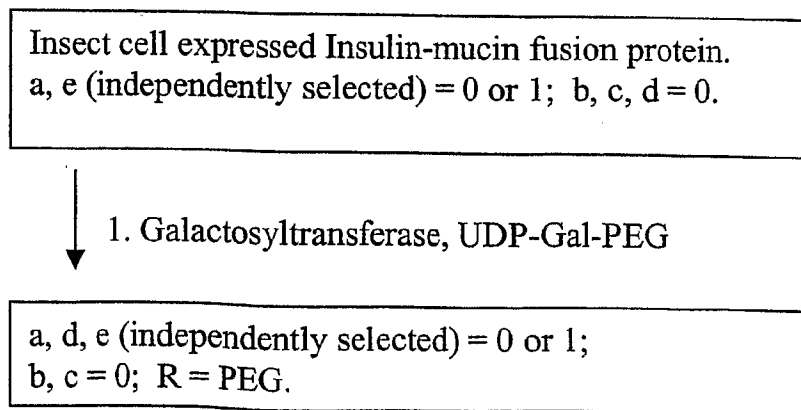


FIG. 45G

204/498

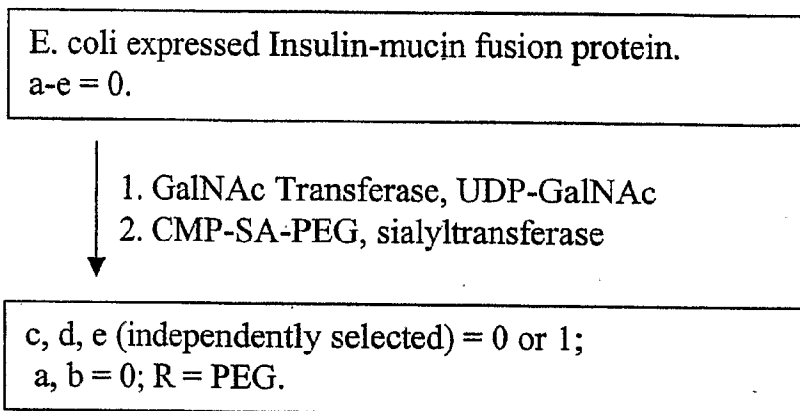
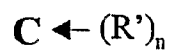
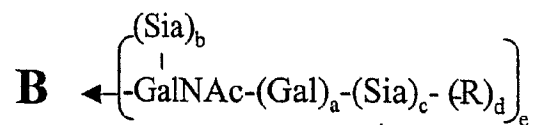
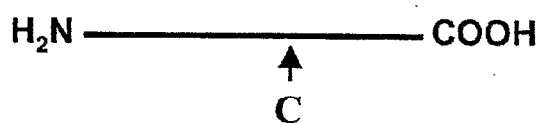
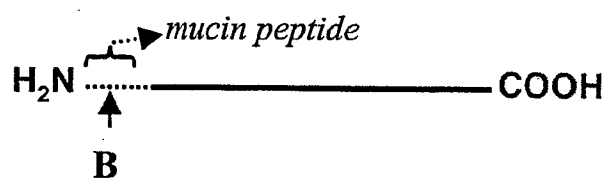
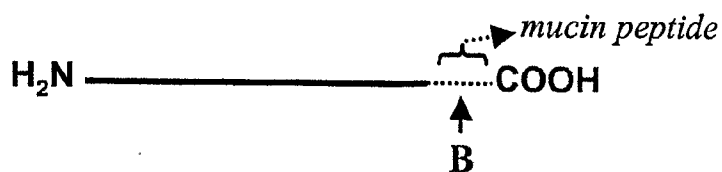


FIG. 45H



205/498



a-c, e (independently selected) = 0 or 1;  
 d = 0; R = modifying group, mannose,  
 oligo-mannose.

FIG. 45I

206/498

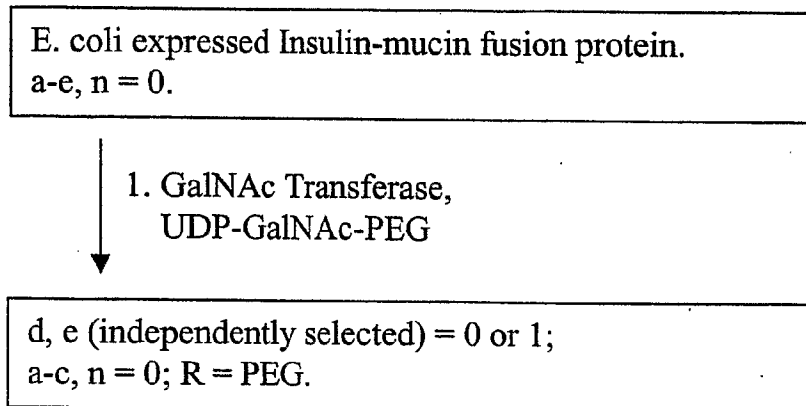


FIG. 45J

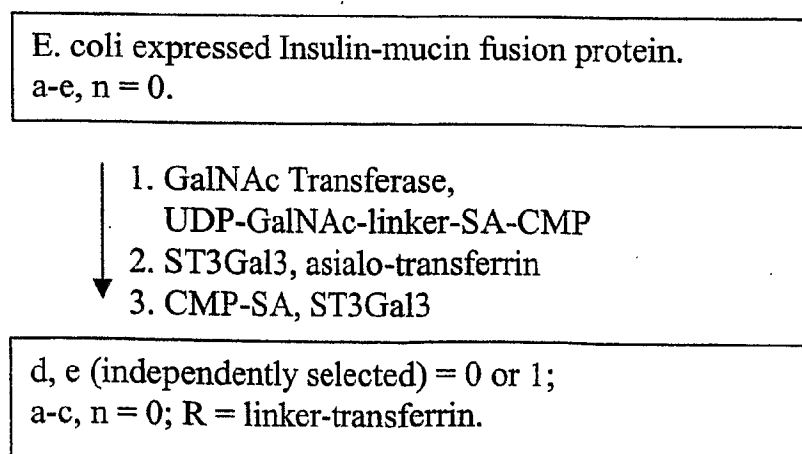


FIG. 45K

207/498

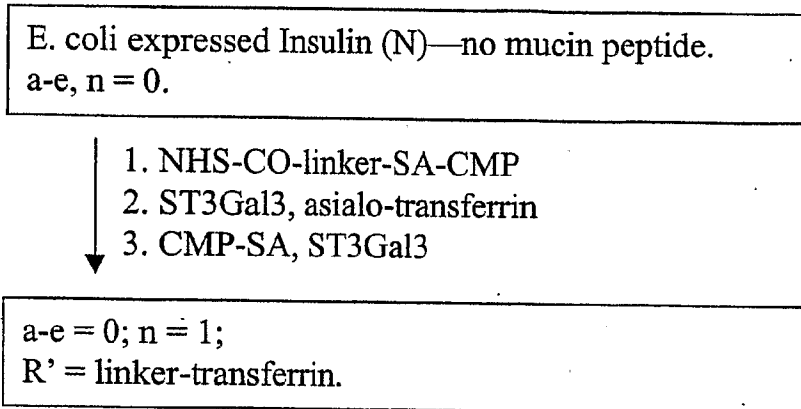
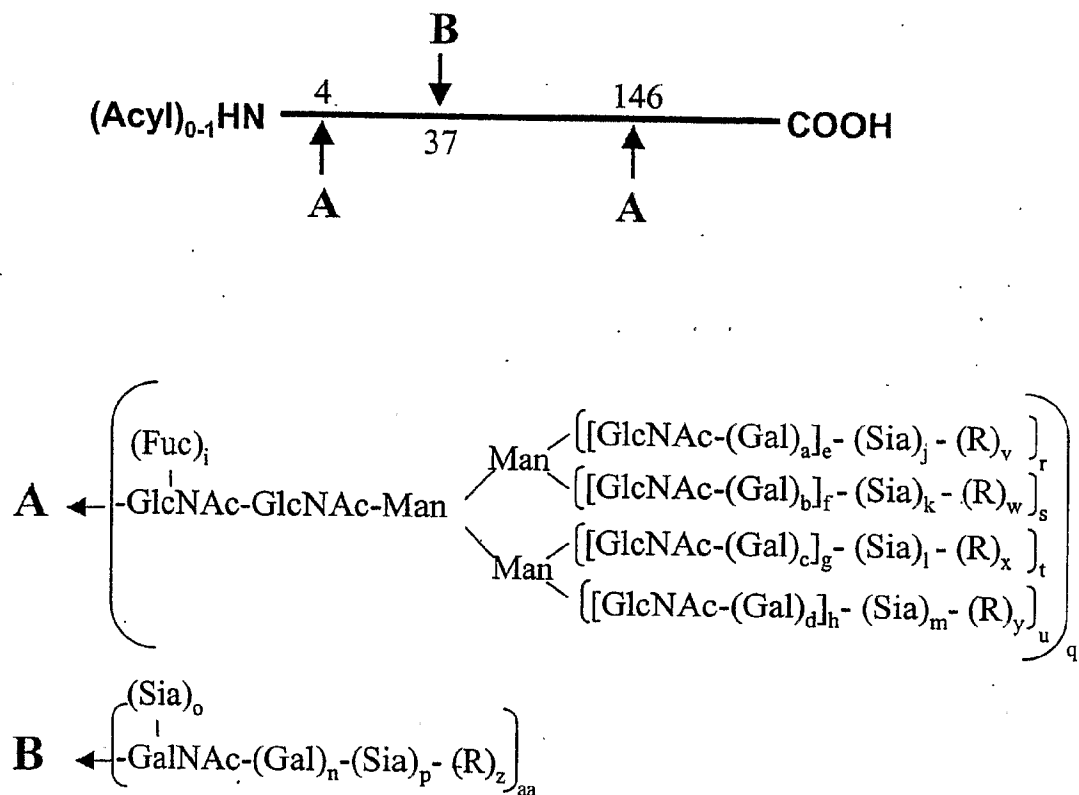


FIG. 45L

208/498



a-d, i, n-u, aa (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 6.  
 j-m (independently selected) = 0 to 100.  
 v-y = 0; R = polymer, glycoconjugate.

FIG. 46A

209/498

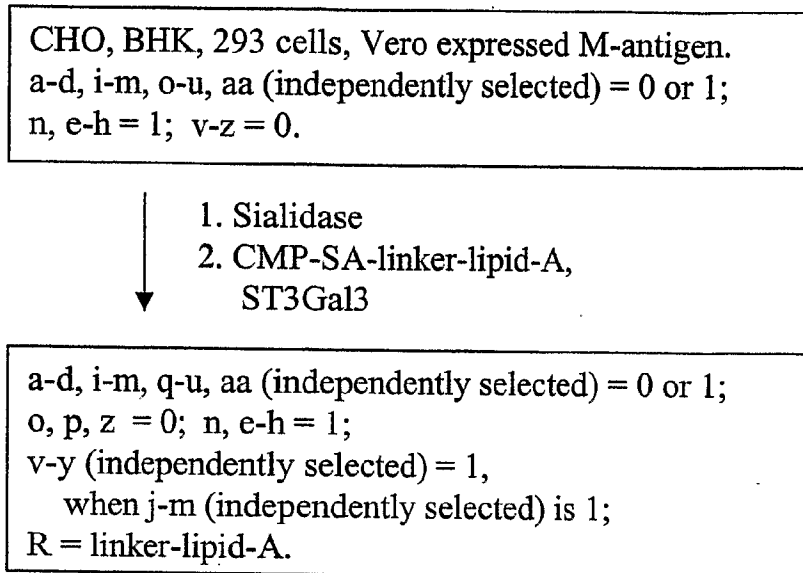


FIG. 46B

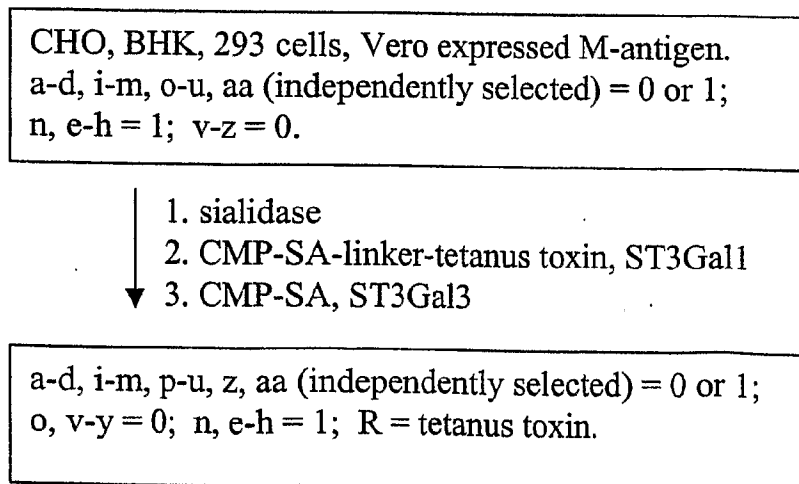


FIG. 46C

210/498

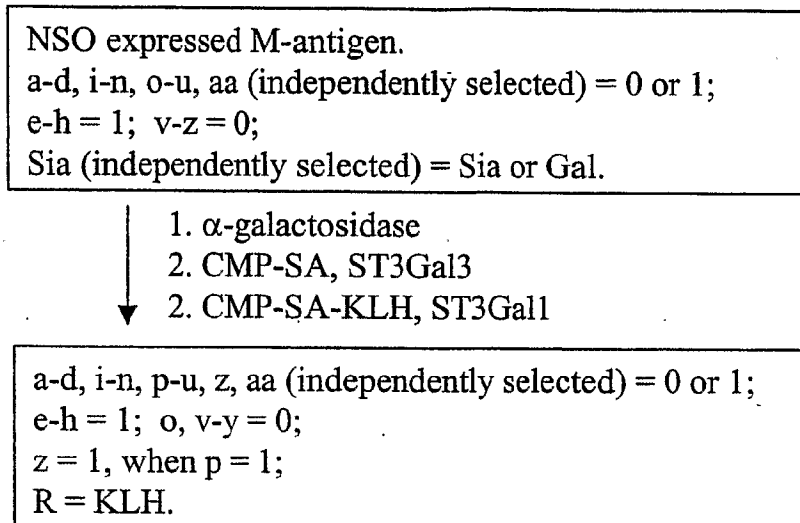


FIG. 46D

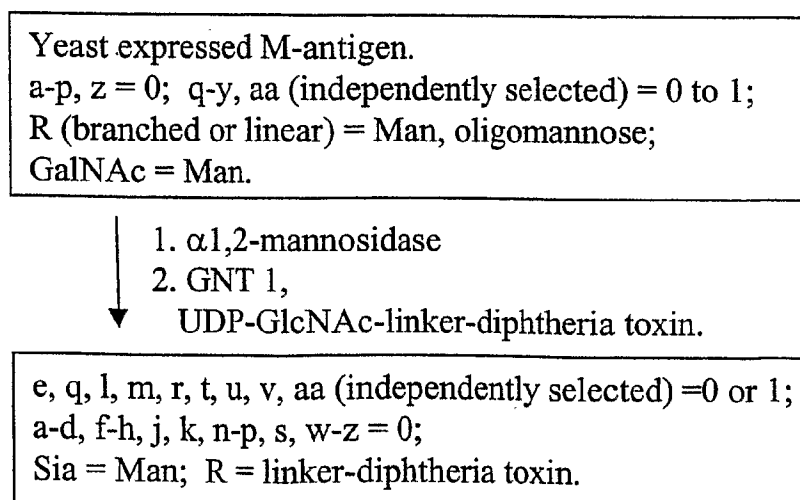


FIG. 46E

211/498

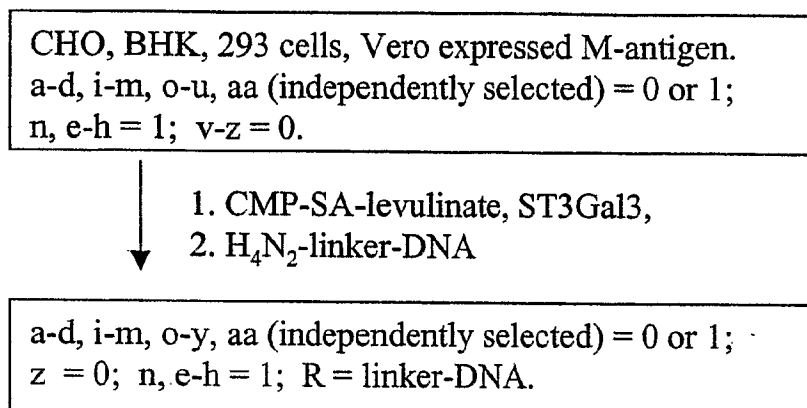


FIG. 46F

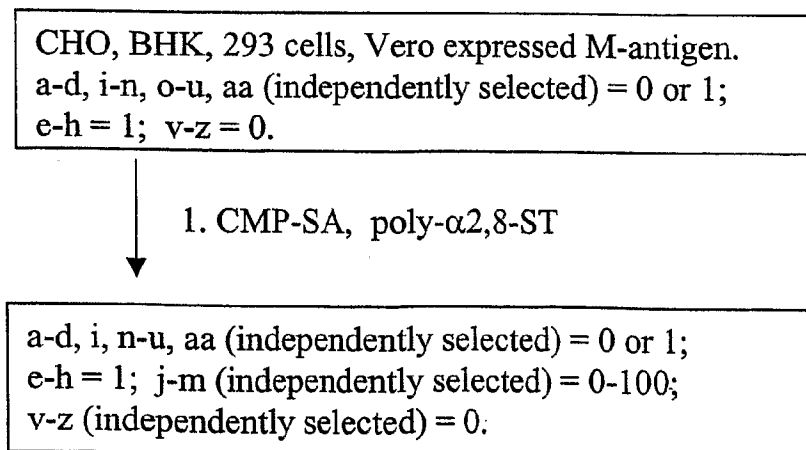
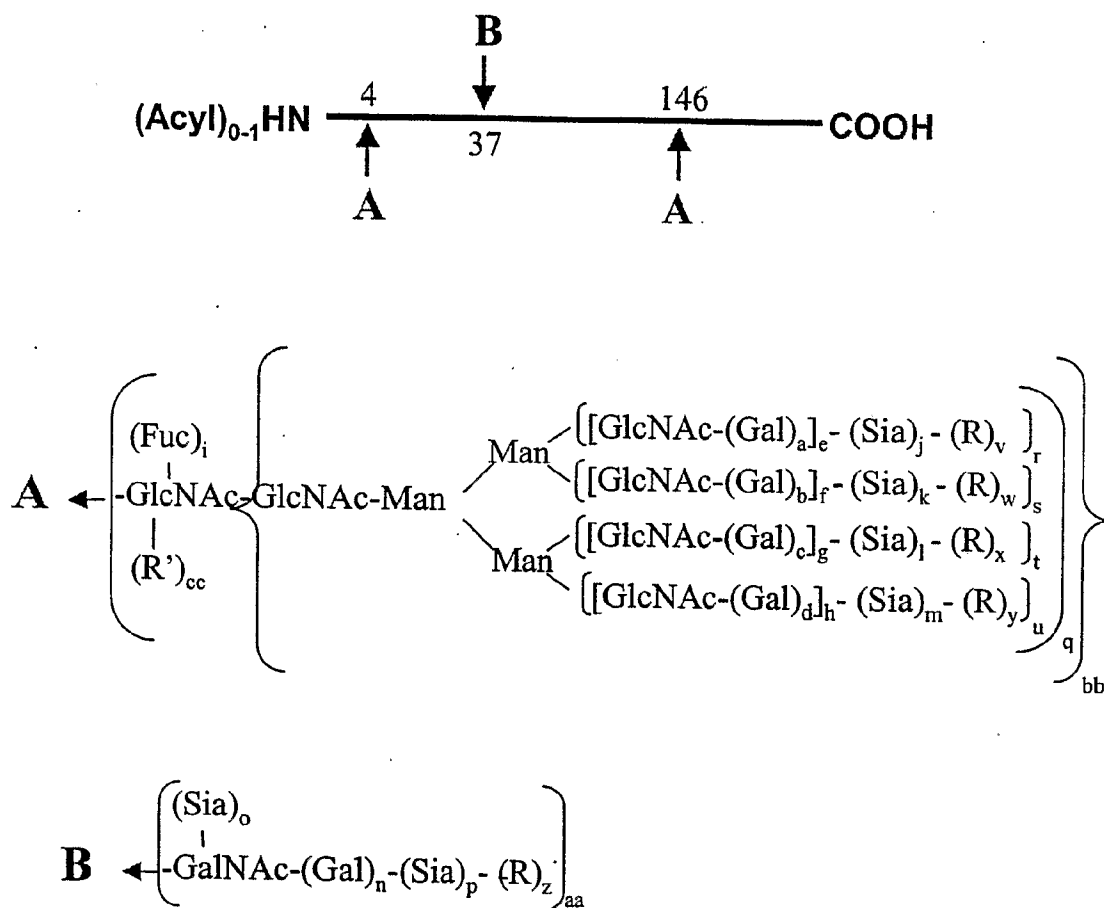


FIG. 46G

212/498



a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46H



213/498

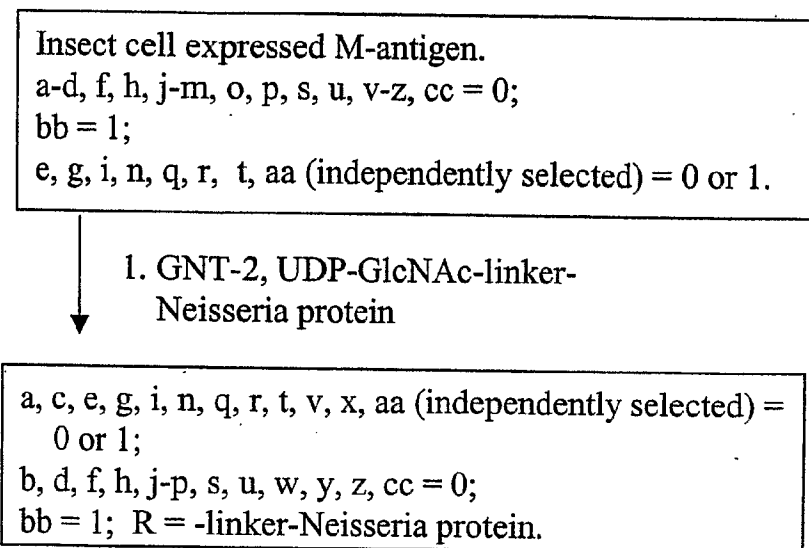


FIG. 46I

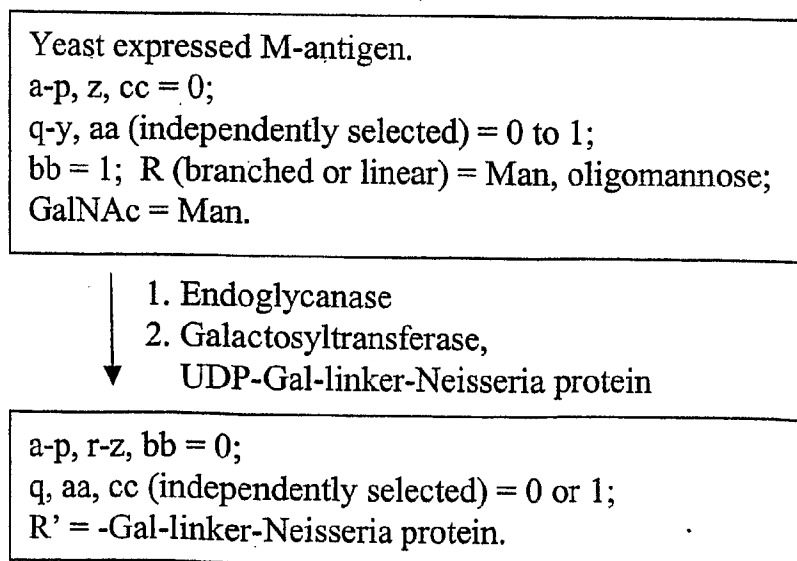


FIG. 46J

214/498


Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

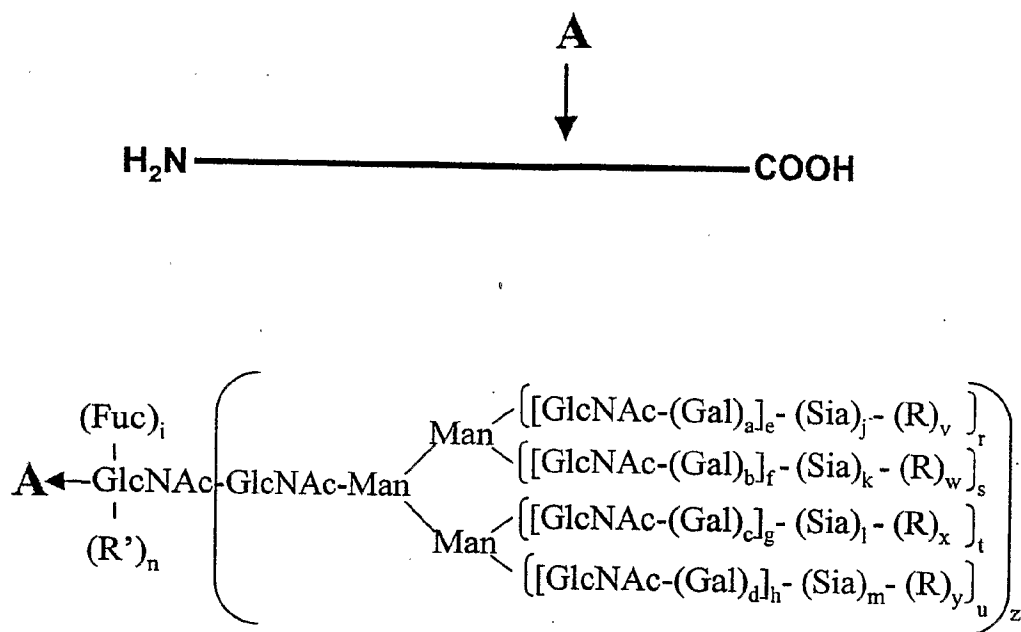
GalNAc = Man.

- 
1. mannosidases
  2. GNT 1 & 2, UDP-GlcNAc
  3. UDP-Gal, Galactosyltransferase,
  4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;  
b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 46K

215/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 47A

216/498

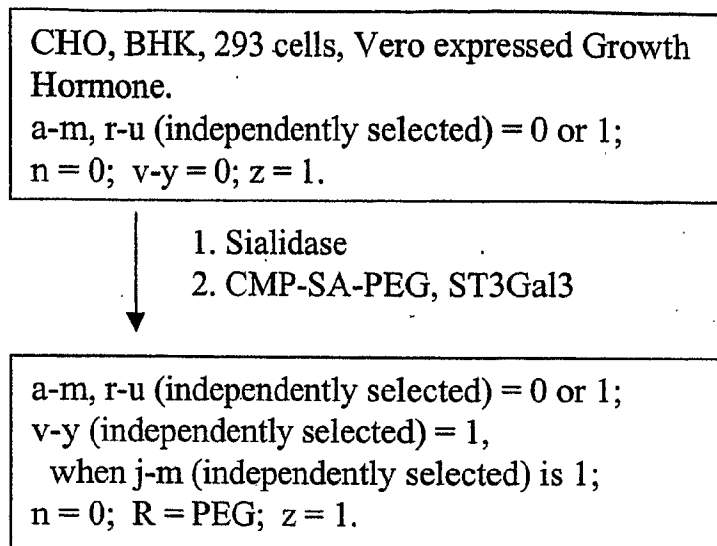


FIG. 47B

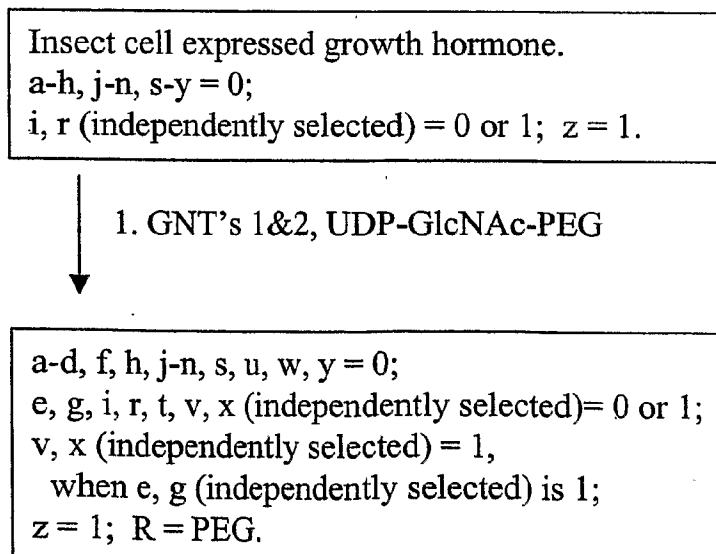


FIG. 47C

217/498

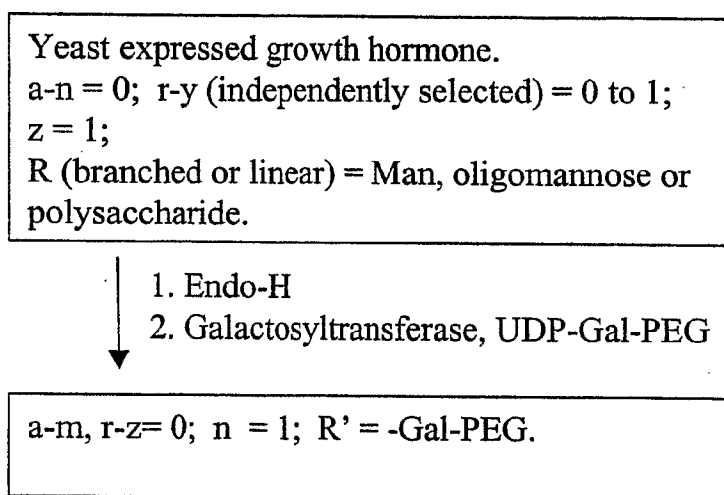
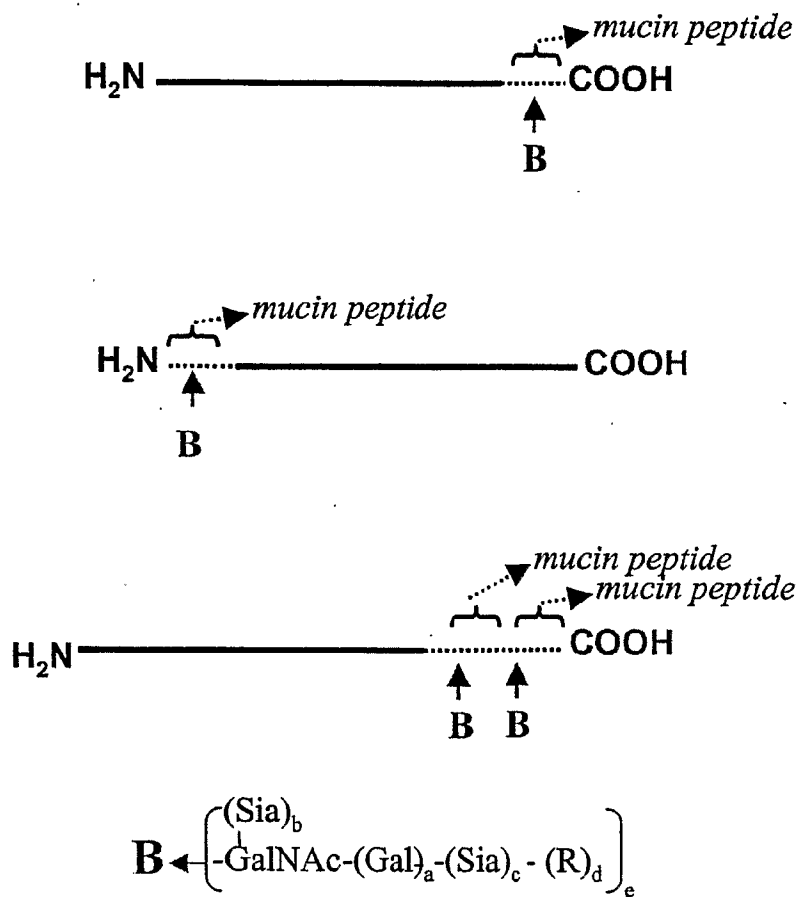


FIG. 47D

218/498



a-c, e (independently selected) = 0 or 1;  
d = 0;  
R = modifying group, mannose, oligo-  
mannose.

FIG. 47E

219/498

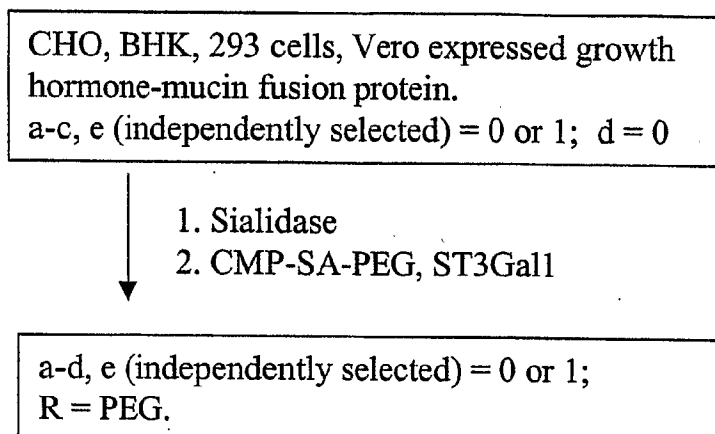


FIG. 47F

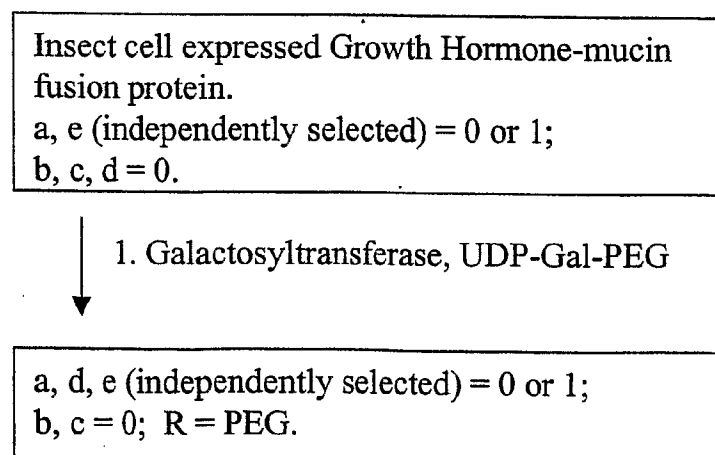


FIG. 47G

220/498

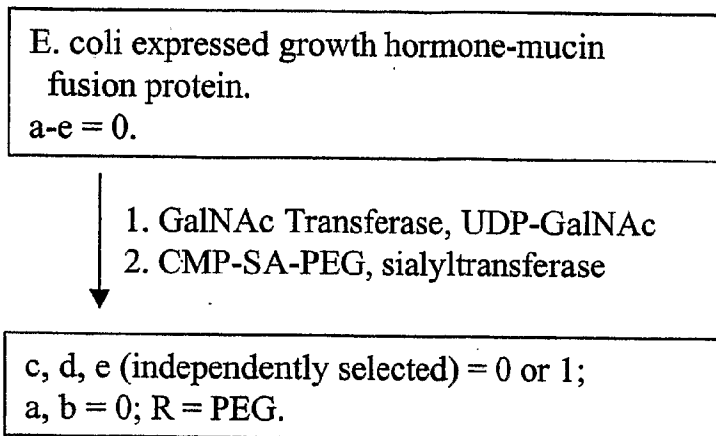


FIG. 47H

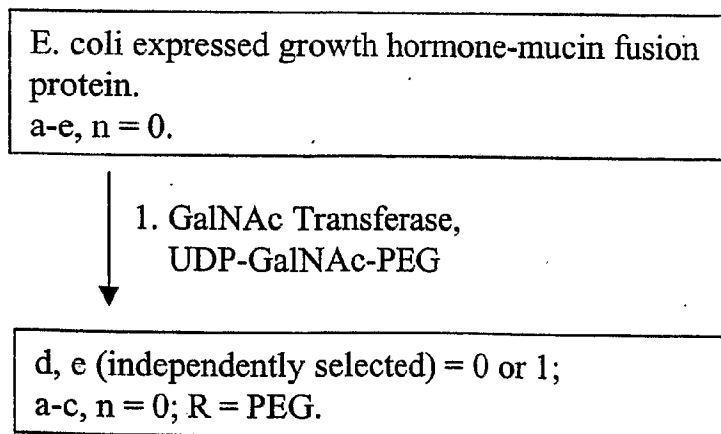


FIG. 47I



221/498

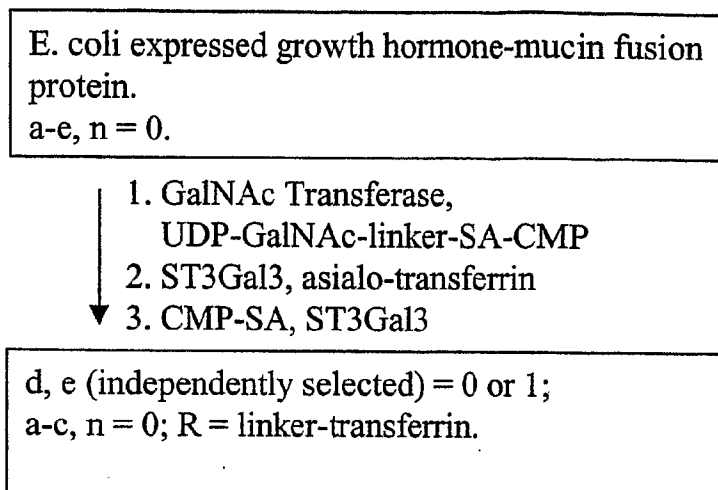


FIG. 47J

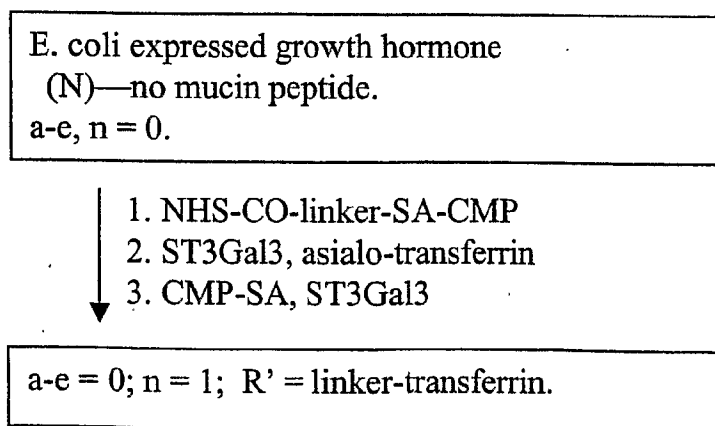
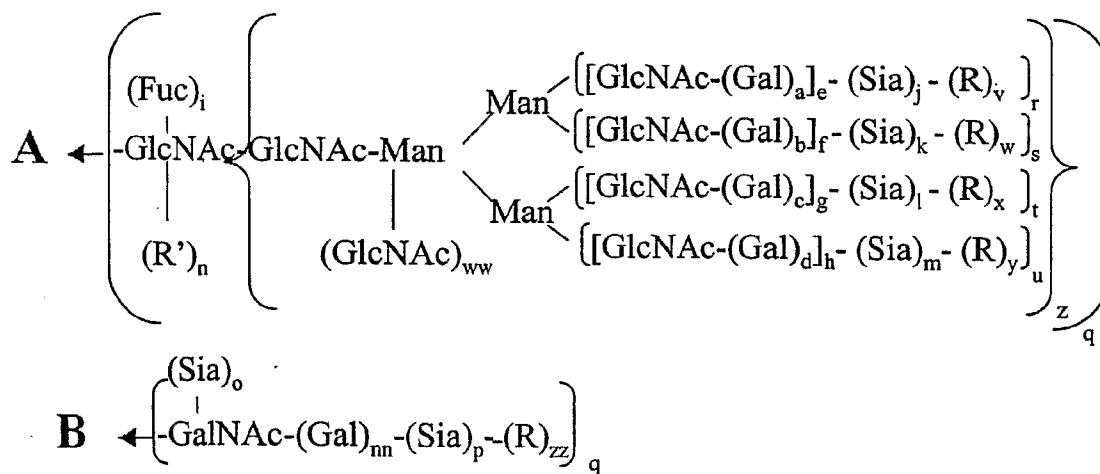
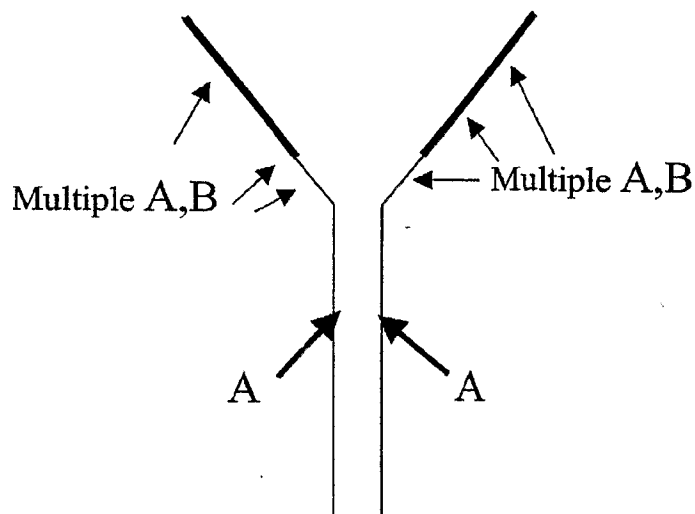


FIG. 47K

222/498



a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

223/498

CHO, BHK, 293 cells, Vero or transgenic animals  
expressed TNF Receptor IgG Fusion.  
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓  
1. CMP-SA, ST3Gal1  
2. galactosyltransferase, UPD-Gal  
3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero expressed  
TNF Receptor IgG Fusion.  
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓  
1. sialidase  
2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;  
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 48C

224/498

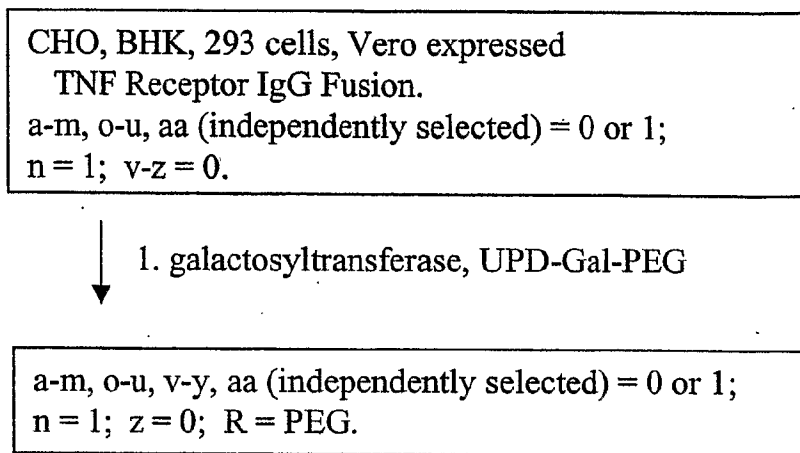


FIG. 48D

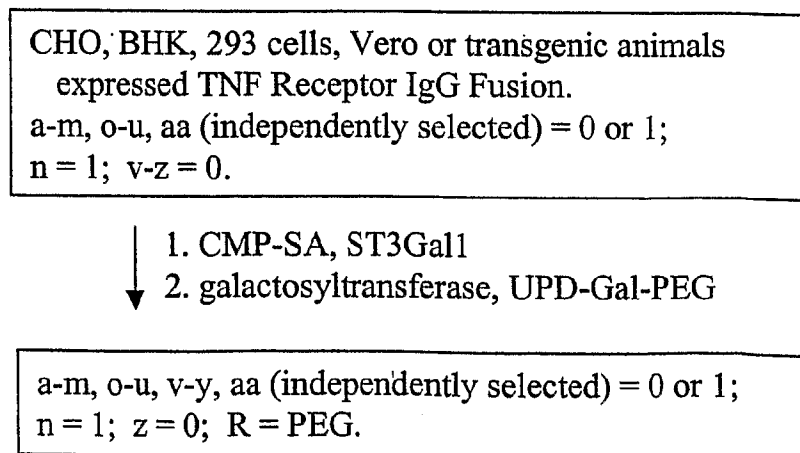


FIG. 48E

225/498

CHO, BHK, 293 cells, Vero or transgenic animals  
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

↓  
1. CMP-SA-levulinate, ST3Gal1  
2. H<sub>4</sub>N<sub>2</sub>-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 48F

CHO, BHK, 293 cells, Vero expressed  
TNF Receptor IgG Fusion.

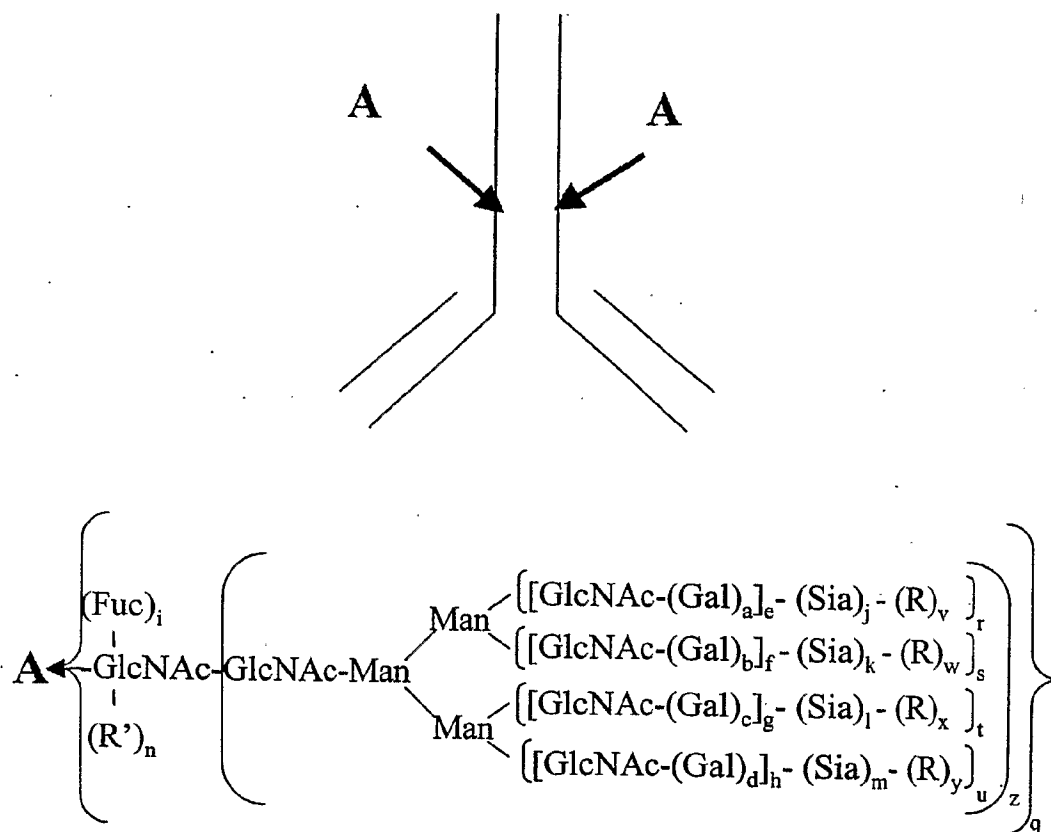
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

↓  
1. CMP-SA-PEG, α2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;  
n = 1; j-m, p (independently selected) = 0 to 2;  
v-z (independently selected) = 1,  
when j-m, p (independently selected) is 2;  
R = PEG.

FIG. 48G

226/498



a-d, i, l, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-k (independently selected) = 0 or 1.

M = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

227/498

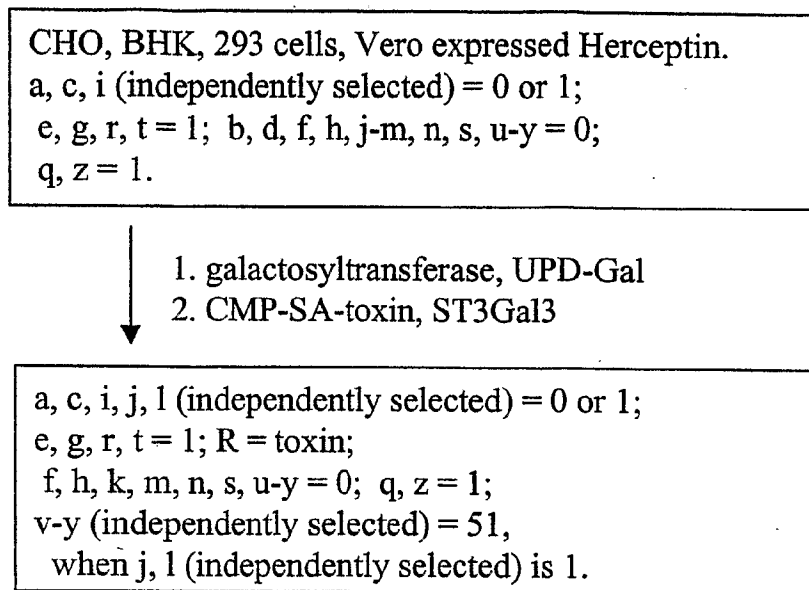


FIG. 49B

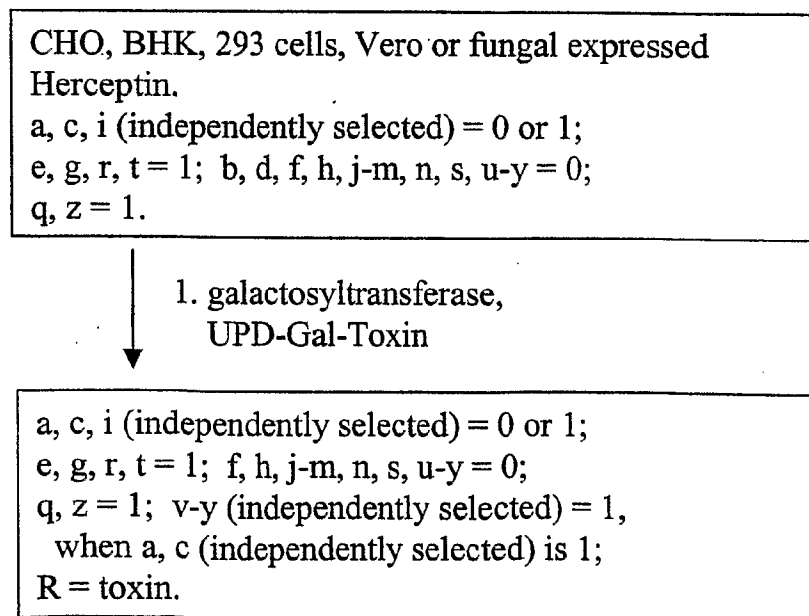


FIG. 49C

228/498

Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - ▼ 3.. CMP-SA-radioisotope complex, ST3Gal3

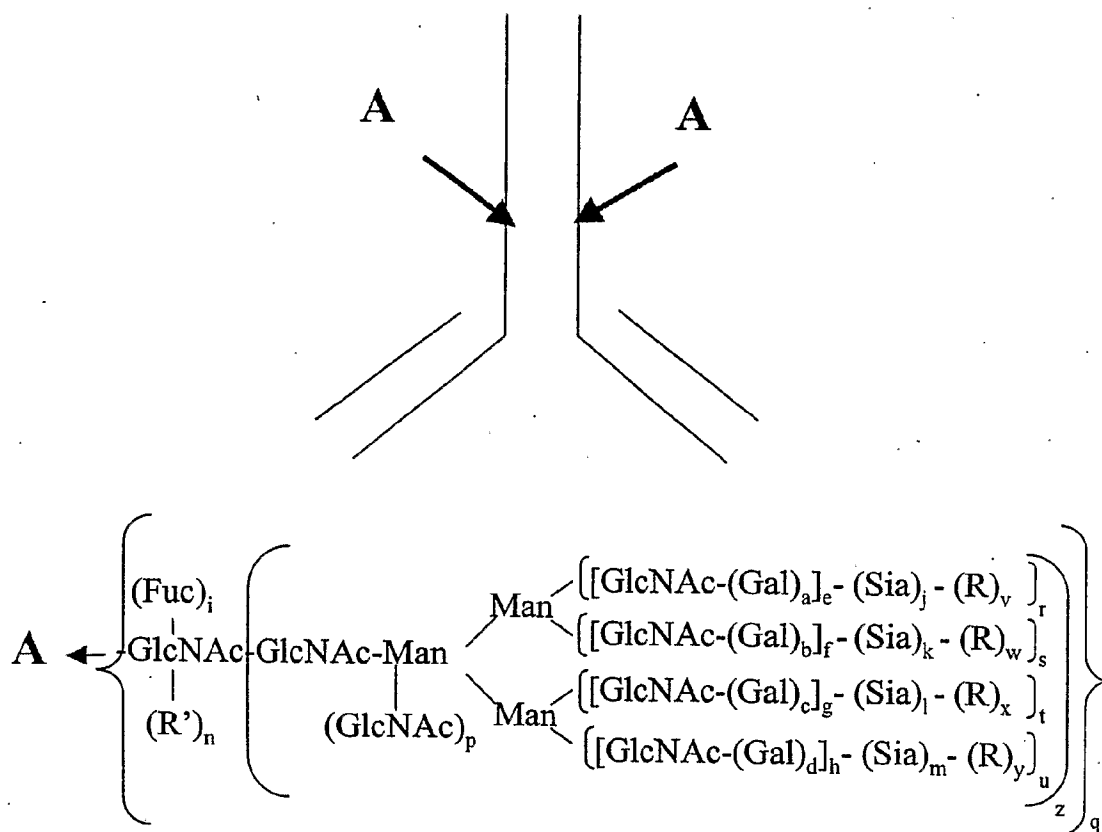
a-m, r-z= 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D



229/498



a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

$j$ -m (independently selected) = 0 or 1.

$$n, v-y=0; z=0 \text{ or } 1;$$

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

**FIG. 50A**

230/498

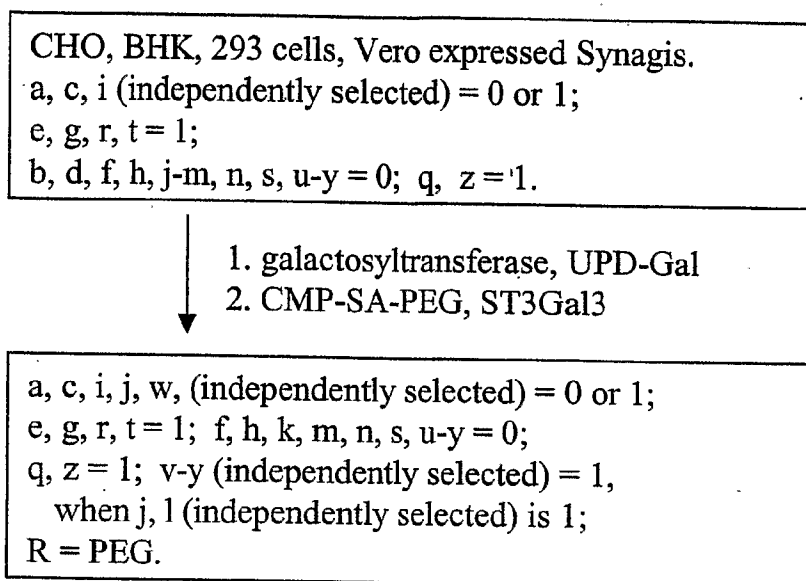


FIG. 50B

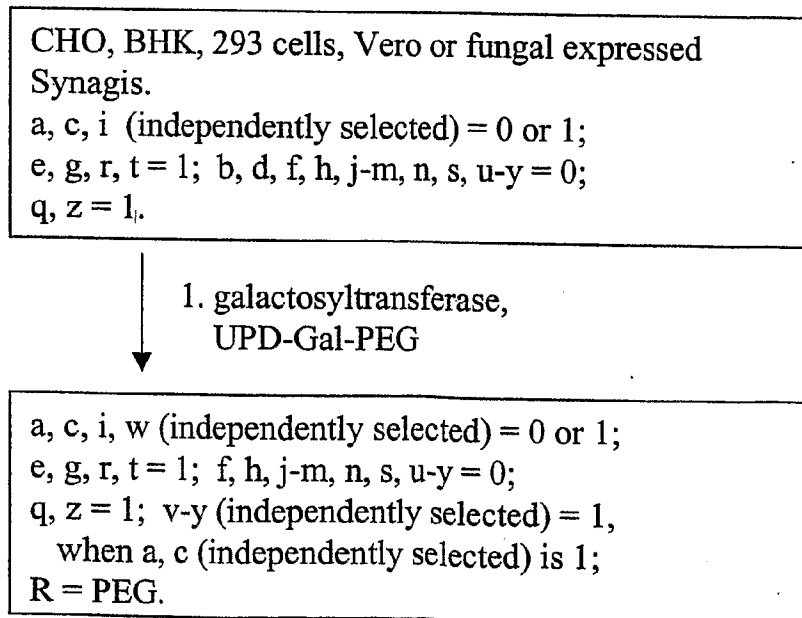


FIG. 50C

231/498

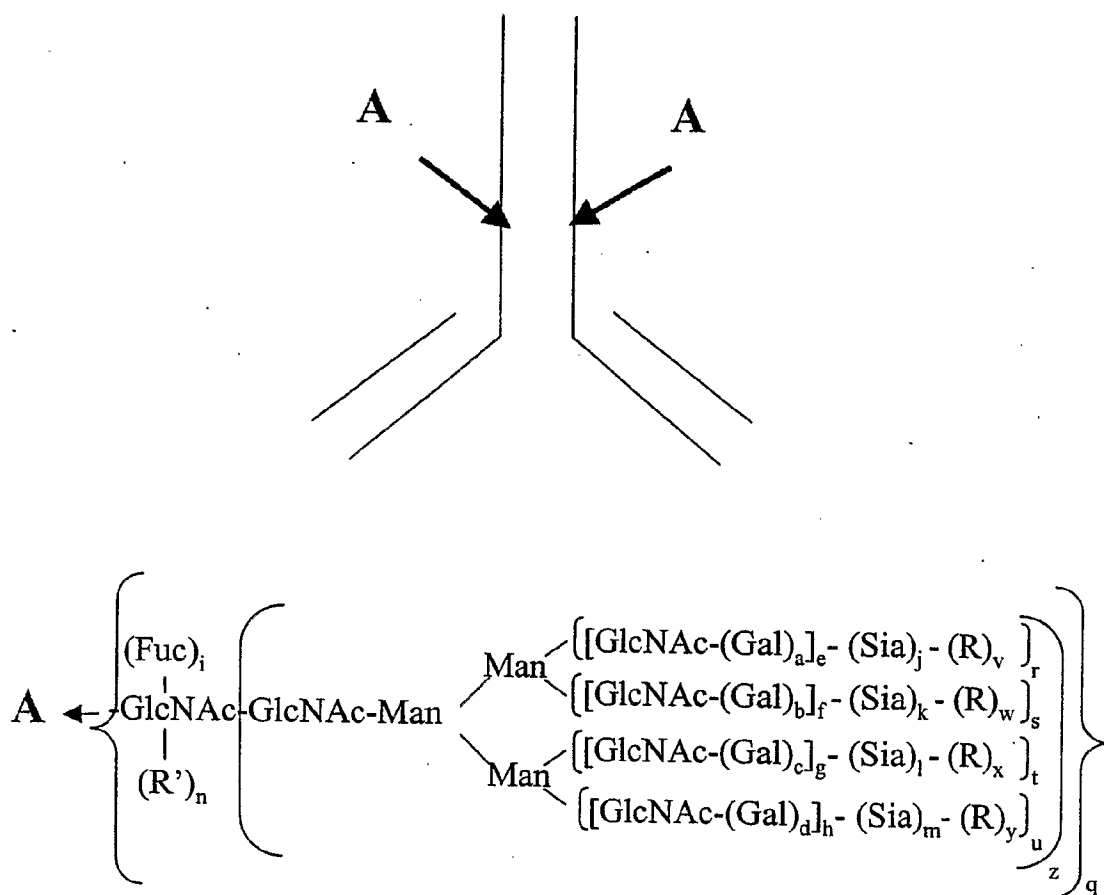
Fungi expressed Synagis.  
e, g, i, r, t (independently selected) = 0 or 1;  
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓  
1. Endo-H  
2. Galactosyltransferase, UDP-Gal  
3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 50D

232/498



a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51A

233/498

CHO, BHK, 293 cells, Vero expressed Remicade.  
 a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
 q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
 e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;  
 q, z = 1; v-y (independently selected) = 1,  
 when j, l (independently selected) is 1;  
 R = PEG.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed  
 Remicade.  
 a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
 q, z = 1.



1. galactosyltransferase,  
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;  
 q, z = 1; v-y (independently selected) = 1,  
 when a, c (independently selected) is 1;  
 R = PEG.

FIG. 51C

234/498

Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

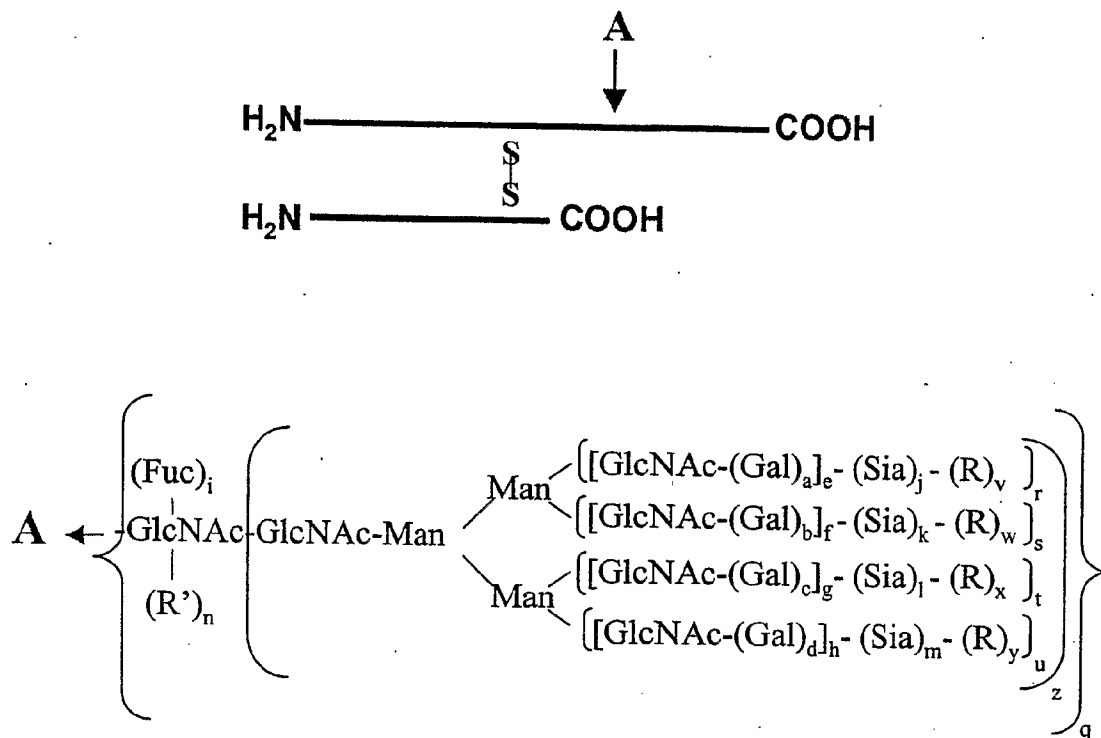
- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

235/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 52A

236/498

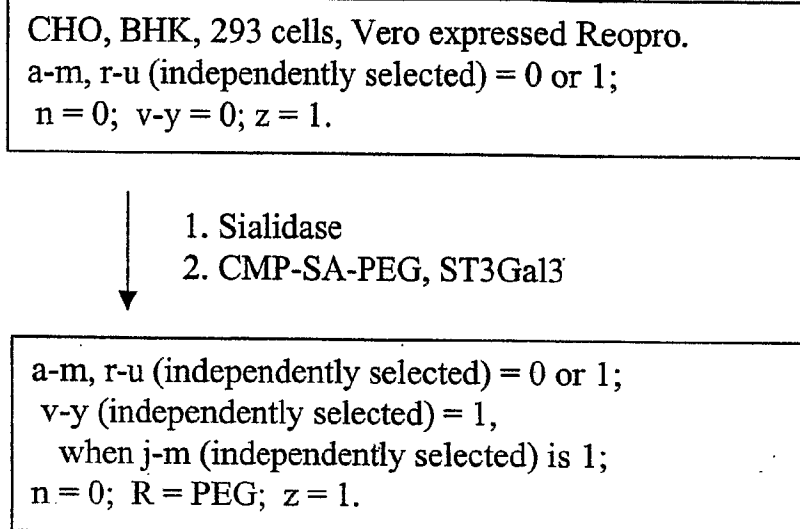


FIG. 52B

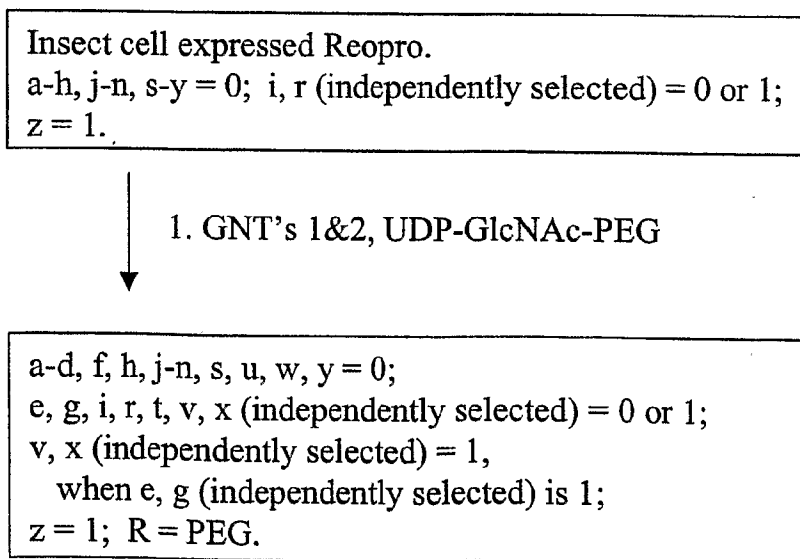


FIG. 52C



237/498

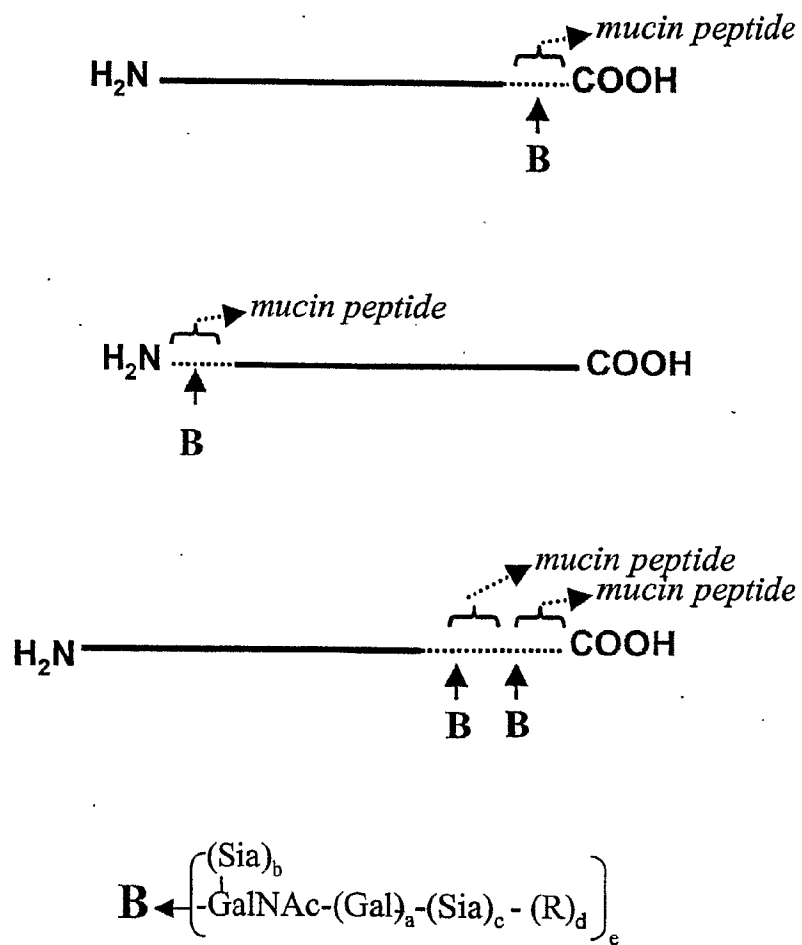
Yeast expressed Reopro.  
a-n = 0; r-y (independently selected) = 0 to 1;  
z = 1;  
R (branched or linear) = Man, oligomannose or  
polysaccharide.

1. Endo-H  
2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 52D

238/498



a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer

FIG. 52E

239/498

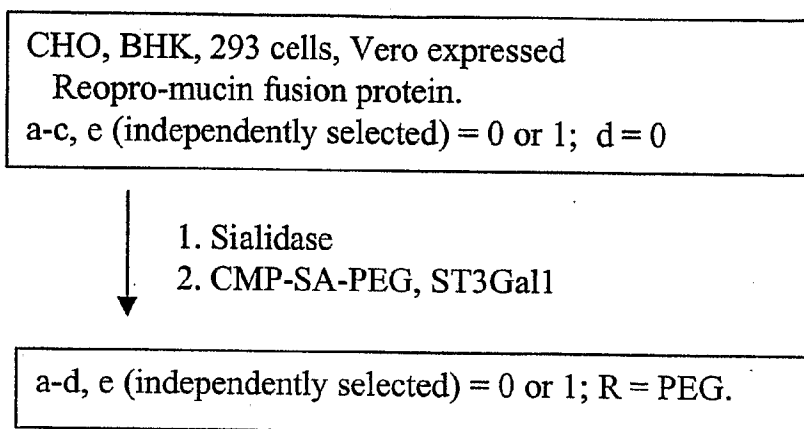


FIG. 52F

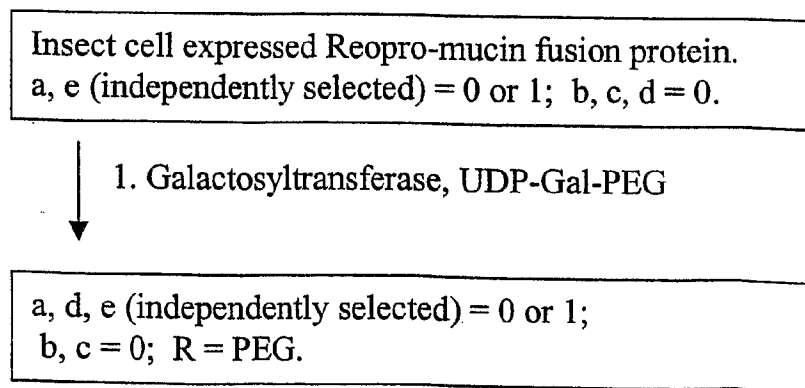


FIG. 52G

240/498

E. coli expressed Reopro-mucin fusion protein.  
a-e = 0.

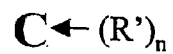
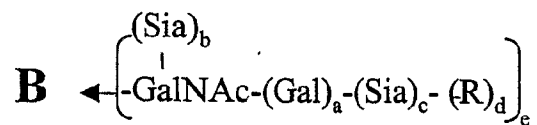
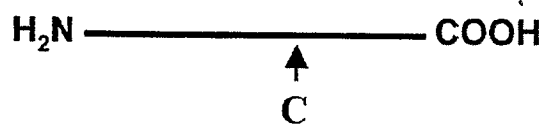
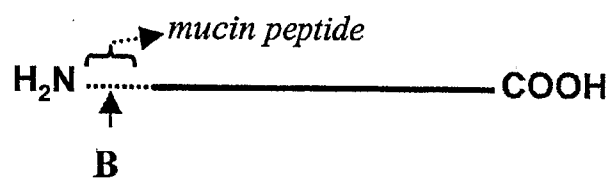
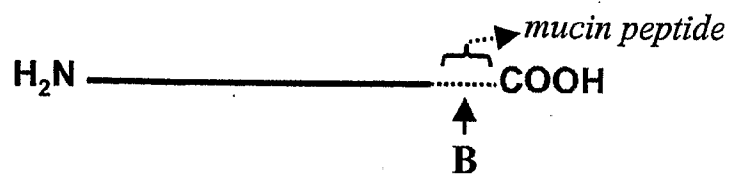


1. GalNAc Transferase, UDP-GalNAc
2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;  
a, b = 0; R = PEG.

FIG. 52H

241/498



a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer, linker.

FIG. 52I

242/498

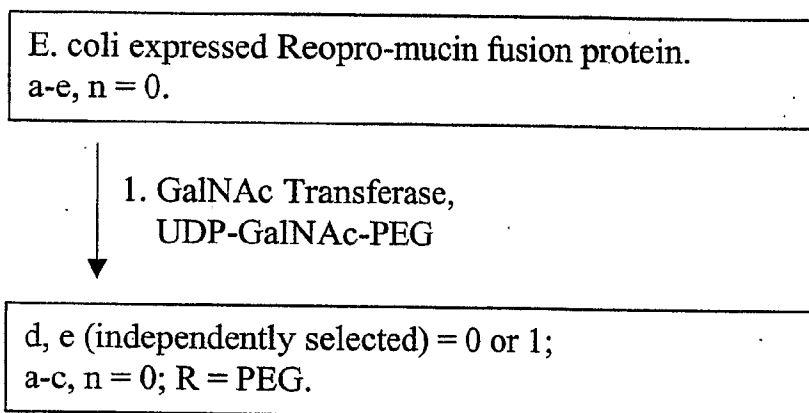


FIG. 52J

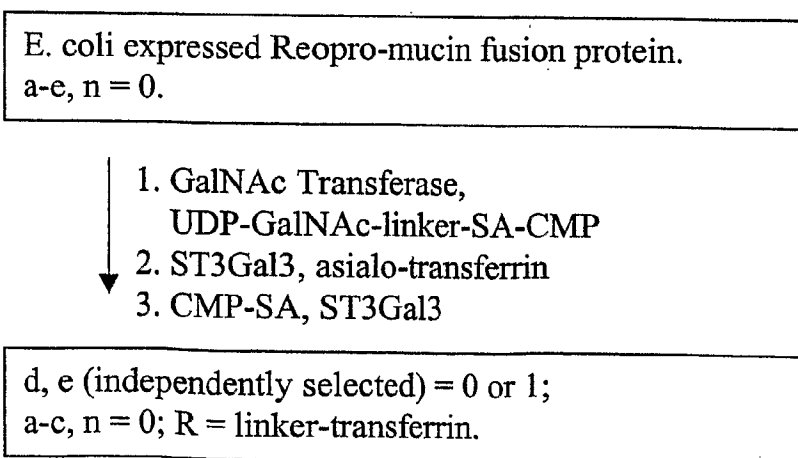


FIG. 52K

243/498

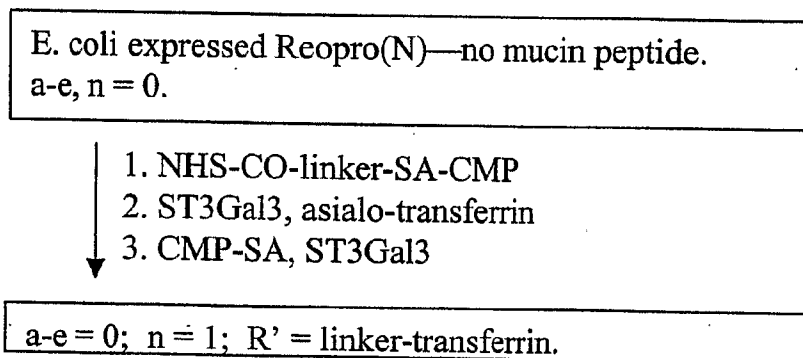
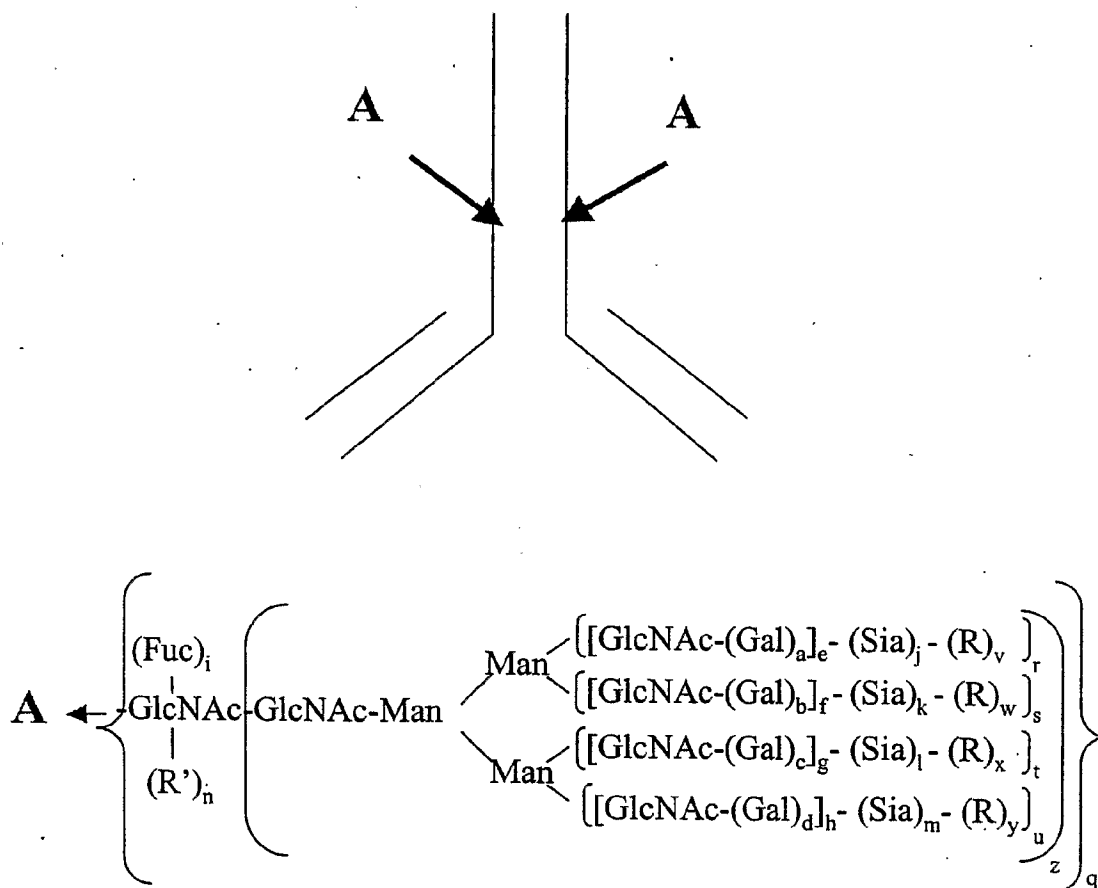


FIG. 52L

244/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 53A



245/498

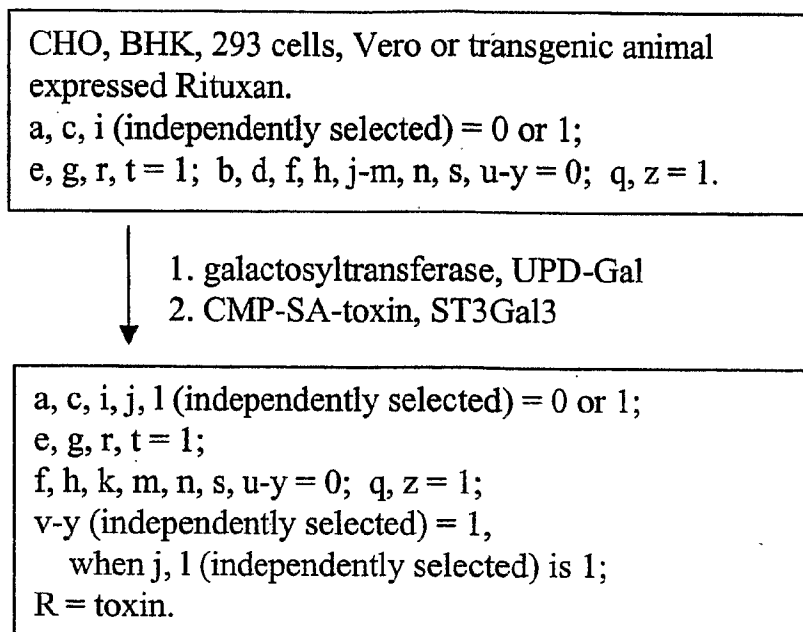


FIG. 53B

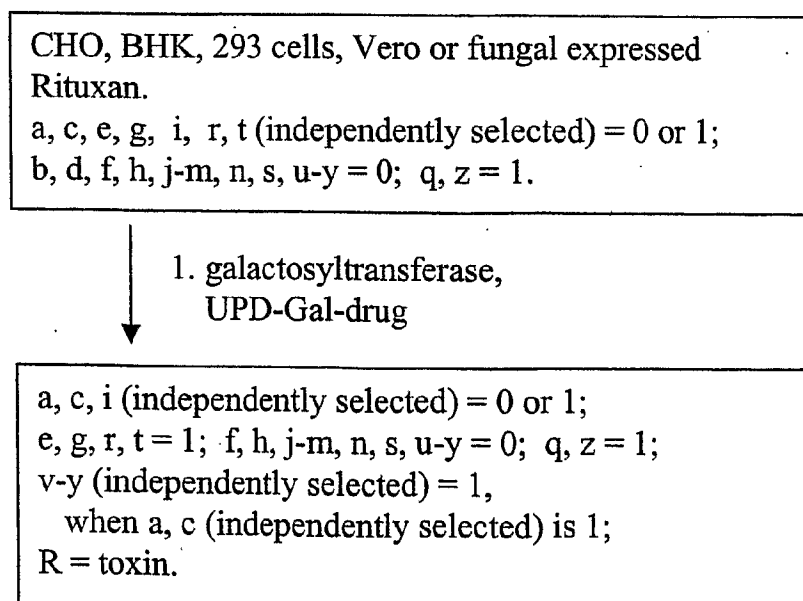


FIG. 53C

246/498

Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

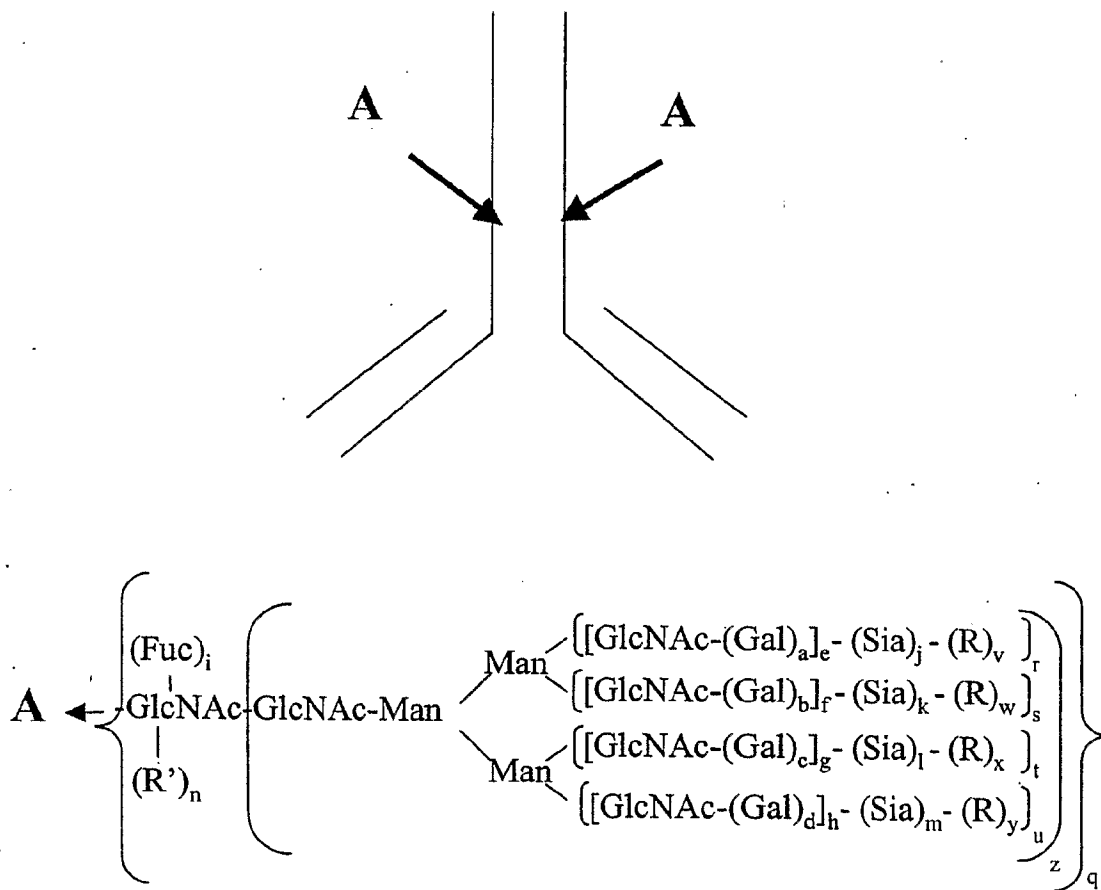
- ↓ 1. Endo-H  
2. Galactosyltransferase, UDP-Gal  
↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 53D

247/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,  
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 53E

248/498

CHO, BHK, 293 cells, Vero or transgenic animal  
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
q, z = 1.



1. galactosyltransferase, UDP-Gal  
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;  
q, z = 1; v-y (independently selected) = 1,  
when j, l (independently selected) is 1;  
R = PEG.

FIG. 53F

Fungi, yeast or CHO expressed Rituxan.

e, g, i, r, t, v, x (independently selected) = 0 or 1;  
a-d, f, h, j-m, n, s, u, w, y = 0; q, z = 1;  
R (independently selected) = mannose, oligomannose,  
polymannose.

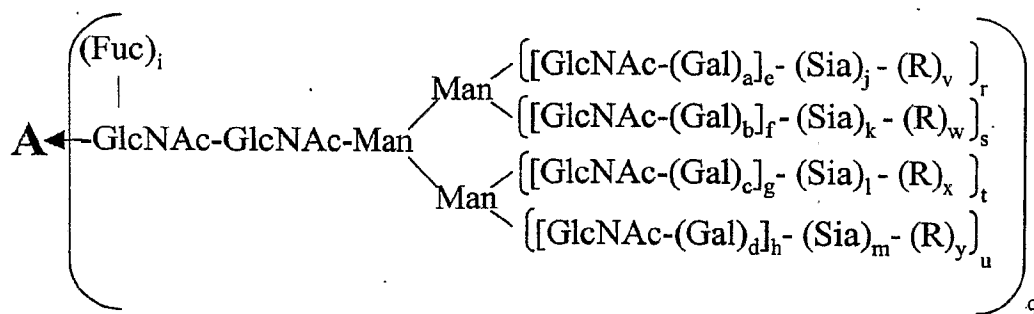
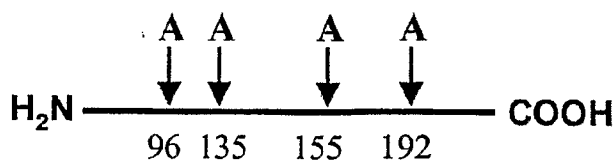


1. mannosidases (alpha and beta)  
2. GNT-I,II, UDP-GlcNAc  
3. Galactosyltransferase, UDP-Gal-radioisotope

a-m, r-z = 0; q, n = 1;  
R' = -Gal-radioisotope complex.

FIG. 53G

249/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = mannose, polymer.

FIG. 54A

250/498

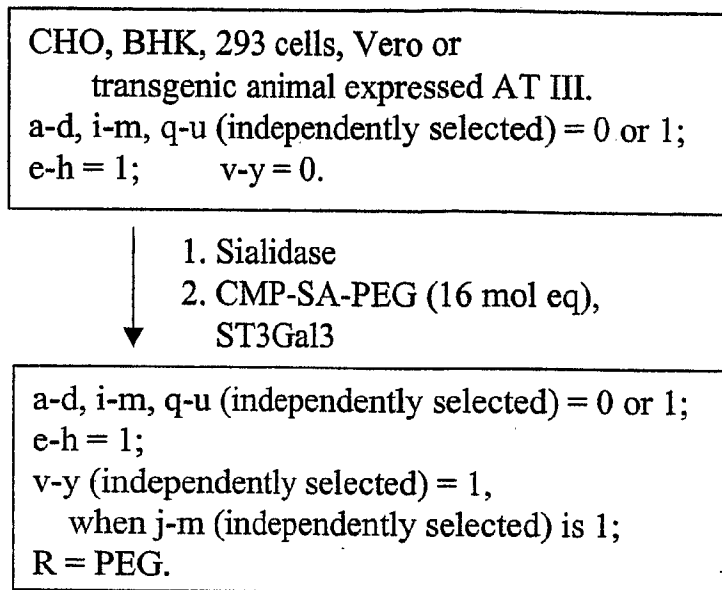


FIG. 54B

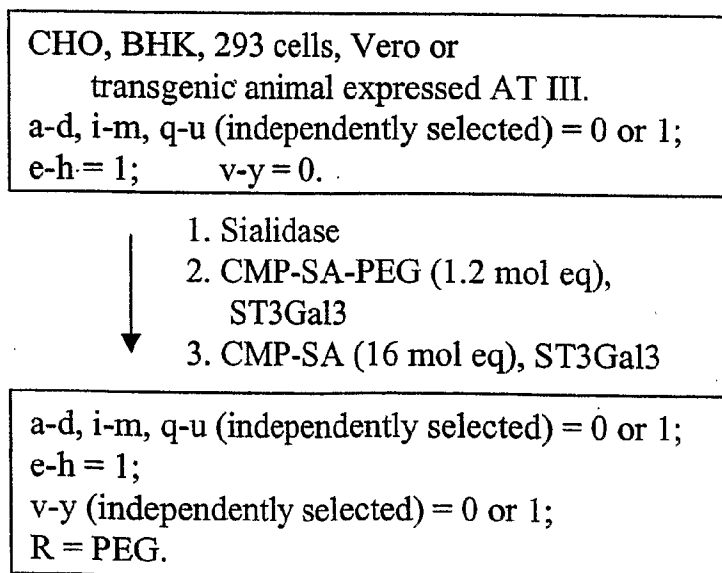


FIG. 54C

251/498

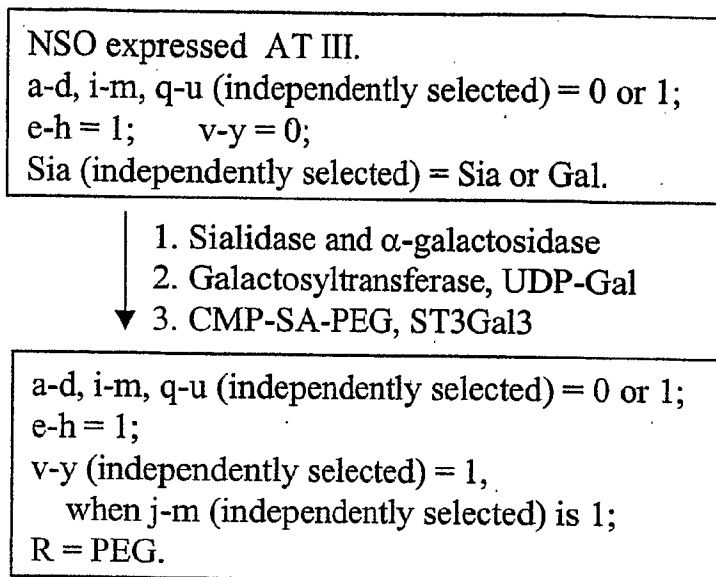


FIG. 54D

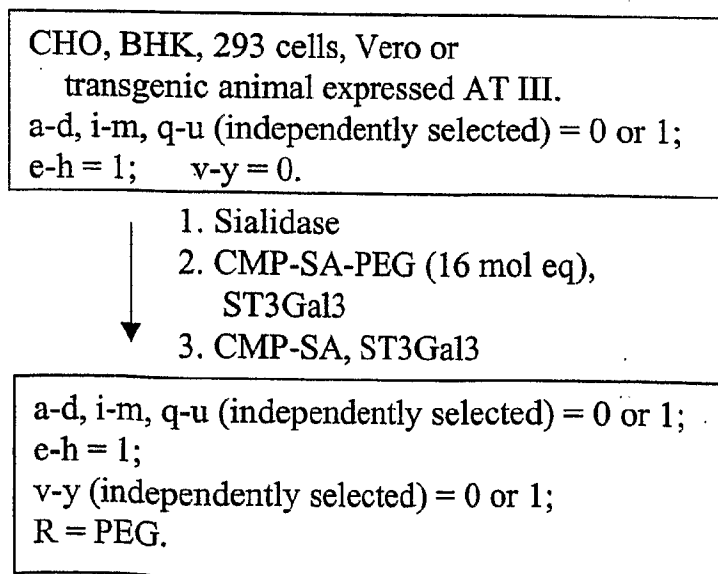


FIG. 54E

252/498

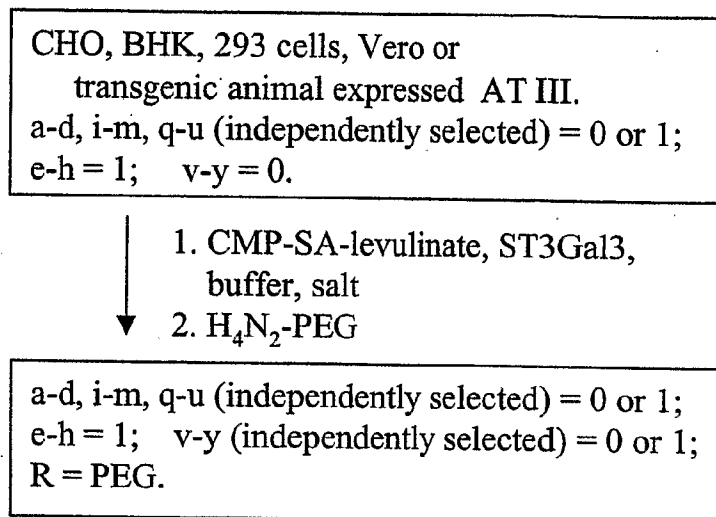


FIG. 54F

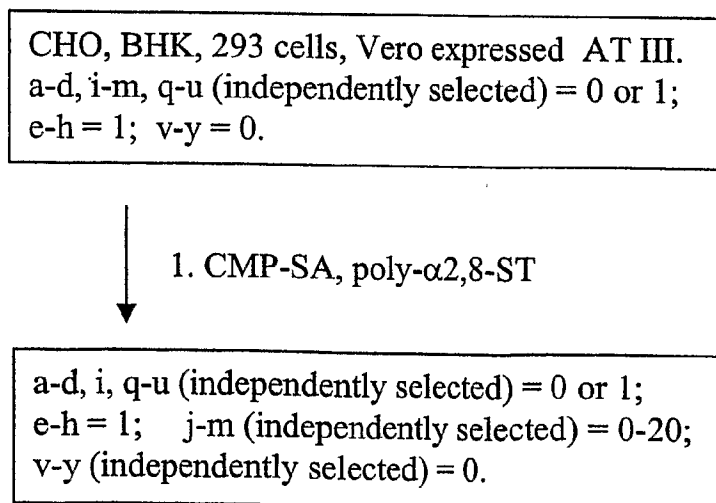
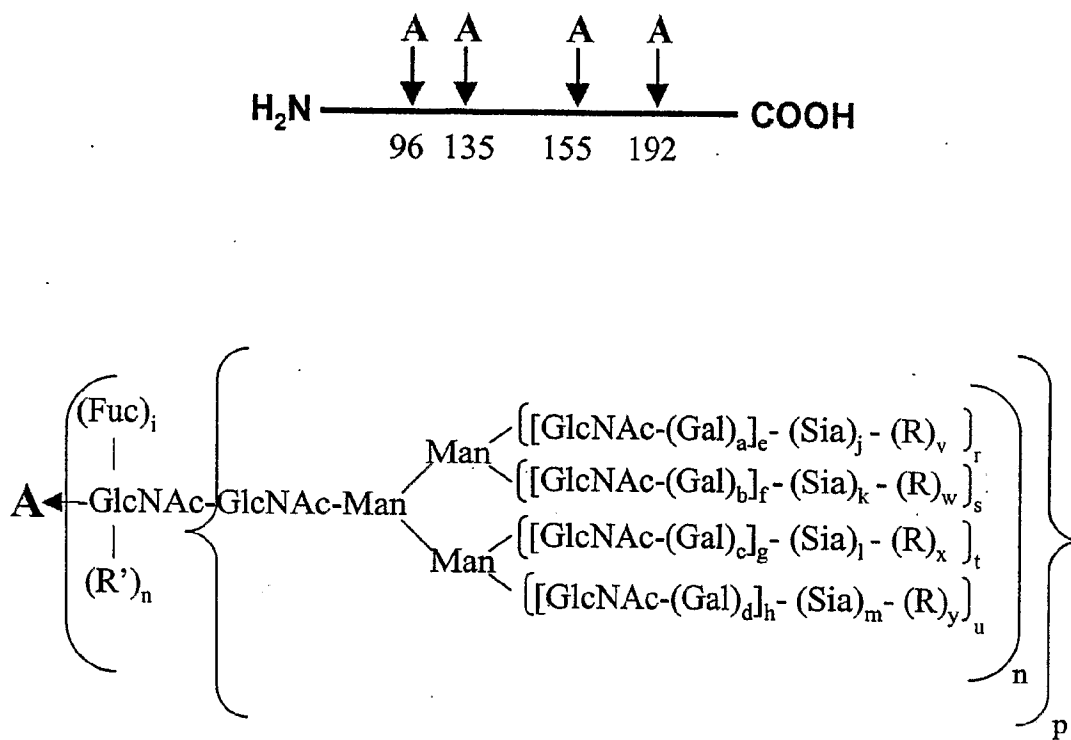


FIG. 54G



253/498



a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100.

R = polymer, linker, mannose.

R' = H, sugar, glycoconjugate.

FIG. 54H

254/498

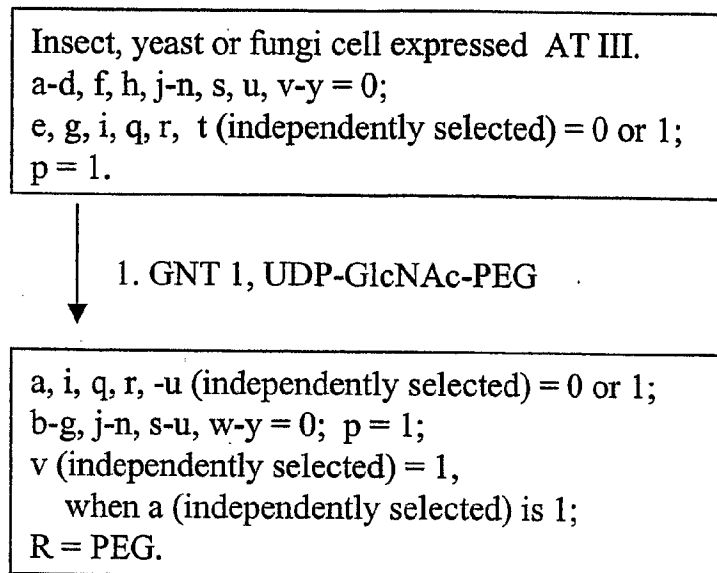


FIG. 54I

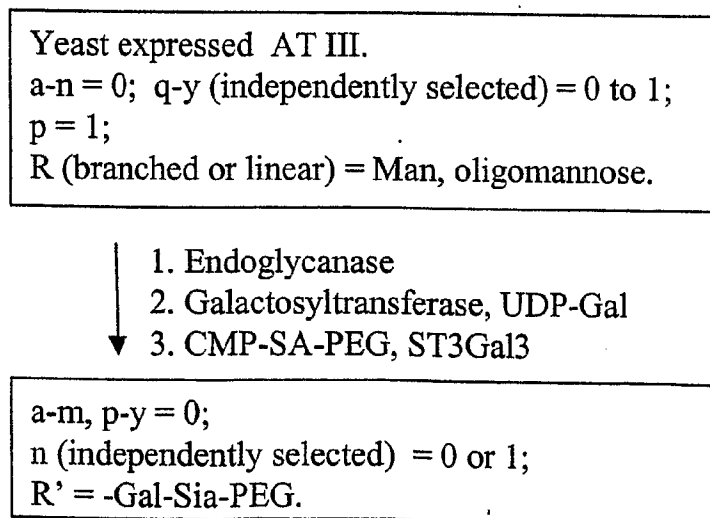


FIG. 54J

255/498

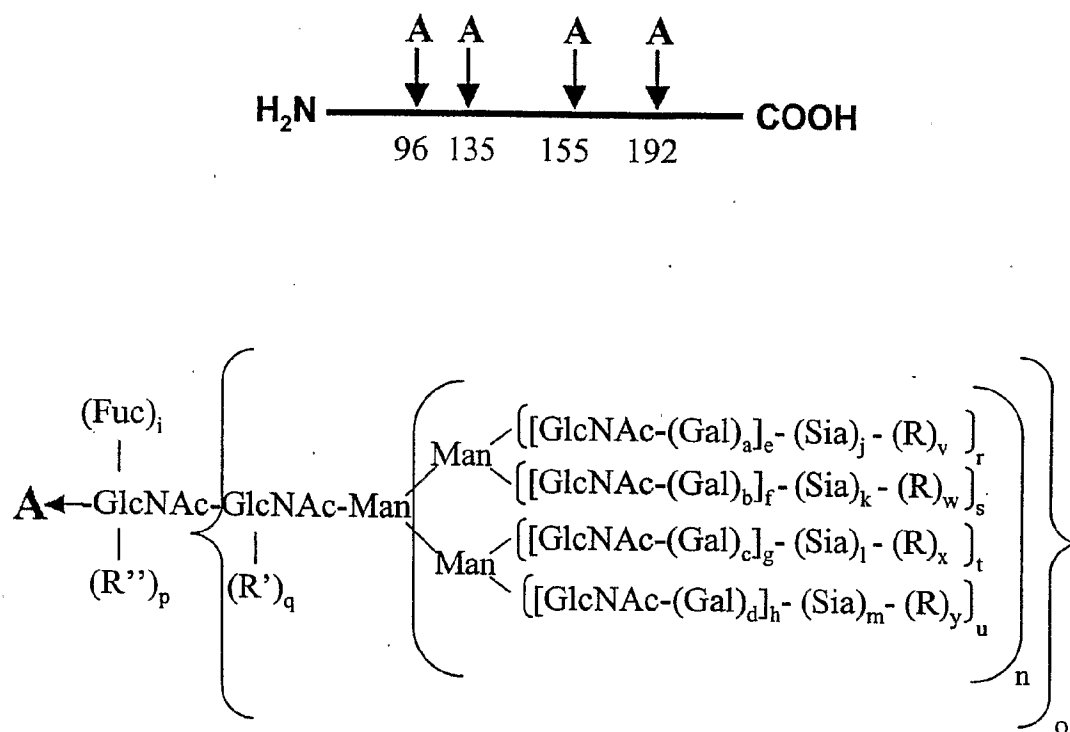
CHO, BHK, 293 cells, Vero expressed AT III.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, transferrin  
treated with endoglycanase

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 54K

256/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer.

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 54L

257/498

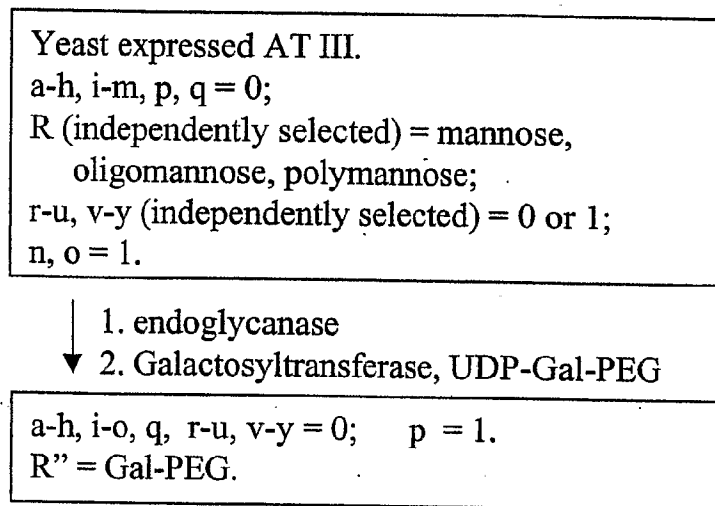


FIG. 54M

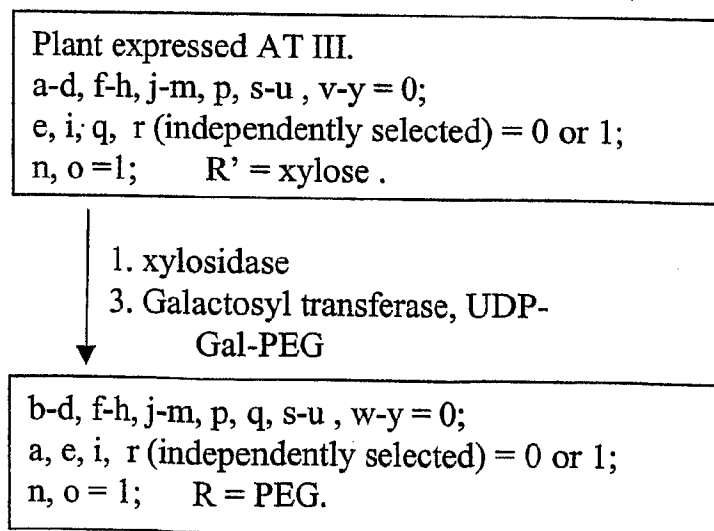


FIG. 54N

258/498

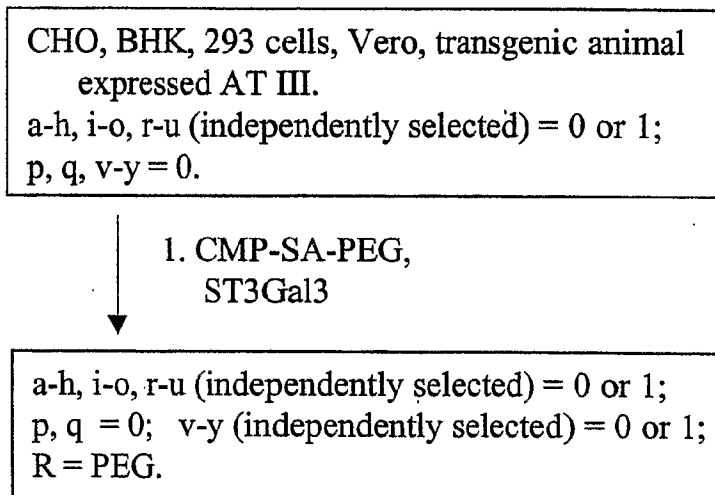
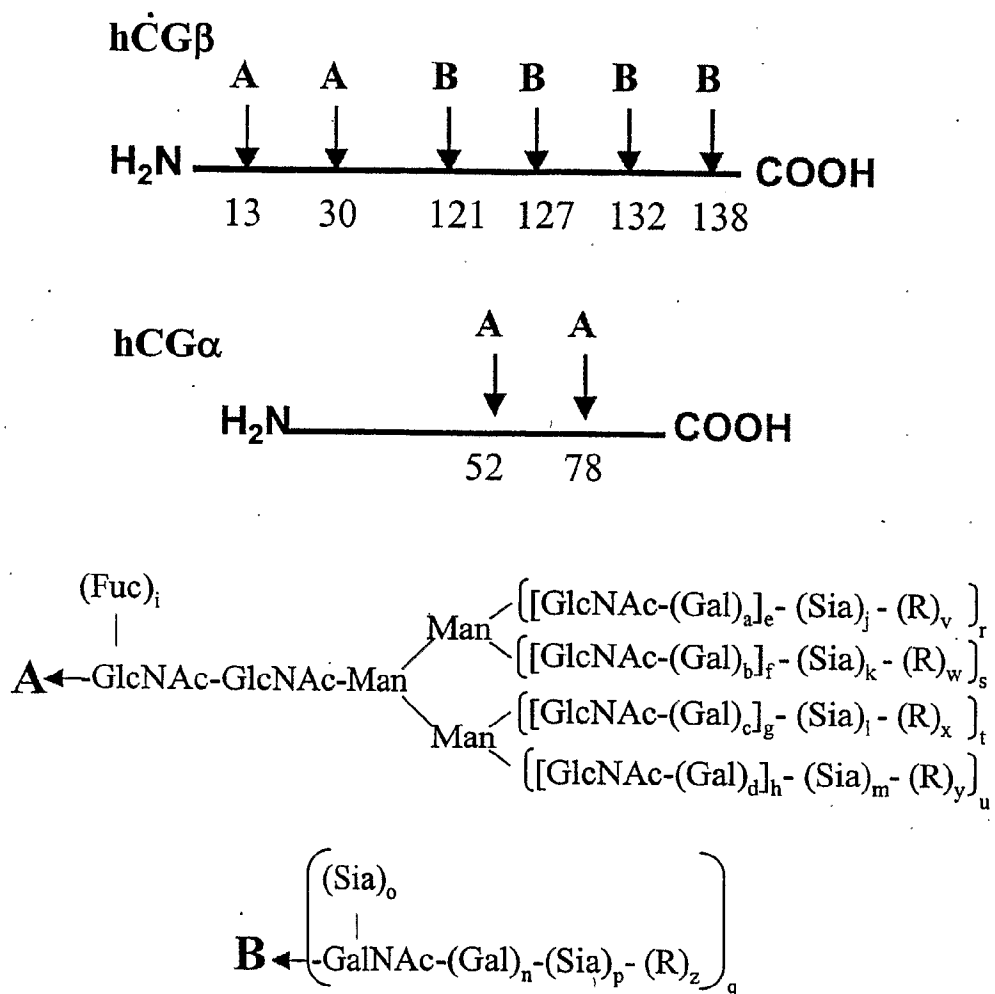


FIG. 540

259/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer

FIG. 55A

260/498

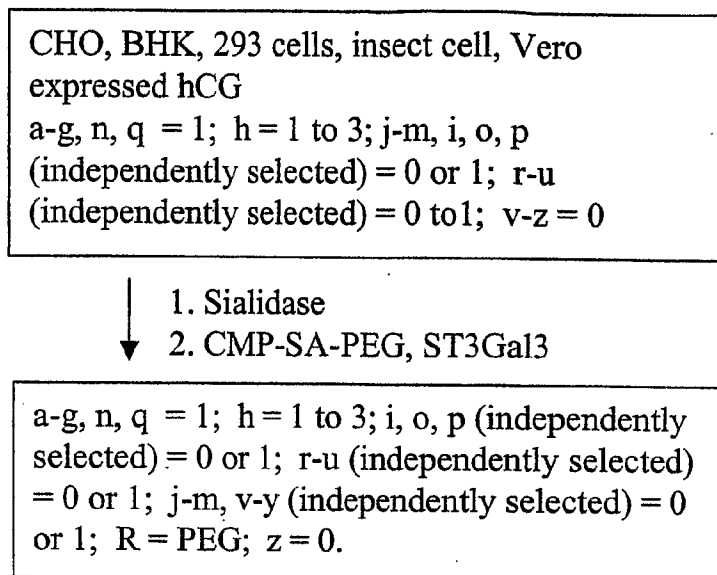


FIG. 55B

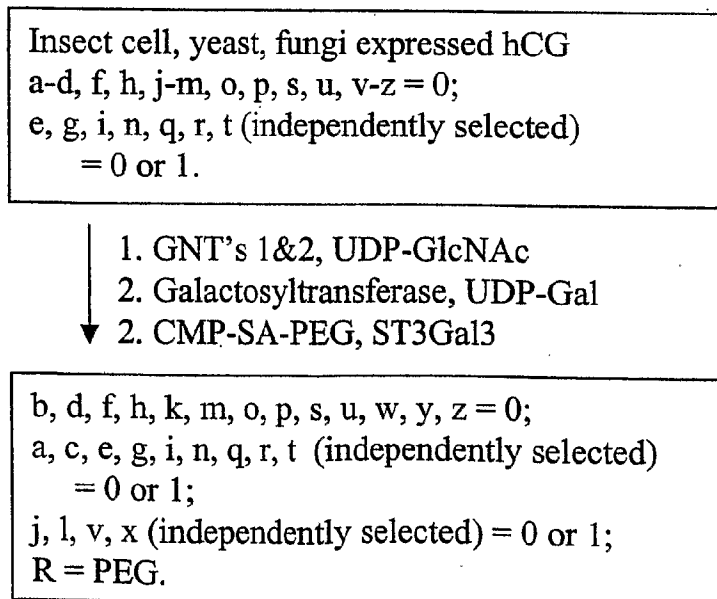


FIG. 55C



261/498

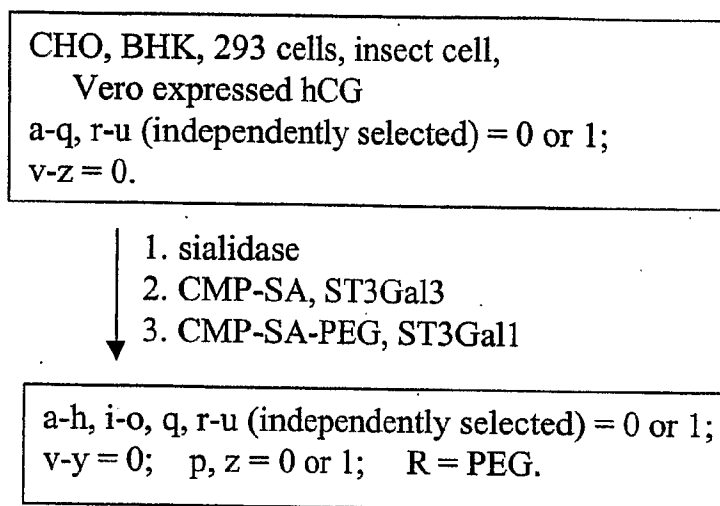


FIG. 55D

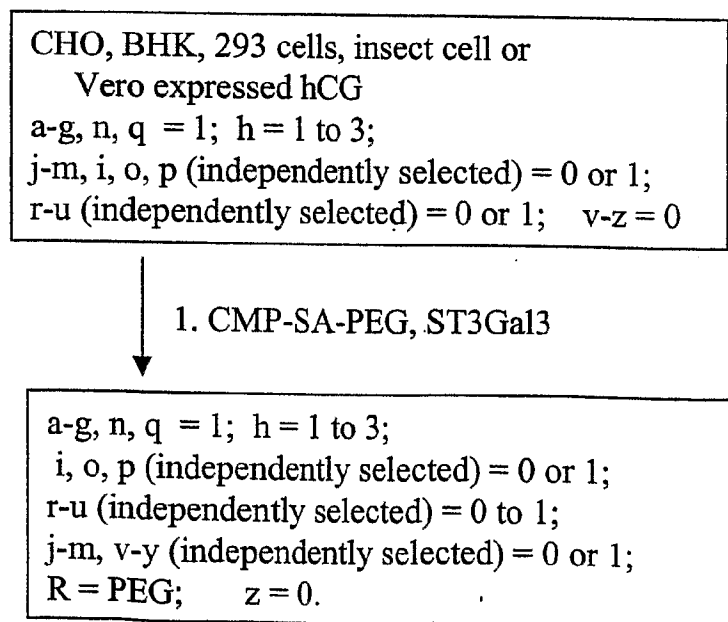


FIG. 55E

262/498

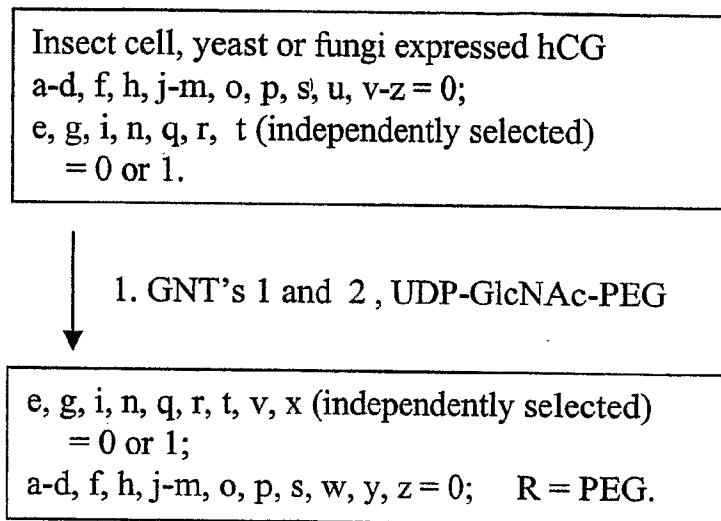


FIG. 55F

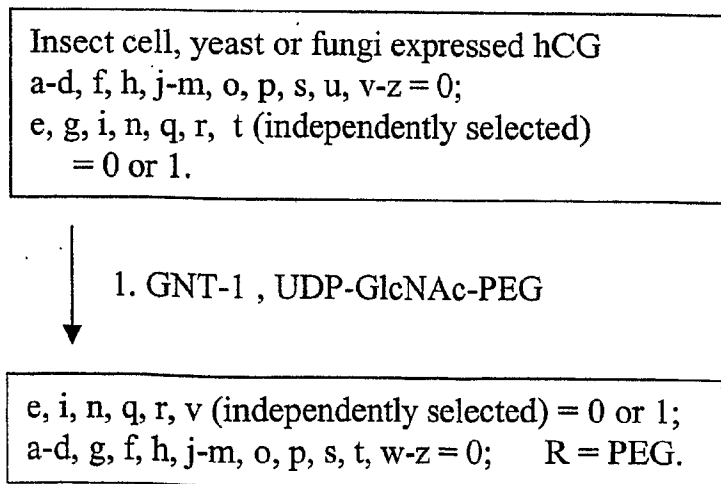


FIG. 55G

263/498

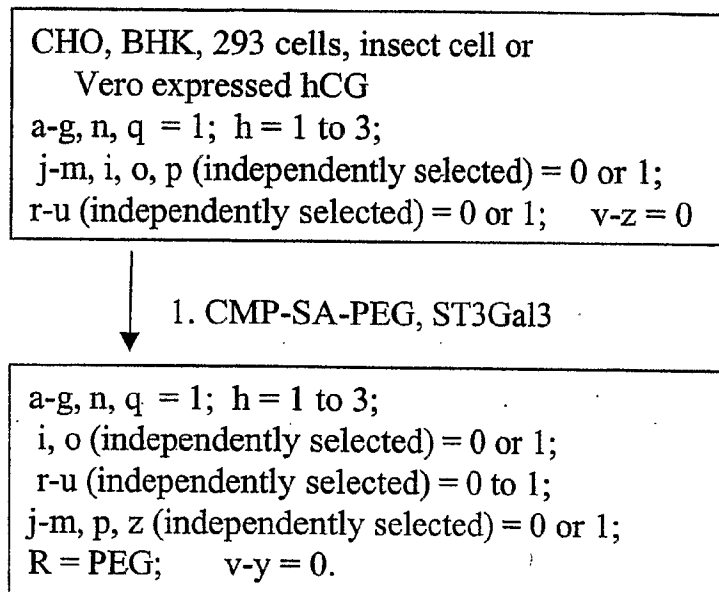


FIG. 55H

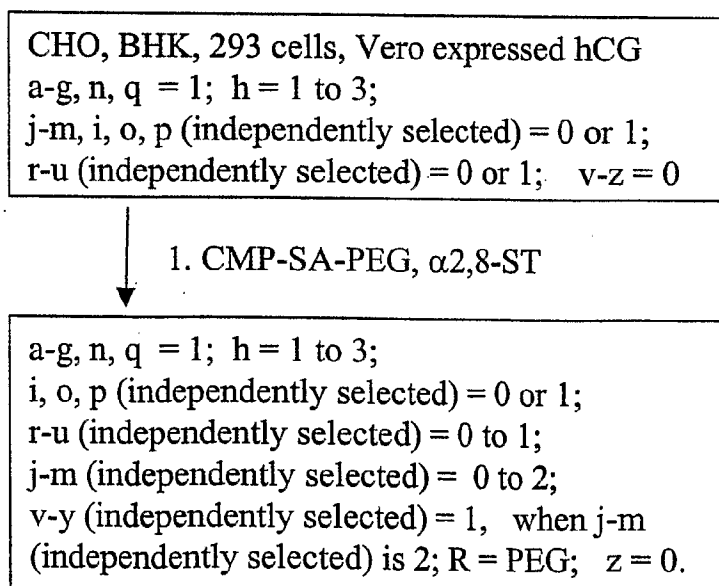


FIG. 55I

264/498

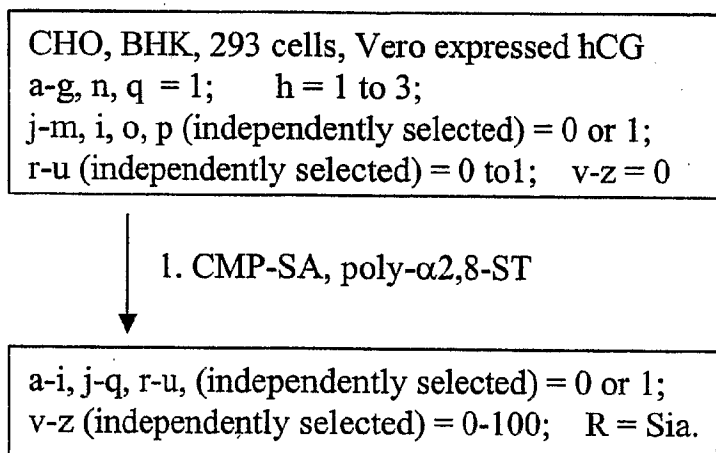
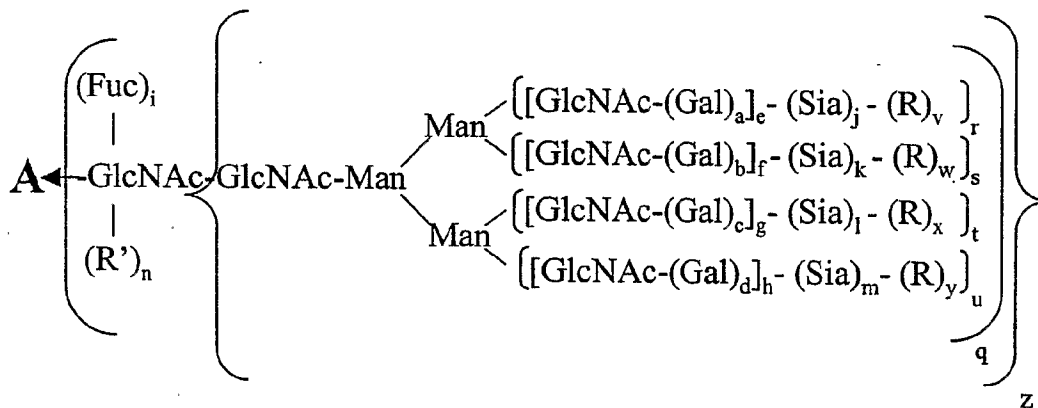
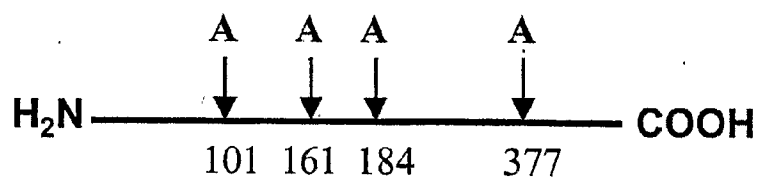


FIG. 55J

265/498



a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 56A

266/498

CHO, BHK, 293 cells, insect cells, Vero expressed  
and secreted alpha-galactosidase  
a-h, i-m, q-u (independently selected) = 0 or 1;  
z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Endo-H  
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;  
n, v-y = 0; z = 1; and when z = 0 and q = 1,  
then n (independently selected) = 0 or 1;  
R' = Gal-PEG-transferrin.

FIG. 56B

CHO, BHK, 293 cells, Insect cells,  
Vero expressed and secreted alpha-galactosidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1; n, v-y  
= 0; and when a-n = 0, then r-u (independently selected) = 0  
or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Sialidase  
2. CMP-SA-linker-Mannose-6-phosphate  
ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1;  
n = 0; z = 1; R = mannose-6-phosphate; and when a-n  
= 0, then r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

FIG. 56C

267/498

NSO expressed alpha-galactosidase.  
 a-d, i-m, q-u (independently selected) = 0 or 1;  
 e-h = 1; v-y = 0;  
 Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-linker-mannose-6-phosphate  
sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;  
 v-y (independently selected) = 1, when j-m (independently  
 selected) is 1; R = mannose-6 phosphate

FIG. 56D

CHO, BHK, 293 cells, Insect cells, Vero expressed and  
 secreted alpha-galactosidase  
 a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
 n, v-y = 0; and when a-n = 0, then r-u (independently  
 selected) = 0 or 1; v-y (independently selected) = 0-100;  
 R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
  2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0; z  
 = 1; R = PEG; and when a-n = 0, then r-u (independently  
 selected) = 0 or 1; v-y = 0-100; R = mannose or mannose  
 with mannose-6-phosphate.

FIG. 56E

268/498

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-galactosidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,  
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate;  
v-y (independently selected) = 0 or 1;  
R = mannose-linker-ApoE.

FIG. 56F

CHO, BHK, 293 cells, Insect cells, Vero, yeast,  
fungi expressed alpha-galactosidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H  
2. galactosyltransferase,  
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;  
R' = galactose-linker-alpha2-macroglobulin.

FIG. 56G



269/498

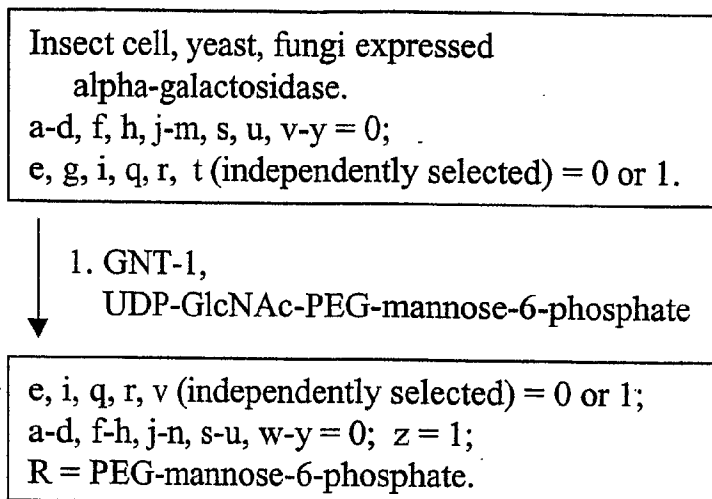


FIG. 56H

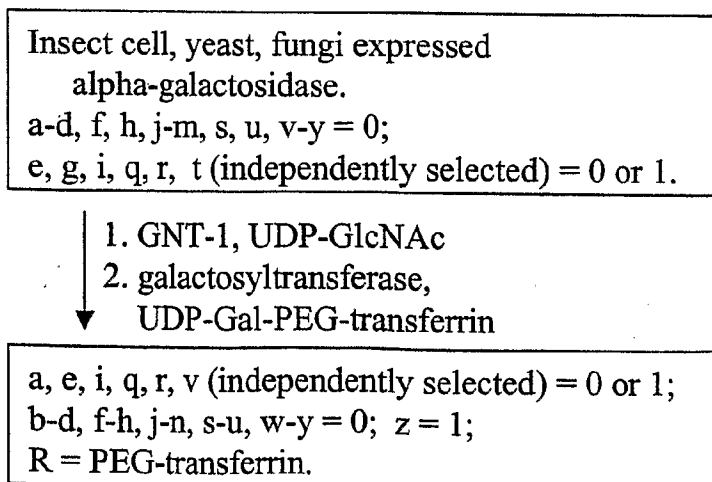


FIG. 56I

270/498

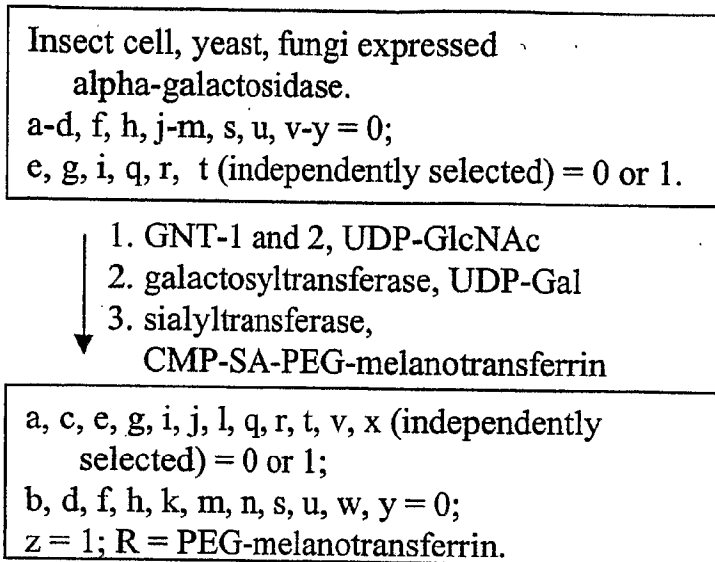
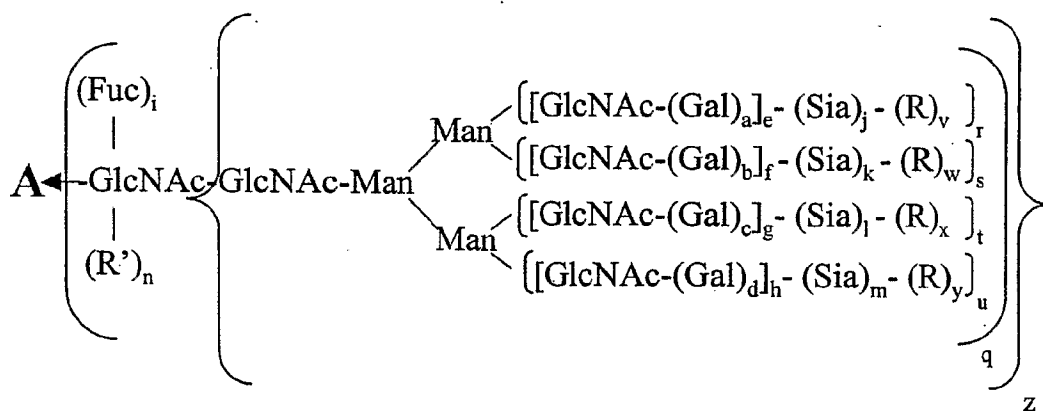
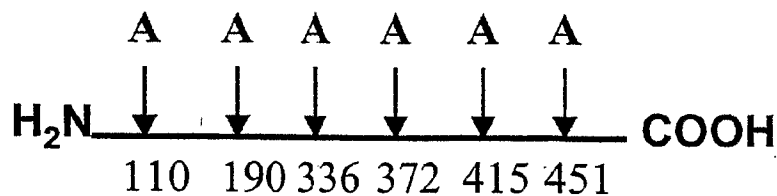


FIG. 56J

271/498



a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 57A

272/498

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Endo-H  
↓  
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;  
n, v-y = 0; z = 1; and when z = 0 and q = 1, then n  
(independently selected) = 0 or 1; R' = Gal-PEG-transferrin.

FIG. 57B

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Sialidase  
↓  
2. CMP-SA-linker-Mannose-6-phosphate ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;  
z = 1; R = mannose-6-phosphate; and when a-n = 0,  
then r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

FIG. 57C

273/498

NSO expressed alpha-iduronidase.

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;  
v-y = 0; Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  - ↓ 3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = mannose-6 phosphate

FIG. 57D

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
  2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;  
z = 1; R = PEG; and when a-n = 0, then r-u  
(independently selected) = 0 or 1; v-y = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

FIG. 57E

274/498

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-iduronidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,  
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1; j-m (independently  
selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate;  
v-y (independently selected) = 0 or 1;  
R = mannose-linker-ApoE.

FIG. 57F

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-iduronidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1;  
z = 1; r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H  
2. galactosyltransferase,  
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;  
R' = galactose-linker-alpha2-macroglobulin.

FIG. 57G

275/498

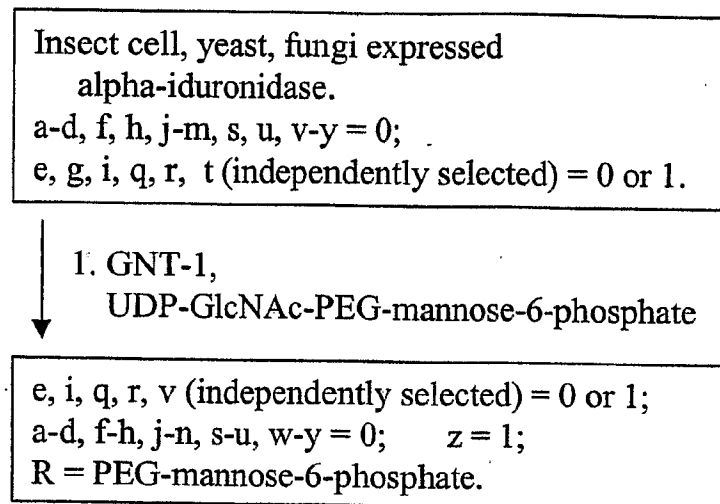


FIG. 57H

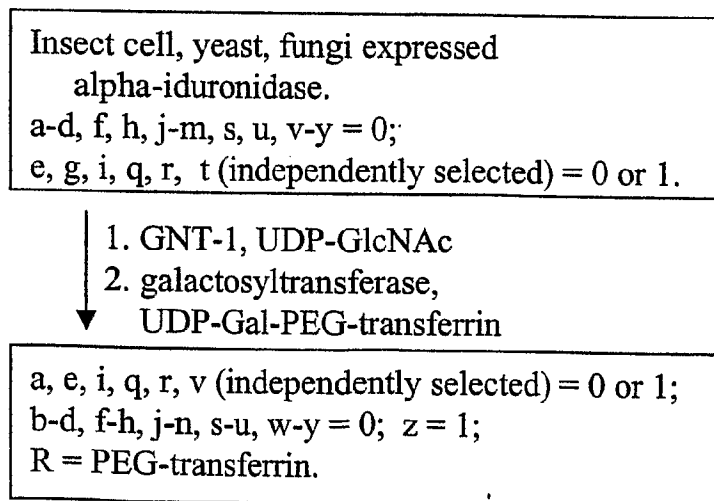


FIG. 57I

276/498

Insect cell, yeast, fungi expressed  
alpha-iduronidase.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.

- ↓ 1. GNT-1 and 2, UDP-GlcNAc  
2. galactosyltransferase, UDP-Gal  
3. sialyltransferase,  
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x

(independently selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0; z = 1;

R = PEG-melanotransferrin.

FIG. 57J



277/498

FIG. 58A

ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT  
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG  
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT  
GCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTG  
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA  
GCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT  
CCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTGCGCCG  
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC  
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT  
TTCCAGCGCCGGGCAGGAGGGGTCTGGTTGCCTCCCATCTGCAGAG  
CTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG  
A

FIG. 58B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu  
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr  
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro  
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser  
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe  
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro  
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val  
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His  
Leu Ala Gln Pro

278/498

FIG. 59A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA  
AGAATATAGTTATCAAGTTAAGTAAAATGTCAATAGCCTTTTAATTTA  
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAAACATTAACTTTAT  
ACTTTTAAATTTAATGTATAGAATAGAGATATACATAGGATATGTAAA  
TAGATACACAGTGTATATGTGATTAAAATATAATGGGAGATTCAATC  
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC  
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA  
AAGAGTGTATAAAGAAAGCAAAAAGAGAAGTAGAAAGTAACACAGG  
GGCATTGGAAGAAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC  
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC  
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA  
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT  
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGG  
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTCTTTTCTCC  
TGCTTGAAGGACAGACATGACTTTGGATTTCCCCAGGAGGAGTTTGG  
CAACCAGTTCCAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGA  
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT  
GGGATGAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAG  
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA  
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT  
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTGT  
GCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCTTTTTCTTTGTCA  
ACAAACTTGCAAGAAAGTTTAAGAAGTAAGGAATGAAAACCTGGTTCA  
ACATGGAAATGATTTTCATTGATTCGTATGCCAGCTCACCTTTTTATG  
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT  
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTAG  
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT  
ATCTATTTAAATATTTTTAAAATATTATTTAATTAACTATTTATAAAC  
AACTTATTTTTGTTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA  
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTGTGTTGTT  
CATTGAACTTTTGCTATGGAACCTTTGTAAGTTGTTTATTCTTTAAAATG  
AAATTCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA  
CTTCATTTGTCCATCAATATTATATTCAAGATATAAGTAAAAATAAAC  
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC  
TAACAAATACAATTCTGCTCTCTTGTGTATTTGATTTTTGTATGAAAA  
AAACTAAAAATGGTAATCATACTTAATTATCAGTTATGGTAAATGGT  
ATGAAGAGAAGAAGGAACG

279/498

## FIG. 59B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser  
Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr  
Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala  
Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr  
Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu  
Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val  
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe  
Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val  
Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu  
Arg Ser Lys Glu

## FIG. 59C

ATGGCCCTCCTGTTCCCTCTACTGGCAGCCCTAGTGATGACCAGCTAT  
AGCCCTGTTGGATCTCTGGGCTGTGATCTGCCTCAGAACCATGGCCTA  
CTTAGCAGGAACACCTTGGTGCTTCTGCACCAAATGAGGAGAATCTCC  
CCTTTCTTGTGTCTCAAGGACAGAAGAGACTTCAGGTTCCCCCAGGAG  
ATGGTAAAAGGGAGCCAGTTGCAGAAGGCCCATGTCATGTCTGTCTCT  
CCATGAGATGCTGCAGCAGATCTTCAGCCTCTTCCACACAGAGCGCTC  
CTCTGCTGCCTGGAACATGACCCTCCTAGACCAACTCCCACTGGACT  
TCATCAGCAACTGCAACACCTGGAGACCTGCTTGCTGCAGGTAGTGG  
GAGAAGGAGAATCTGCTGGGGCAATTAGCAGCCCTGCACTGACCTTG  
AGGAGGTACTTCCAGGGAATCCGTGTCTACCTGAAAGAGAAGAAATA  
CAGCGACTGTGCCTGGGAAGTTGTCAGAATGGAAATCATGAAATCCT  
TGTTCTTATCAACAAACATGCAAGAAAGACTGAGAAGTAAAGATAGA  
GACCTGGGCTCATCTTGA

## FIG. 59D

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr Ser Pro Val  
Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr  
Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu Lys Asp  
Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser Gln Leu Gln Lys  
Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His  
Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr  
Gly Leu His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe  
Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Val  
Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met Gln Glu Arg  
Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser

280/498

FIG. 60A

ATGACCAACAAGTGTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC  
ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCCCTACAAAGA  
AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG  
GCTTGAATATTGCCTCAAGGACAGGATGAACTTTGACATCCCTGAGG  
AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGCATTGACC  
ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA  
TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA  
TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC  
TGGAGAAAGAAGATTTTACCAGGGGAAACTCATGAGCAGTCTGCAC  
CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA  
GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA  
ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT  
CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTTCAAGCATTCTTC  
AACCAGCAGATGCTGTTTAAAGTGACTGATGGCTAATGTACTGCAAAT  
GAAAGGACACTAGAAGATTTTGAATTTTATTAAATTATGAGTTATT  
TTTATTTAT TTAAATTTTATTTTGGAAAATAAATTATTTTGGTGC

FIG. 60B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala  
Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp  
Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu  
Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln  
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp  
Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile  
Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val  
Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

281/498

FIG. 61A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG  
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT  
CCTGCACCGGCGCCGGCGCGCCAACGCGTTCCTGGAGGAGCTGCGGC  
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA  
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC  
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA  
GAATGGGGGGCTCCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCT  
GCCTCCCTGCCTTCGAGGGGCCGGAACGTGTGAGACGCACAAGGATGAC  
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG  
TGACCACACGGGCACCAAGCGCTCCTGTGCGGTGCCACGAGGGGTACT  
CTCTGCTGGCAGACGGGGTGTCTGTCACACCCACAGTTGAATATCCA  
TGTGGAAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAACCCCA  
AGGCCGAATTGTGGGGGGGCAAGGTGTGCCCCAAAGGGGAGTGTCCA  
TGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC  
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA  
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC  
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG  
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACCAACGACATC  
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTGGTG  
CCCCTCTGCCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC  
GTGCGCTTCTCATTTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGG  
CGCCACGGCCCTGGAGCTCATGGTGCTCAACGTGCCCCGGCTGATGA  
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT  
ATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA  
CTCCTGCAAGGGGGACAGTGGAGGCCACATGCCACCCACTACCGGG  
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA  
ACCGTGGGCCACTTTGGGGGTGTACACCAGGGTCTCCAGTACATCGA  
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCAGGAGTCCTCC  
TGCGAGCCCCATTTCCC

282/498

FIG. 61B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys  
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg  
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys  
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg  
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys  
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro  
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val  
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg  
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro  
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys  
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln  
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile  
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile  
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg  
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp  
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu  
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser  
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu  
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg  
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp  
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg  
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly  
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met  
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

283/498

FIG. 62A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC  
CATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTT  
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA  
TTCAGGTAAATTGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAAT  
GTATGGAAGAAAAGTGTAGTTTTGAAGAACCACGAGAAGTTTTTGAA  
AACACTGAAAAGACAACCTGAATTTTGGAAGCAGTATGTTGATGGAGA  
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG  
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGA  
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG  
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT  
GAGGGATATCGACTTGCAGAAAACCAGAAGTCCTGTGAACCAGCAGT  
GCCATTTCCATGTGGAAGAGTTTCTGTTTCACAACTTCTAAGCTCAC  
CCGTGCTGAGGCTGTTTTTCCTGATGTGGACTATGTAAATCCTACTGA  
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA  
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA  
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA  
GGCTCTATCGTTAATGAAAAATGGATTGTAAGTCTGCTGCCCCTGTGTT  
GAAACTGGTGTAAAATTACAGTTGTTCGCAGGTGAACATAATATTGA  
GGAGACAGAACATACAGAGCAAAAGCGAAATGTGATTTCGAGCAATT  
ATTCCTCACCACAACCTACAATGCAGCTATTAATAAGTACAACCATGA  
CATTGCCCTTCTGGAACTGGACGAACCCTTAGTGCTAAACAGCTACG  
TTACACCTATTTGCATTGCTGACAAGGAATACACGAACATCTTCCTCA  
AATTTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA  
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTTGAC  
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT  
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG  
ATAGTGGGGGACCCCATGTTACTGAAGTGGAAGGGACCAGTTTCTTA  
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAATA  
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAA  
AAACAAAGCTCACTTAATGAAAGATGGATTTCCAAGGTTAATTCATT  
GGAATTGAAAATTAACAG

284/498

FIG. 62B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu  
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala  
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe  
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu  
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr  
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys  
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn  
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys  
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu  
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser  
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr  
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser  
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe  
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val  
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr  
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn  
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn  
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr  
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly  
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln  
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe  
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser  
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu  
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr  
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr



285/498

FIG. 63A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG  
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCA  
GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC  
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCC  
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAG  
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG  
GGGGGTTTCAAAGTGGAAGAACACACGGCGTGCCACTGCAGTACTTG  
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT  
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT  
GTGAGATAAACTCTCCTTTTCTTACCATAACCACTTTGACACGCTTC  
AAGGATATACTGCAGCTTTACTGCCTTCCTCCTTATCCTACAGTACAA  
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAGCTTG  
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 63B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu  
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu  
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe  
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn  
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His  
Lys Ser

286/498

FIG. 63C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC  
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA  
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG  
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCCC  
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT  
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC  
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG  
ATTGTACTGTGCGAGGCCTGGGGCCCAGCTACTGCTCCTTTGGTGAAA  
TGAAAGAATAA

FIG. 63D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys  
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe  
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val  
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val  
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr  
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys  
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

287/498

FIG. 64A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC  
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT  
GCACCGCCGAGCTTCCCGGGATGAGGGCCCCCGGTGTGGTCACCCGG  
CGCGCCCCAGGTGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG  
GTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTCG  
CTCCCTCTGGGCCTCCCAGTCCTGGGCGCCCCACCACGCCTCATCTGT  
GACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG  
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT  
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGAT  
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG  
CTGTGCGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC  
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG  
CCTTCGCAGCCTCACCCTCTGCTTCGGGCTCTGCGAGCCCAGAAGG  
AAGCCATCTCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA  
ATCACTGCTGACACTTTCCGCAAACCTCTTCCGAGTCTACTCCAATTC  
CTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG  
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC  
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC  
GTCGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA  
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC  
AACTCTGAGATCTAAGGATGTCACAGGGCCAACCTGAGGGGCCAGAG  
CAGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG  
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC  
AGGACACGCTTTGGAGGCGATTTACCTGTTTTTCGCACCTACCATCAGG  
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG  
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA  
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCTCTGG  
CTCTCATGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGA  
ACTGAAACCACCAAAAAAAAAAAAAA

288/498

FIG. 64B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu Leu Ser  
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser  
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr  
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys  
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val  
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu  
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser  
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile  
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe  
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr  
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

FIG. 65

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala  
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn  
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly  
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg  
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val  
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly  
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr  
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly  
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

289/498

FIG. 66A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT  
CTCTGCACCCGCCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGC  
ATGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGA  
GAACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAT  
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT  
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCCTTG  
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA  
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA  
ACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG  
TCCAGGAGTGA

FIG. 66B

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro  
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu  
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr  
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg  
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro  
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu  
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

290/498

FIG. 67A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG  
GGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGA  
AAACCTTAAGAAATATTTTAATGCAGGTCATTCAGATGTAGCGGATA  
ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT  
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACT  
TTTTAAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA  
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG  
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT  
GAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTG  
AACTGTCGCCAGCAGCTAAAACAGGGAAGCGAAAAAGGAGTCAGAT  
GCTGTTTCGAGGTCGAAGAGCATCCCAGTAA

FIG. 67B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu  
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr  
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile  
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser  
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val  
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys  
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln  
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys  
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

291/498

FIG. 68A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT  
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA  
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC  
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC  
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA  
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC  
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA  
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC  
CAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT  
GACCACCGGCAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG  
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC  
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG  
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAG  
GAGCTTGACAGAGACACAGTTTTTGTCTCTGGTGAATTACATCTTCTT  
AAAGGCCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG  
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG  
AAGCGTTTAGGCATGTTTAAACATCCAGCACTGTAAGAAGCTGTCCAG  
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT  
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC  
CACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGC  
CAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAA  
GAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG  
CTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAG  
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC  
TGCTGGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCCGA  
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATAC  
CAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAT  
AACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC  
CTGGATGACATTAAAGAAGGGTTGAGCTGG

292/498

FIG. 68B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser  
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe  
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe  
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp  
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala  
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln  
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val  
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val  
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys  
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val  
Phe Ala LeuVal Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val  
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser  
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro  
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys  
Phe Leu Glu Asn Glu AspArg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile  
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys  
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala  
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro  
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val  
Val Asn Pro Thr Gln Lys



293/498

FIG. 69A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTTT  
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT  
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCA  
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC  
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCGTGGGCATCAGGT  
GCCCCGCCCTGCATCCCTAAAAGCTTTCGGCTACAGCTCGGTGGTGTGT  
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCGACCTTTCCT  
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG  
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG  
GCCTGCTACTGACCCTGCAGCCAGAACAGAAAGTTCCAGAAAGTGAAG  
GGATTTGGAGGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC  
CTGTACCCCCCTGCCCAAATTTGCTACTTAAATCGTACTTCTCTGAA  
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA  
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCCA  
GTTGCACAACCTTCAGCCTCCCAGAGGAAGATACCAAGCTCAAGATAC  
CCCTGATTCACCGAGCCCTGCAGTTGGCCCAGCGTCCCGTTTCACTCC  
TTGCCAGCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG  
GTGAATGGGAAGGGGTCACTCAAGGGACAGCCCGGAGACATCTACC  
ACCAGACCTGGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG  
AGCACAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT  
GCTGGGCTGTTGAGTGGATAACCCCTTCCAGTGCCTGGGCTTCACCCCT  
GAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCCTACCCTCGCC  
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACGC  
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC  
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCT  
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA  
ACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGG  
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC  
CACAGCATCATCACGAACCTCCTGTACCATGTGGTCGGCTGGACCGAC  
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA  
CTTTGTCGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTTA  
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC  
TGAGGGCTCCCAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC  
TGGACGCAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTCTG  
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG  
CTGTGGGCTTCCTGGAGACAATCTCACCTGGCTACTCCATTACACCT  
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGG  
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG  
TGACTAAAGAGGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

294/498

FIG. 69A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCCCTCTAGGTGGT  
GCCCAGGGCTGGAGGCCCCCTAGAAAAAGATCAGTAAGCCCCAGTGTC  
CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT  
TGGAAACT

FIG. 69B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser  
Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser  
Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys  
Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr  
Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly  
Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln  
Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu  
Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser  
Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser  
Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser  
Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu  
Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys  
Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile  
Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu  
His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu  
Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp  
Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg  
Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val  
Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu  
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro  
Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser  
Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn  
Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu  
Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr  
Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys  
Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu  
Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn  
Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu  
Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

295/498

FIG. 70A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG  
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCGATTTCAGAA  
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAAACGCA  
GATGATATACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA  
GCAACCGGGTGGAAATATTGCTGGTGCAACAGTGGCAGGGCACAGTGC  
CACTCAGTGCCTGTCAAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG  
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTTCGTGTGCCAGTG  
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCA  
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCAC  
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG  
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG  
GCCTGGGGAACCACTACTGCAGAAACCCAGATCGAGACTCAAA  
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCT  
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG  
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC  
CTCCTGCCTCCCGTGGAATTCATGATCCTGATAGGCAAGGTTTACAC  
AGCACAGAACCCCAAGTGCCCAGGCACTGGGCCTGGGCAAACATAATT  
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG  
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC  
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG  
GAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCT  
TTGCCAAGCACAGGAGGTCGCCGGGAGAGCGGTTCTGTGCGGGGGC  
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG  
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA  
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA  
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT  
TGCGCTGCTGCAGCTGAAATCGGATTTCGTCCCGCTGTGCCCAGGAGA  
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG  
CCGGAAGTGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC  
CTTGTCTCCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTCAGACT  
GTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAG  
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCC  
CAGGCAAACCTTGACGACGCCTGCCAGGGCGATTTCGGGAGGCCCCCT  
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT  
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG  
GTTACCAACTACCTAGACTGGATTTCGTGACAACATGCGACCGTGACC  
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

296/498

FIG. 70B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val  
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr  
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp  
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly  
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn  
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro  
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu  
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys  
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp  
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp  
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser  
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr  
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met  
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu  
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His  
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser  
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe  
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser  
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser  
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly  
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys  
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu  
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg  
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu  
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn  
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro  
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly  
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg  
Asp Asn Met Arg Pro

297/498

FIG. 71A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA  
TGTACAGGATGCAACTCCTGTCTTGCATTGCACTAATTCTTGCACCTG  
TCACAAACAGTGCACCTACTTCAAGTTCGACAAAGAAAACAAAGAAA  
ACACAGCTACAACCTGGAGCATTACTGCTGGATTTACAGATGATTTTG  
AATGGAATTAATAATTACAAGAATCCCAAACCTCACCAGGATGCTCAC  
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC  
AGTGTCTAGAAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA  
GCTCAAAGCAAAAACCTTCACTTAAGACCCAGGGACTTAATCAGCAA  
TATCAACGTAATAGTTCTGGAACATAAGGGATCTGAAACAACATTCA  
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC  
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA  
TTAAGTGCTTCCCACTTAAACATATCAGGCCTTCTATTTATTTATTTA  
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG  
TAACTATTATTCTTAATCTTAAACATAAATATGGATCTTTTATGAT  
TCTTTTTGTAAAGCCCTAGGGGCTCTAAAATGGTTTACCTTATTTATCC  
CAAAAATATTTATTATTATGTTGAATGTTAAATATAGTATCTATGTAG  
ATTGGTTAGTAAACCTATTTAATAAATTTGATAAATATAAAAAAAAAA  
AAACAAAAAAAAAAAA

FIG. 71B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn  
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu  
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn  
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr  
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val  
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser  
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu  
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys  
Gln Ser Ile Ile Ser Thr Leu Thr

298/498

FIG. 72A-1

ATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTTCGATTCT  
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGTCA  
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG  
ATTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT  
GTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACAT  
CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCC  
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT  
TCCCATCCTGTCAAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCT  
TCTGAGGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG  
AAGATGATAAAGTCTTCCCTGGTGGAAAGCCATACATATGTCTGGCAG  
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC  
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG  
CCTCATTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG  
AAAAGACACAGACCTTGCACAAATTTATACTACTTTTTTGCTGTATTTG  
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATGCA  
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG  
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA  
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA  
GTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCAT  
CGCCAGGCGTCCTTGGAAATCTCGCCAATAACTTTCCTTACTGCTCAA  
ACACTCTTGATGGACCTTGGACAGTTTCTACTGTTTTTGTCTATCTCTT  
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT  
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG  
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG  
ATGATGACAACCTCTCCTTTCCTTTATCCAAATTCGCTCAGTTGCCAAGA  
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC  
TGGGACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGAAGTTATAAA  
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA  
AAAAGTCCGATTTATGGCATAACAGATGAAACCTTTAAGACTCGTG  
AAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG  
AAGTTGGAGACACACTGTTGATTATATTTAAGAATCAAGCAAGCAGA  
CCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTAT  
TCAAGGAGATTACCAAAGGTGTAAAACATTTGAAGGATTTTCCAAT  
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAG  
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA  
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC  
TCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACAGATA  
ATGTCAGACAAGAGGAATGTCATCCTGTTTTCTGTATTTGATGAGAAC  
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTTCTCCCCAATCCA  
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT  
GCACAGCATCAATGGCTATGTTTTTGATAGTTTGCAGTTGTGAGTTTG  
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTGGAGCACAGA  
CTGACTTCCTTTCTGTCTTCTCTCTGGATATACCTTCAAACACAAAAT

299/498

FIG. 72A-2

GGTCTATGAAGACACACTCACCTATTCCCATTCTCAGGAGAACTGT  
CTTCATGTGCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA  
ACTCAGACTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT  
AGTTGTGACAAGAACAACACTGGTGATTATTACGAGGACAGTTATGAAGA  
TATTTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA  
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCCAAAAGCAATTT  
AATGCCACCACAATTCCAGAAAATGACATAGAGAAGACTGACCCTTG  
GTTTGCACACAGAACACCTATGCCTAAAATACAAAATGTCTCCTCTA  
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT  
CCTTATCTGATCTCCAAGAAGCCAAATATGAGACTTTTTTCTGATGATC  
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA  
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCCC  
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAACTGGGGGACAACTG  
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTAGTACATCA  
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT  
GATAATACAAGTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT  
AGTCAATTAGATACCACTCTATTTGGCAAAAAGTCATCTCCCCTTACT  
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATAATGATTCAA  
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA  
AAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGGAAAAGA  
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGTT  
AGCATCTCTTTGTTAAAGACAAACAAAACCTTCCAATAATTCAGCAACT  
AATAGAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG  
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAA  
AAGTGACACCTTTGATTCATGACAGAATGCTTATGGACAAAAATGCT  
ACAGCTTTGAGGCTAAATCATATGTCAAATAAACTACTTCATCAAA  
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGCCCCATTCCACCA  
GATGCACAAAATCCAGATATGTCGTTCTTTAAGATGCTATTCTTGCCA  
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA  
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG  
AAAAATCTGTGGAAGGTCAGAATTTCTTGCTGAGAAAAACAAAGTG  
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA  
TGGTTTTTCCAAGCAGCAGAAACCTATTTCTTACTAACTTGGATAATT  
TACATGAAAATAATACACACAATCAAGAAAAAAAATTCAGGAAGA  
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC  
AGATACATACAGTGACTGGCACTAAGAATTTTCATGAAGAACCTTTTC  
TACTGAGCACTAGGCCAAAATGTAGAAGGTTTCATATGACGGGGCATA  
TGCTCCAGTACTTCAAGATTTTAGGTCATTAAATGATTCAACAAATAG  
AACAAAGAAACACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA  
AACTTGGAAGGCTTGGGAAATCAAACCAGCAAATTGTAGAGAAATAT  
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAATTTTG  
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCACTA

FIG. 72A-3

300/498

GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC  
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCCCTCACAC  
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC  
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAATAGA  
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTA  
TATATCTGACCAGGGTCCTATTCCAAGACAACCTCTTCTCATCTTCCAG  
CAGCATCTTATAGAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT  
TTCTTACAAGGAGCCAAAAAATAACCTTTCTTTAGCCATTCTAACC  
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG  
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC  
GAAACCAGACTTGCCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA  
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAAACTAGCAATG  
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA  
CAGAGGGAGCGATTAAGTGGAATGAAGCAAACAGACCTGGAAAAGT  
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAAGACTCCCTCCAA  
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC  
AAAAGAAGAGTGGAATCCCAAGAGAAGTCACCAGAAAAAACAGCT  
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAGCAAT  
CATGCAATAGCAGCAATAAATGAGGGACAAAATAAGCCCGAAATAG  
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA  
AACCCACCAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC  
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT  
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAATC  
AGAGCCCCCGCAGCTTTCAAAGAAAAACACGACACTATTTTATTGCTG  
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT  
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAAGAAAGT  
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT  
GGAGAACTAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC  
AGAAGTTGAAGATAATATCATGGTAACCTTCAGAAATCAGGCCTCTC  
GTCCCTATTCTTCTATTCTAGCCTTATTTCTTATGAGGAAGATCAGAG  
GCAAGGAGCAGAACCTAGAAAAAAGCTTTGTCAAGCCTAATGAAACCA  
AACTTACTTTTGGAAAGTGCAACATCATATGGCACCCACTAAAGAT  
GAGTTTGAAGTGCAGGCTGATTGGACCCCTTCTGGTCTGCCACACT  
AACACACTGAACCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT  
TGCTCTGTTTTTCACCATCTTTGATGAGACCAAAGCTGGTACTTCACT  
GAAAATATGGAAAGAACTGCAGGGCTCCCTGCAATATCCAGATGGA  
AGATCCCACTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA  
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA  
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAACATCCATTCT  
ATTCATTTCAGTGGACATGTGTTCACTGTACGAAAAAAGAGGAGTA  
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGAGACAGTGGA



FIG. 72A-4

301/498

AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGAATGCCTTATTGG  
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA  
TAAGTGTGAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT  
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG  
CCAGACTTCATTATTCCGGATCAATCAATGCCTGGAGCACCAAGGAG  
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTCAC  
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT  
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA  
CTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATG  
TGGATTCACTCTGGGATAAAACACAATATTTTTTAACCCTCCAATTATTG  
CTCGATACATCCGTTTGCACCCAACTCATTATAGCATTTCGCAGCACTC  
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT  
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA  
TCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAAGCTCGA  
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA  
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA  
CAGGAGTAACTACTCAGGGAGTAAAATCTCTGCTTACCAGCATGTAT  
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC  
TCTCTTTTTTTCAGAATGGCAAAGTAAAGGTTTTTTCAGGGAAATCAAGA  
CTCCTTCACACCTGTGGTGAACCTCTCTAGACCCACCGTTACTGACTCG  
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG  
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC  
CACTGCAGCACCTGCCACTGCCGTACCTCTCCCTCCTCAGCTCCAGG  
GCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGC  
AGACACTGCCTTGAAGCCTCCTGAATTAACCTATCATCAGTCCCTGCATT  
TCTTTGGTGGGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACTCTTA  
CCTATTTTCTGCAGCTGCTCCCAGATTACTCCTTCCTTCCAATATAACT  
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTCTTCCCTG  
AAAAGTTAGGCCTCTCAGAGTCACCACTTCCCTCTGTTGTAGAAAACT  
ATGTGATGAAACTTTGAAAAAGATATTTATGATGTTAACATTTTCAGGT  
TAAGCCTCATACGTTTAAAATAAAACTCTCAGTTGTTTATTATCCTGA  
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT  
GGAGTCAAAAGGCAAATCATTTGGACAATCTGCAAAATGGAGAGAA  
TACAATAACTACTACAGTAAAGTCTGTTTCTGCTTCCTTACACATAGA  
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA  
AACTAGCATTCTTAAACTGAGAATTATAGATGGGGTTCAAGAATCCC  
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAATGTGC  
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT  
GACCAATAAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG  
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA  
AAATGATGA

FIG. 72B-1

302/498

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser  
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser  
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe  
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His  
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile  
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro  
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr  
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly  
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro  
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn  
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys  
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser  
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg  
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu  
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro  
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln  
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp  
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu  
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn  
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val  
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys  
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr  
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn  
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr  
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro  
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser  
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg  
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile  
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg  
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser  
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn  
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg  
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln  
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val  
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu  
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys  
His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val  
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe

FIG. 72B-2

303/498

Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr  
Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn  
Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln  
Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp  
Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu  
Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu  
Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn  
Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val  
Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr  
Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu  
Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu  
Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly  
Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn  
Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly  
Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly  
Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu  
Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp  
Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser  
Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp  
Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser  
Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala  
Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg  
Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro  
Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu  
Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly  
Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp  
Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile  
Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr  
Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln  
Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg  
Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys  
Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val  
Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe  
Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu  
Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn  
Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu  
Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile  
Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile  
Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro

## FIG. 72B-3 304/498

Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu  
Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr  
Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr  
Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser  
Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro  
Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu  
Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys  
Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu  
Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu  
Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile  
Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly  
Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg  
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg  
Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu  
Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg  
Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp  
Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val  
Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro  
Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg  
Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro  
Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu  
Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val  
Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr  
Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu  
Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln  
Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu  
Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr  
Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro  
Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly  
Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys  
Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr  
Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu  
His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr  
Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln  
Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala  
Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile  
Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser  
Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly  
Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile

FIG. 72B-4

305/498

Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr  
His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn  
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr  
Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu  
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu  
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln  
Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser  
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe  
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu  
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg  
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr

306/498

FIG. 73A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC  
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG  
GCGCGCCTGCTTCTCTGCGTCCTGGTCGTGAGCGACTCCAAAGGCAGC  
AATGAAC TTCATCAAGTTCATCGAACTGTGACTGTCTAAATGGAGGA  
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC  
CCAAAGAAATTCGGAGGGGCAGCACTGTGAAATAGATAAGTCAAAAAC  
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG  
ACACCATGGGCCGGCCCTGCCTGCCCTGGA ACTCTGCCACTGTCCTTC  
AGCAAACGTACCATGCCACAGATCTGATGCTCTTCAGCTGGGCCTGG  
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGCGACCCTGG  
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTTCCAAGAGTGCATGGT  
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT  
TAAAATTTTCAGTGTGGCCAAAAGACTCTGAGGCCCCCGCTTTAAGATTA  
TTGGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGT TTGCGGCC  
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG  
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT  
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTCGCTCAA  
GGCTTAACTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAC  
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC  
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA  
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA  
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA  
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA  
AGCTGATTTCCCACCGGGAGTGTGAGCAGCCCCACTACTACGGCTCTG  
AAGTCACCACCAAAATGCTGTGTGCTGCTGACCCACAGTGGAAAACA  
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA  
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC  
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC  
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA  
GGGTCCCCAGGGAGGAAACGGGGCACCACCCGCTTTCTTGCTGGTTGTC  
ATTTTTGCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA  
AGAT

307/498

## FIG. 73B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser  
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly  
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys  
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn  
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro  
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg  
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His  
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys  
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile  
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr  
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys  
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu  
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys  
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg  
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro  
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys  
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr  
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp  
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val  
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser  
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

308/498

FIG.74A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA  
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAATTGTCATCA  
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC  
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGGCGCTGCTG  
GCACTGGCGGCCCTACTGCAGGGGGGCCGTGTCCCTGAAGATCGCAGC  
CTTCAACATCCAGACATTTGGGGGAGACCAAGATGTCCAATGCCACCCT  
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT  
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG  
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT  
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTCGTGTA  
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG  
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT  
GTCAGGTTCTTCTCCCGGTTACAGAGGTCAGGGAGTTTGCCATTGTT  
CCCCTGCATGCGGCCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT  
CTATGACGTCTACCTGGATGTCCAAGAGAAAATGGGGCTTGGAGGACG  
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT  
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC  
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT  
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTC  
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG  
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG  
CTGAAGTGAGCAGCCCCTCCCCACACCAGTTGAACTGCAG



309/498

FIG. 74B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Leu Leu Gln  
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys  
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile  
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu  
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro  
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln  
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile  
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp  
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln  
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser  
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln  
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
Glu Val Met Leu Lys

310/498

FIG. 75A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG  
CCCTGTGGATGCGCCTCCTGCCCCTGCTGGCGCTGCTGGCCCTCTGGG  
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGGCTCAC  
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT  
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA  
GGTGGAGCTGGGCGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG  
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT  
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG  
CAGCCCGCAGGCAGCCCCCACC CGCCCTCCTGCACCGAGAGAGA  
TGGAATAAAGCCCTTGAACCAGC

FIG. 75B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly  
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val  
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr  
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro  
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile  
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

311/498

FIG. 76A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT  
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCCT  
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA  
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC  
GGGCCAGGGTTCACCCCAACACACGGCGGTCTTTTGGGGTGGAGCCC  
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCCTG  
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC  
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAACCTCCACAACA  
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGCCTATATTTTCCT  
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCCTGTTCCGACTACTGTC  
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC  
ATGGAGAGCACAACATCAGGATTCCTAGGACCCCTGCTCGTGTTACA  
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT  
AGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGAGCACCCACGTG  
TCCTGGCCAAAATTTCGCAGTCCCAACCTCCAATCACTCACCAACCTC  
TTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT  
ATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTC  
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA  
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT  
CAAGGAACCTCTATGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC  
GGAAACTGCACTTGTAATCCCATCCCATCATCCTGGGCTTTCGCAAGA  
TTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA  
GTGCCATTTGTTCAGTGGTTCGCAGGGCTTTCCCCCACTGTTTGGCTTT  
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT  
TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC  
ATTGA

312/498

FIG. 76B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro  
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn  
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile  
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu  
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro  
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg  
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu  
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val  
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp  
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu  
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser  
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr  
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu  
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu  
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala  
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn  
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp  
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala  
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro  
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu  
Trp Val Tyr Ile

313/498

FIG. 77A

CGAACCCTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA  
CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC  
CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGC  
CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT  
TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG  
AAGTATTCATTCCCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG  
TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA  
CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA  
GCCCCGTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG  
CGCCTCTGACAGCAACGTCTATGACCTCCTAAAGGACCTAGAGGAAG  
GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT  
GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA  
CAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG  
GAAGGACATGGCAAGGTTCGAGACATTCCTGCGCATCGTGCAGTGCCG  
CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG  
TGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT  
GCCCACCAGCCTTGTCTAATAAAATTAAGTTGCATC

FIG. 77B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu  
Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp  
Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln  
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr  
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp  
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly  
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile  
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

314/498

FIG. 78A

ATGTATTCCAATGTGATAGGAACTGTAACCTCTGGAAAAAGGAAGGT  
TTATCTTTTGTCTTGCTGCTCATTGGCTTCTGGGACTGCGTGACCTGT  
CACGGGAGCCCTGTGGACATCTGCACAGCCAAGCCGCGGGACATTCC  
CATGAATCCCATGTGCATTTACCGCTCCCCGGAGAAGAAGGCAACTG  
AGGATGAGGGGCTCAGAACAGAAGATCCCGGAGGCCACCAACCGGCG  
TGTCTGGGAACTGTCCAAGGCCAATTCCCGCTTTGCTACCACTTTCTA  
TCAGCACCTGGCAGATTCCAAGAATGACAATGATAACATTTTCCTGTG  
ACCCCTGAGTATCTCCACGGCTTTTGCTATGACCAAGCTGGGTGCCTG  
TAATGACACCCTCCAGCAACTGATGGAGGTATTTAAGTTTGACACCAT  
ATCTGAGAAAACATCTGATCAGATCCACTTCTTCTTTGCCAAACTGAA  
CTGCCGACTCTATCGAAAAGCCAACAAATCCTCCAAGTTAGTATCAGC  
CAATCGCCTTTTTTGGAGACAAATCCCTTACCTTCAATGAGACCTACCA  
GGACATCAGTGAGTTGGTATATGGAGCCAAGCTCCAGCCCCTGGACT  
TCAAGGAAAATGCAGAGCAATCCAGAGCGGCCATCAACAAATGGGGT  
TCCAATAAGACCGAAGGCCGAATCACCGATGTCATTCCCTCGGAAGC  
CATCAATGAGCTCACTGTTCTGGTGCTGGTTAACACCATTTACTTCAA  
GGGCCTGTGGAAGTCAAAGTTCAGCCCTGAGAACACAAGGAAGGAAC  
TGTTCTACAAGGCTGATGGAGAGTCGTGTTTCAAGCATCTATGATGTACC  
AGGAAGGCAAGTTCCGTTATCGGCGCGTGGCTGAAGGCACCCAGGTG  
CTTGAGTTGCCCTTCAAAGGTGATGACATCACCATGGTCCTCATCTTG  
CCCAAGCCTGAGAAGAGCCTGGCCAAGGTGGAGAAGGAACCTCACCCC  
AGAGGTGCTGCAGGAGTGGCTGGATGAATTGGAGGAGATGATGCTGG  
TGGTCCACATGCCCCGCTTCCGCATTGAGGACGGCTTCAGTTTGAAGG  
AGCAGCTGCAAGACATGGGCCTTGTCGATCTGTTTCAAGCCCTGAAAAG  
TCCAAACTCCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTC  
TCAGATGCATTCCATAAGGCATTTCTTGAGGTAAATGAAGAAGGCAG  
TGAAGCAGCTGCAAGTACCGCTGTTGTGATTGCTGGCCGTTTCGCTAAA  
CCCCAACAGGGTGACTTTCAAGGCCAACAGGCCTTTCCTGGTTTTTAT  
AAGAGAAGTTCCTCTGAACACTATTATCTTCATGGGCAGAGTAGCCA  
ACCCTTGTGTTAAGTAA

315/498

FIG. 78B

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val Tyr Leu Leu  
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser Pro Val Asp  
Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys Ile Tyr Arg Ser  
Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr  
Asn Arg Arg Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr  
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser  
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln  
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Ile His  
Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser  
Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu  
Thr Tyr Gln Asp Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe  
Lys Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr  
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu  
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Ser Pro Glu  
Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser  
Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln  
Val Leu Glu Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys  
Pro Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu  
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg  
Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val Asp  
Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu Gly Arg Asp Asp  
Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser  
Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg  
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn  
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys

316/498

FIG. 79A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCG  
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCAG  
AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCA  
ATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCA  
CTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAGA  
GTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATGGG  
GGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTT  
ATTATCACAAATCTTAA

FIG. 79B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu  
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu  
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe  
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn  
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His  
Lys Ser



317/498

FIG. 79C

ATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC  
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCAT  
CAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCA  
CCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCG  
TGCTGCAGGGGGTCCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACC  
GCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCCGCGCGGCG  
TGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCAC  
TCTGCCGCGCAGCACCCTGACTGCGGGGGTCCCAAGGACCACCCC  
TTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCCTCAAAGGCC  
CCTCCCCCAGCCTTCCAAGCCCATCCCGACTCCCGGGGGCCCTCGGAC  
ACCCCGATCCTCC CACAATAA

FIG. 79D

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr  
Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala  
Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly  
Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val  
Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg  
Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys  
Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp  
Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser  
Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln

318/498

FIG. 80A

ATGCGTCCCCTGCGCCCCCGCGCCGCGCTGCTGGCGCTCCTGGCCTCG  
CTCCTGGCCGCGCCCCCGGTGGCCCCGGCCGAGGCCCCGCACCTGGT  
GCAGGTGGACGCGGCCCGCGCGCTGTGGCCCCCTGCGGGCGCTTCTGGA  
GGAGCACAGGCTTCTGCCCCCGCTGCCACACAGCCAGGCTGACCAG  
TACGTCCTCAGCTGGGACCAGCAGCTCAACCTCGCCTATGTGGGCGCC  
GTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCACTGGCTGCTGGA  
GCTTGTCAACCACCAGGGGGTCCACTGGACGGGGCCTGAGCTACAAC  
TCACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCC  
TCCCAGGGTTTGAGCTGATGGGCAGCGCCTCGGGCCACTTCACTGACT  
TTGAGGACAAGCAGCAGGTGTTTGAGTGGAAGGACTTGGTCTCCAGC  
CTGGCCAGGAGATACATCGGTAGGTACGGACTGGCGCATGTTTCCAA  
GTGGAACCTTCGAGACGTGGAATGAGCCAGACCACCACGACTTTGACA  
ACGTCTCCATGACCATGCAAGGCTTCCCTGAACTACTACGATGCCTGCT  
CGGAGGGTCTGCGCGCCGCCAGCCCCGCCCTGCGGCTGGGAGGCCCC  
GGCGACTCCTTCCACACCCACCGCGATCCCCGCTGAGCTGGGGCCTC  
CTGCGCCACTGCCACGACGGTACCAACTTCTTCACTGGGGAGGCGGG  
CGTGCGGCTGGACTACATCTCCCTCCACAGGAAGGGTGCGCGCAGCT  
CCATCTCCATCCTGGAGCAGGAGAAGGTCGTCGCGCAGCAGATCCGG  
CAGCTCTTCCCAAGTTCGCGGACACCCCATTTACAACGACGAGGCG  
GACCCGCTGGTGGGCTGGTCCCTGCCACAGCCGTGGAGGGCGGACGT  
GACCTACGCGGCCATGGTGGTGAAGGTCATCGCGCAGCATCAGAACC  
TGCTACTGGCCAAACACCACCTCCGCCTTCCCCTACGCGCTCCTGAGCA  
ACGACAATGCCTTCTGAGCTACCACCCGCACCCCTTCGCGCAGCGCA  
CGCTCACCGCGCGCTTCCAGGTCAACAACACCCGCCCGCCGCACGTG  
CAGCTGTTGCGCAAGCCGGTGCTCACGGCCATGGGGCTGCTGGCGCT  
GCTGGATGAGGAGCAGCTCTGGGGCCGAAGTGTCGCAGGCCGGGACCG  
TCCTGGACAGCAACCACACGGTGGGCGTCCTGGCCAGCGCCACCGC  
CCCCAGGGCCCCGGCCGACGCCTGGCGCGCCGCGGTGCTGATCTACGC  
GAGCGACGACACCCGCGCCACCCCAACCGCAGCGTCGCGGTGACCC  
TGCGGCTGCGCGGGGTGCCCCCGGCCCGGGCCTGGTCTACGTCACG  
CGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGGCGGCG  
CCTGGGGCCGGCCCGTCTTCCCCACGGCAGAGCAGTTCCGGCGCATGC  
GCGCGGCTGAGGACCCGGTGGCCGCGGCGCCCCGCCCTTACCCGCC  
GGCGGGCCGCCTGACCCTGCGCCCCGCGCTGCGGCTGCCGTGCTTTTG  
CTGGTGACGTGTGTGCGCGCCCCGAGAAGCCGCCCGGGCAGGTCAC  
GCGGCTCCGCGCCCTGCCCTGACCCAAGGGCAGCTGGTTCTGGTCTG  
GTCGGATGAACACGTGGGCTCCAAGTGCCTGTGGACATACGAGATCC  
AGTTCTCTCAGGACGGTAAGGCGTACACCCCGGTCAGCAGGAAGCCA  
TCGACCTTCAACCTCTTTGTGTTTCAGCCAGACACAGGTGCTGTCTCT  
GGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCCCGACCAGGCC  
CTTCTCGGACCCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCC  
CCCATCCCCGGGCAATCCAT GA

319/498

FIG. 80B

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu  
Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val Gln Val Asp Ala Ala  
Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu  
Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala  
Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu  
Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His  
Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu  
Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val  
Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly  
Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp  
Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys  
Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser  
Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp  
Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His  
Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln  
Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala  
Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala  
Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr  
Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro  
His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg  
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala  
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu  
Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala  
Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro  
Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu  
Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp  
Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg  
Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu  
Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala  
Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln  
Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr  
Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro  
Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr  
Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro  
Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

320/498

FIG. 81A

ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCGCT  
TCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACT  
GGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGG  
AGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCAGATTCCCTGC  
ATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGA  
AGGCTGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTG  
GATGGCTCCCCAAAGAGATTCAGAAGGCAGACTTCAGGCAGACCCTC  
AGCGCTTTCCTCATGGGATTCGCCAGCTAGCTAATTATGTTACACAGCA  
AAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGC  
GCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCAGACC  
TTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGT  
GACAGTTTGGAAAATTTGGCAGATGGTTATAAGCACATGTCCTTG GCC  
CTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCTCTT  
TATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGACAGTAC  
TGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGT  
ATAAAGAGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTT  
GATGTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGAT  
TGGCAACTTTGGCCTCAGCTGGAATCAGCAAGTAACTCAGATGGCCCT  
CTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACA  
CATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGC  
CATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGG  
GAGACAACCTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGG  
GCTGTAGCTATGATAAACCGGCAGGAGATTGGTGGACCTCGCTCTTAT  
ACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCTGCC  
TGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTTCTAT  
GAATGGACTTCAAGGTTAAGAAGTCACATAAATCCACAGGCACTGT  
TTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAAAGACTTACT  
TTAA

321/498

FIG. 81B

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe  
Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala  
Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met Cys Asn Leu Asp  
Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys Leu Phe Met Glu Met Ala Glu  
Leu Met Val Ser Glu Gly Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp  
Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln  
Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys  
Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly Ser Phe  
Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys  
Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn Leu Ala Asp Gly Tyr Lys His  
Met Ser Leu Ala Leu Asn Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro  
Leu Tyr Met Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu  
Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro Gly Gly Trp  
Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu Ser Trp Asn Gln Gln  
Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp  
Leu Arg His Ile Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala  
Ile Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn  
Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser Leu Gly Lys  
Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu Leu Pro Val Lys Arg Lys  
Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr  
Val Leu Leu Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu

322/498

FIG. 82A

ATGGCGCCCGTCGCCGTCTGGGCGCGCTGGCCGTCGGACTGGAGCT  
CTGGGCTGCGGCGCACGCCTTGCCCGCCCAGGTGGCATTACACCCTA  
CGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC  
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA  
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG  
GACAGCACATAACCCAGCTCTGGAAGTGGGTTCGAGTGTGCTTGAG  
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACTCAAGCCTGCAC  
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG  
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG  
TGCCGCCCCGGGCTTCGGCGTGGCCAGACCAGGAACTGAAACATCAGA  
CGTGGTGTGCAAGCCCTGTGCCCGGGGACGTTCTCCAACACGACTTC  
ATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACGTGGTGGCCAT  
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA  
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCAGCCAGTGTCC  
ACACGATCCCAACACACGCAGCCAACCTCCAGAACCCAGCACTGCTCC  
AAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG  
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC  
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTCATCATGAC  
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC  
CTCACTTGCCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG  
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA  
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCCACTCGGAACCAGC  
CACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC  
CAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCCAGG  
TCAATGTCACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT  
CACAGTGCTCCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC  
AGCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCCTTCTCCAAGGA  
GGAATGTGCCTTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGG  
GGAGCACCGAAGAGAAGCCCCTGCCCTTGGAGTGCTGATGCTGGG  
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTGCTAGCCAAGG  
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGCCCTGGTCCTT  
CCAGGC

323/498

FIG. 82B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala  
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser  
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys  
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys  
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys  
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln  
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val  
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr  
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val  
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr  
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln  
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro  
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly  
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val  
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro  
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu  
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg  
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly  
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln  
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys  
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro  
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu  
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro  
Asp Ala Gly Met Lys Pro Ser

324/498

## FIG. 83A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro  
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

## FIG. 83B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg  
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg  
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr  
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys  
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln  
Gly Thr Leu Val Thr Val Ser Ser



325/498

FIG. 84A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr  
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp  
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp  
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser  
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr  
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly  
Thr Thr Val Thr Val Ser Ser

FIG. 84B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys  
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser  
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe  
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

326/498

FIG. 85A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA  
GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGC  
ATCCACTGGTATCAGCAAAGAACAATGGTTCTCCAAGGCTTCTCATA  
AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC  
AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT  
GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC  
ACGTTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA  
GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT  
CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAACTGGG  
TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA  
TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG  
AGGTTCAACATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA  
ATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCCAGG  
AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC  
ACAGTCTCC

FIG. 85B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val  
Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln  
Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn  
Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro  
Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser  
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly  
Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu  
Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu  
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr  
Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg  
Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

327/498

FIG. 86A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTCCA  
GGTTCCACTGGTGACGTCAGGCGAGGGCCCCGGAGCCTGCGGGGCAG  
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC  
TGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACGCCGCGGC  
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG  
CCGCAGGAGTCGGTGGGCGCGGGGGGCCGGCGAGGCGGCGGTGCGACA  
AAACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGA  
CCGTGAGTCTTCTTCCCCCAAAACCCAAGGACACCCTCATGATC  
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGA  
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC  
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA  
CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGG  
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA  
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG  
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT  
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT  
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACG  
CCTCCCGTGTTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC  
ACCGTGGAACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC  
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT  
CCCTGTCTCCCGGGAAATGA

328/498

FIG. 86B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser  
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala  
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala  
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro  
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val  
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu  
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

329/498

FIG. 87

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser  
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro  
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

FIG. 88

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys  
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser  
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe  
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr  
Leu Val Thr Val Ser Ala

FIG. 89

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu  
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

FIG. 90

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg  
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser  
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
Thr Leu Val Thr Val Ser Ser

330/498

FIG. 91

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser  
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu  
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro  
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
 Ser Phe Asn Arg Gly Glu Cys

FIG. 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg  
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser  
 Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
 Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His  
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp  
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

331/498

FIG. 93A

ATGGATTTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA  
GTCATAATGTCCAGAGGGCAAATTGTTCTCTCCCAGTCTCCAGCAATC  
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGCCAG  
CTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGATCCTC  
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC  
TGTTTCGCTTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT  
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT  
GGACTAGTAACCCACCCACGTTCTGGAGGGGGGACCAAGCTGGAAATC  
AAA

FIG. 93B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser  
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu  
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln  
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser  
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn  
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

332/498

FIG. 94A

ATGGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG  
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG  
CCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATTT  
ACCAGTTACAATATGCACTGGGTAAAACAGACACCTGGTCGGGGCCT  
GGAATGGATTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAA  
TCAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA  
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG  
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC  
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 94B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser  
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys  
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys  
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp  
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser  
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr  
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly  
Thr Thr Val Thr Val Ser Ala



333/498

FIG. 95A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAAGCCTCCTCACTACTTCT  
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA  
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGGCGGAAGTGGGGCG  
GAGTTAGGGGCGGGATGGGGCGGAGTTAGGGGCGGGACTATGGTTGCT  
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT  
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC  
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA  
CACACATTCCACAGAATTAATTCCCCTAGTTATTAATAGTAATCAATT  
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA  
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC  
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA  
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT  
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG  
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT  
TATGGGACTTTCCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA  
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGATAGC  
GGTTTGACTCACGGGGATTTCCTCAAGTCTCCACCCCATTTGACGTCAATG  
GGAGTTTGTTTTTGGCACCAAAATCAACGGGACTTTCCAAAAATGTCGTA  
ACAACCTCCGCCCCATTGACGCAAATGGGGCGGTAGGCGTGTACGGTGG  
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG  
GAGACGCCATCACAGATCTCTACCATGAGGGTCCCCGCTCAGCTCCT  
GGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGATGGTACCAA  
GGTGGAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTTCCC  
GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCT  
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG  
ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACACAGAGCAG  
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAG  
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC  
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAG  
TGTTGAATTCAGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCT  
GTGACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTG  
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCT  
TGACCCTGGAAGGTGCCACTCCCCTGTCCTTTTCCCTAATAAAATGAGG  
AAATTGCATCGCATTGTCTGAGTAGGTGTCAATTCTATTCTGGGGGGTG  
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG  
GCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGAC  
AGCTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGC  
CCGCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCCTACTT  
GGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT  
TTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGA  
TTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTTTTGGCAC

334/498

FIG. 95B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTG  
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG  
AGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGAACACAGACCC  
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTA  
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT  
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC  
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC  
CCTGACCAGCGGCGTGCACACCTTCCCGGTGTCTACAGTCCTCAGG  
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG  
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA  
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA  
TGCCACCGTGCCAGCACCTGAATCCTGGGGGGACCGTCAGTCTTC  
CTCTTCCCCCCTAAAACCAAGGACACCCTCATGATCTCCCGGACCCCT  
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT  
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA  
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC  
GTCCTCACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA  
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  
CCCCCATCCCGGGATGAGCTGACCAGGAACCAGGTCAGCCTGACCTG  
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA  
GCAATGGGCAGCCGGAGAACAATAAGACCACGCCTCCCGTGCTG  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG  
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA  
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG  
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGTG  
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT  
TCTAGTTGCCAGCCATCTGTTGTTTGCCCTCCCCCGTGCCTTCCTTGA  
CCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAA  
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGGG  
TGGGGCAGGACAGCAAGGGGGGAGGATTGGGAAGACAATAGCAGGCA  
TGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAGC  
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA  
ATGAGAAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGAT  
TGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT  
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG  
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT  
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC  
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT  
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG  
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

335/498

FIG. 95C

GCTGCGATTTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG  
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAACTGCAT  
CGTCGCCGTGTCCCAAATATGGGGATTGGCAAGAACGGAGACCTAC  
CCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC  
ACAACCTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAG  
GAAAACCTGGTTCTCCATTCTGAGAACAAATCGACCTTTAAAGGACA  
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACCACCACGAGGA  
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA  
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG  
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT  
CTTTGTGACAAGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCC  
AGAAATTGATTTGGGGAAATATAAACTTCTCCCAGAATACCCAGGCG  
TCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAA  
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGC  
TCCCCTCCTAAAGTCATGCATTTTTATAAGACCATGGGACTTTTGCTG  
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGT  
TTGCCCCCTCCCCCGTGCTTCCCTTGACCCTGGAAGGTGCCACTCCCAC  
TGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG  
GTGTCAATTCTATTCTGGGGGGGTGGGGGTGGGGCAGGACAGCAAGGGGG  
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT  
ATGGAACCAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT  
ATTTGCATAATGAGAAAAAAAGGAAAAATTAATTTTAACACCAATTCA  
GTAGTTGATTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACA  
GTGTTCTCTGCACAGATAAGGACAAACATTATTCAGAGGGAGTACCC  
AGAGCTGAGACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGA  
AATATGCTTGTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGG  
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGG  
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC  
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAA  
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  
GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT  
GTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGA  
CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTAT  
CGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTGCTCGACGTTG  
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG  
CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATC  
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC  
CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCG  
GATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATC  
AGGGGCTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCGCGCATG  
CCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG

336/498

FIG. 95D

AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC  
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG  
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGT  
GCTTTACGGTATCGCCGCTTCCCGATTTCGCAGCGCATCGCCTTCTATC  
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGAC  
CGACCAAGCGACGCCCAACCTGCCATCACGAGATTTTCGATTCCACCG  
CCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCG  
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC  
ACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATA  
GCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTT  
GTGGTTTGTCCAAACTCATCAATCTATCTTATCATGTCTGGATCGCGG  
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC  
TGTGTGAAATTGTTATCCGCTCACAAATCCACACAACATACGAGCCGG  
AGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCAC  
ATTAATTGCGTTGCGCTCACTGCCCCGCTTTCAGTCGGGAAACCTGTC  
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT  
TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTC  
GGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA  
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA  
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC  
TGCGGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAATC  
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC  
CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC  
CTGCCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTG  
GCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC  
GTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC  
CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA  
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG  
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA  
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA  
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA  
CAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATT  
ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC  
GGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTAAAGGGATTTTGG  
TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAA  
AATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG  
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC  
TATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC  
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC  
GAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA  
GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTC  
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTTCG

337/498

FIG. 95E

CAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTACAGGCATCGTGG  
TGTCACGCTCGTCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCCAAC  
GATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTT  
AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTG  
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC  
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT  
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA  
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC  
ATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG  
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACCTGATCTTCA  
GCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGG  
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAA  
TACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTA  
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA  
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

338/498

FIG. 96A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT  
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA  
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAACTGGGGCG  
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT  
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT  
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC  
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA  
CACACATTCCACAGAATTAATTCCCCTAGTTATTAATAGTAATCAATT  
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA  
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCC  
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA  
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT  
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG  
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT  
TATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA  
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATACC  
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCCATTGACGTCAATG  
GGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA  
ACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGG  
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG  
GAGACGCCATCACAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT  
CAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT  
TGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA  
GGTCACAATGACTTGCAAGGGCCAGCTCAAGTGTAAGTTACATCCACT  
GGTTCCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCA  
CATCCAACCTGGCTTCTGGAGTCCCTGTTCGCTTCAGTGGCAGTGGGT  
CTGGGACTTCTTACTCTCTCACAAATCAGCAGAGTGGAGGCTGAAGATG  
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCG  
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT  
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCC  
TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA  
CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG  
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA  
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC  
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT  
CAACAGGGGAGAGTGTTGAATTCAGATCCGTTAACGGTTACCAACTA  
CCTAGACTGGATTTCGTGACAACATGCGGCCGTGATATCTACGTATGAT  
CAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTC  
CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCC

339/498

FIG. 96B

TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT  
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG  
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA  
GCTGGGGCTCGACAGCTATGCCAAGTACGCCCCCTATTGACGTCAATG  
ACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG  
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT  
GGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTTG  
ACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTT  
TGTTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAAC  
CCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC  
TATATAAGCAGAGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGA  
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT  
CGCTGTTGCTACGCGTGTCTGTCCCAGGTACAACCTGCAGCAGCCTGG  
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG  
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAACAGA  
CACCTGGTTCGGGGCCTGGAATGGATTGGAGCTATTTATCCCGGAAAT  
GGTGATACTTCCTACAATCAGAAGTTCAAAGGCAAGGCCACATTGAC  
TGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGA  
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG  
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCACC  
GTCTCTGCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  
TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT  
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG  
CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG  
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG  
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC  
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACAC  
ATGCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT  
CCTCTTCCCCC AAAACCAAGGACACCCTCATGATCTCCCGGACCCC  
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG  
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG  
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG  
CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA  
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC  
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT  
GCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACACCT  
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG  
AGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCT  
GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAA  
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG  
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG  
GTAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTTCGT

340/498

FIG. 96C

GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC  
TTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTG  
ACCCTGGAAGGTGCCACTCCCAGTGTCTTTCTAATAAAATGAGGAA  
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGG  
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC  
ATGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAG  
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCAT  
AATGAGAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGA  
TTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT  
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG  
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT  
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC  
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT  
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG  
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTGCGATTTTCG  
CGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC  
CCCGCTGCCATCATGGTTCGACCATTGAACTGCATCGTCGCCGTGTCC  
CAAAATATGGGGATTGGCAAGAACGGAGACCTACCCTGGCCTCCGCT  
CAGGAACGAGTTCAAGTACTTCCAAAGAATGACCACAACCTCTTCAG  
TGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGTTC  
TCCATTCTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTT  
CTCAGTAGAGAACTCAAAGAACCACCACGAGGAGCTCATTTTCTTGC  
CAAAAGTTTGGATGATGCCTTAAGACTTATTGAACAACCGGAATTGG  
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCTGTTTACC  
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG  
ATCATGCAGGAATTTGAAAGTGACACGTTTTTCCCAGAAATTGATTTG  
GGGAAATATAAACTTCTCCCAGAATACCCAGGCGTCCTCTCTGA  
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA  
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCCCTCCTAA  
AGCTATGCATTTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA  
GCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCC  
CCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAGTGTCTTTCTTA  
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT  
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA  
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGC  
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTTATTTGCATAATG  
AGAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGATTGA  
GCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCTGCA  
CAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAGACT  
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTC  
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT  
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA  
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG



341/498

FIG. 96D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA  
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTG  
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC  
AGCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC  
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA  
CGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGG  
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG  
TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCA  
ATGCGGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCAC  
CAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGG  
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC  
CAGCCGAACGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAG  
GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG  
GAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTG  
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA  
AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTAT  
CGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA  
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGAC  
GCCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTCTATGA  
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT  
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTT  
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT  
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAA  
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC  
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT  
TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTG  
TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT  
GCGCTCACTGCCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCA  
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGC  
GCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTTCGTTCCGGCT  
GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA  
CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA  
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC  
ATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT  
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC  
CCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC  
CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA  
ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAA  
GCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTT  
ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

342/498

FIG. 96E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG  
TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC  
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC  
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGC  
TGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAA  
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC  
TCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATC  
AAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAAATGAAGTTTTAA  
ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG  
CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC  
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG  
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC  
ACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCG  
AGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTA  
ATTGTTGCCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAGTTTGC  
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGT  
TTGGTATGGCTTCATTCAGCTCCGTTCCCAACGATCAAGGCGAGTTA  
CATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTC  
CGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTA  
TGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCT  
TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA  
TGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACC  
GCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCT  
TCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCC  
ATGTAACCCACTCGTGCACCCAAGTATCTTCAGCATCTTTTACTTTCA  
CCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAA  
AAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCT  
TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG  
ATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGC  
GCACATTTCCCCGAAAAGTGCCACCT

343/498

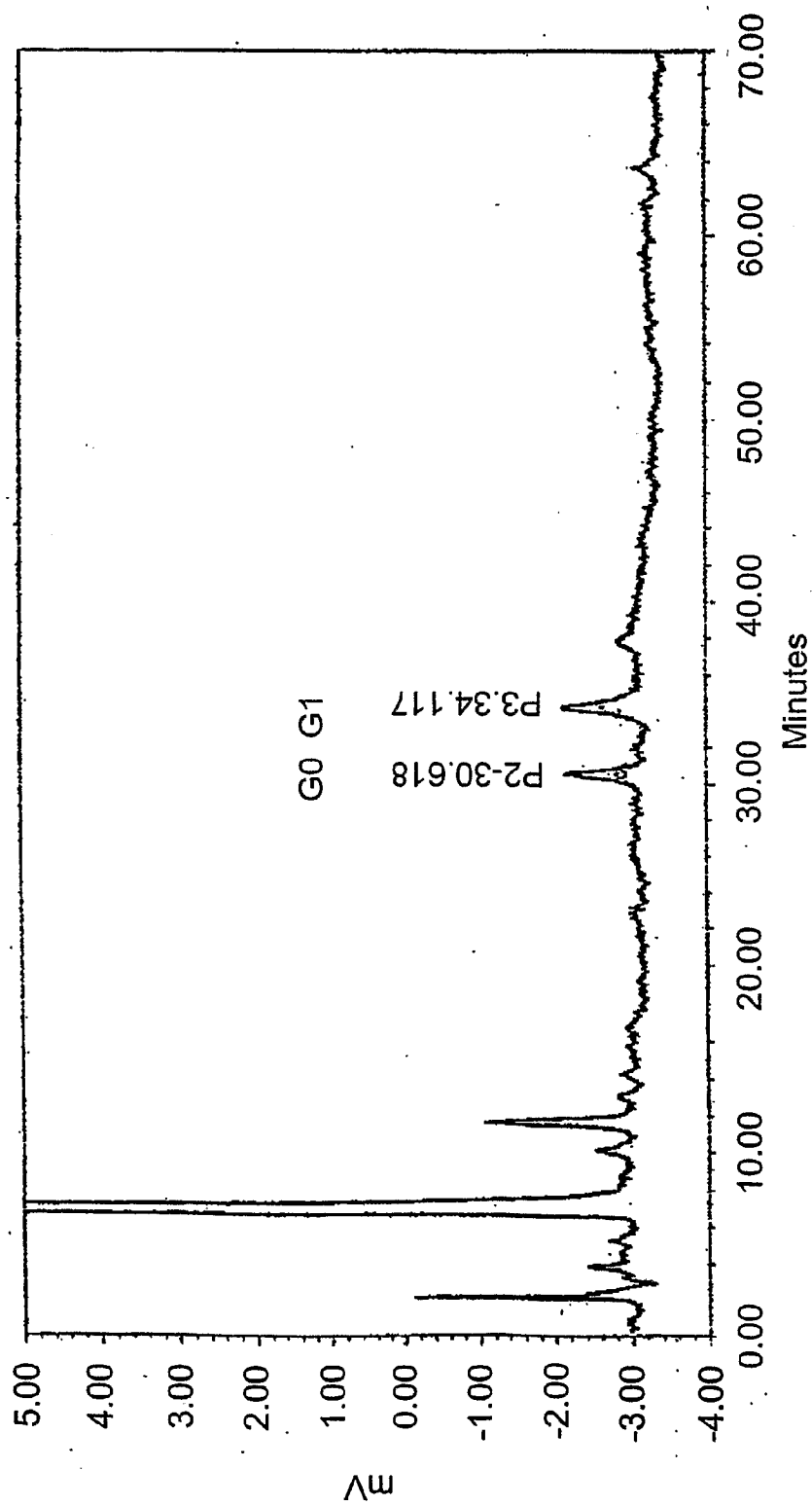


FIG. 97A

344/498

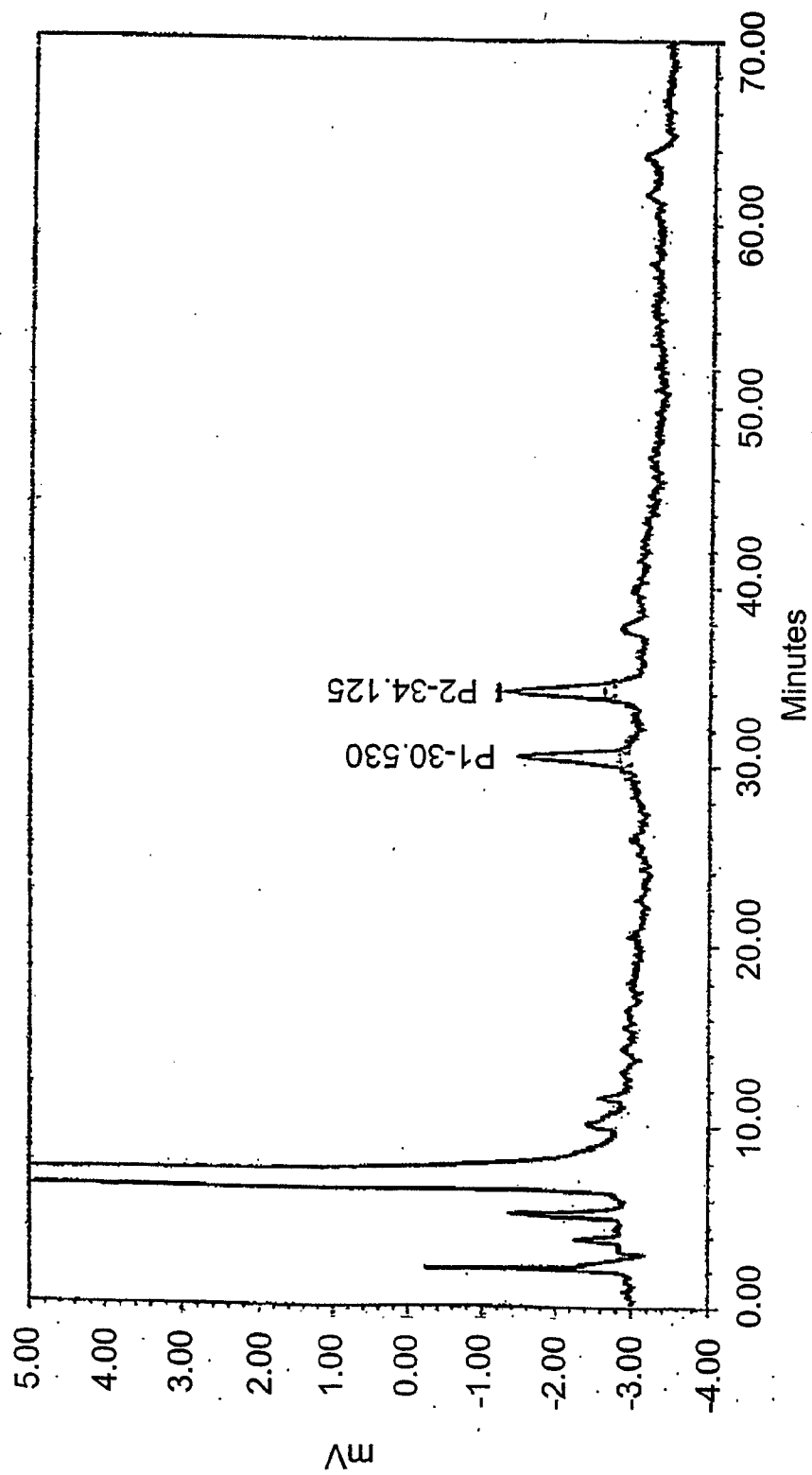


FIG. 97B

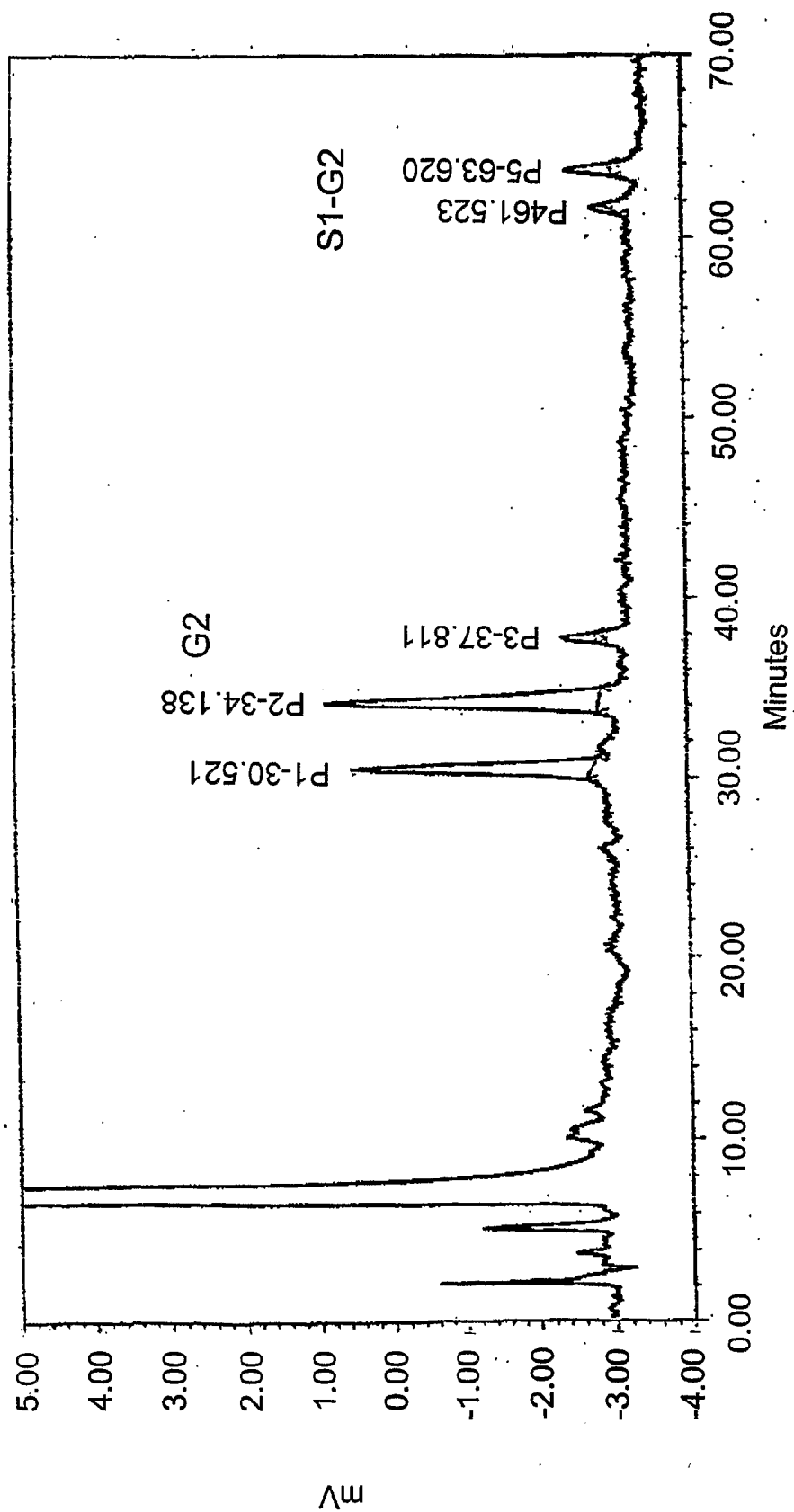


FIG. 97C

346/498

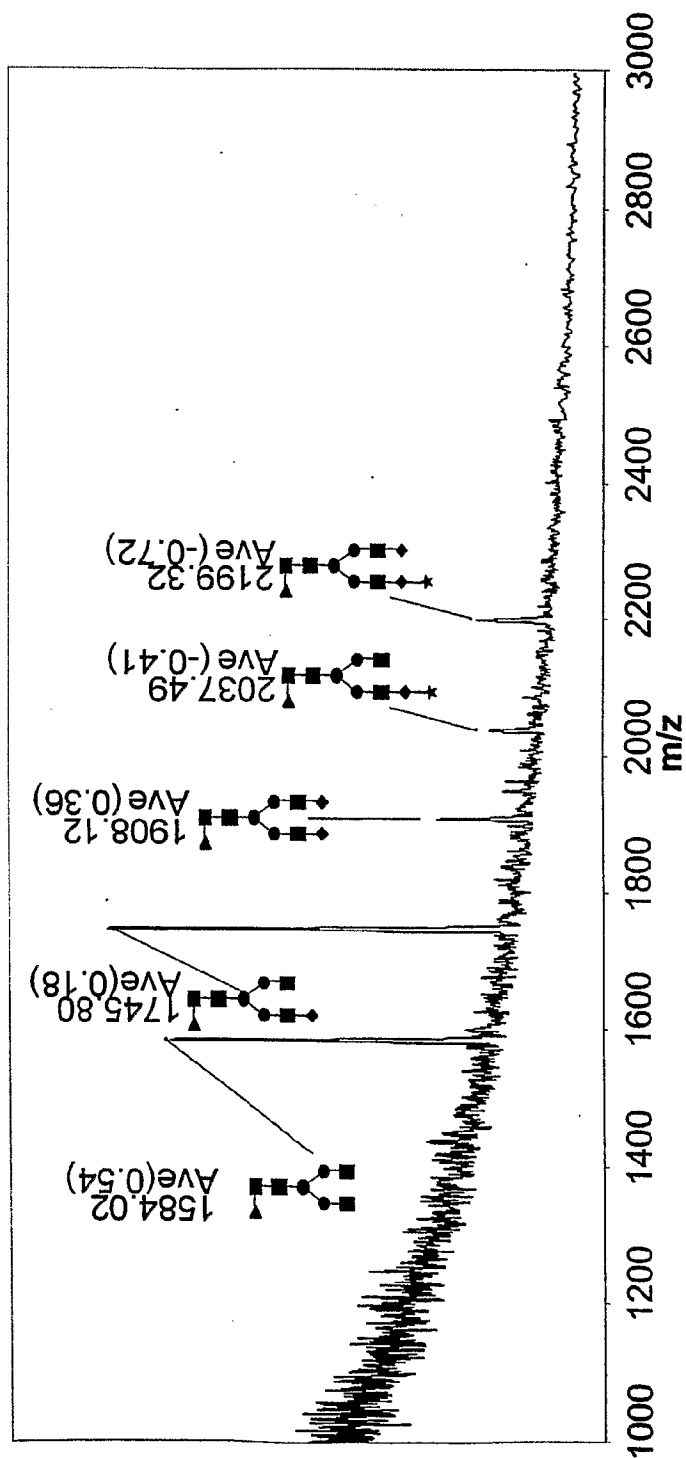


FIG. 98A

347/498

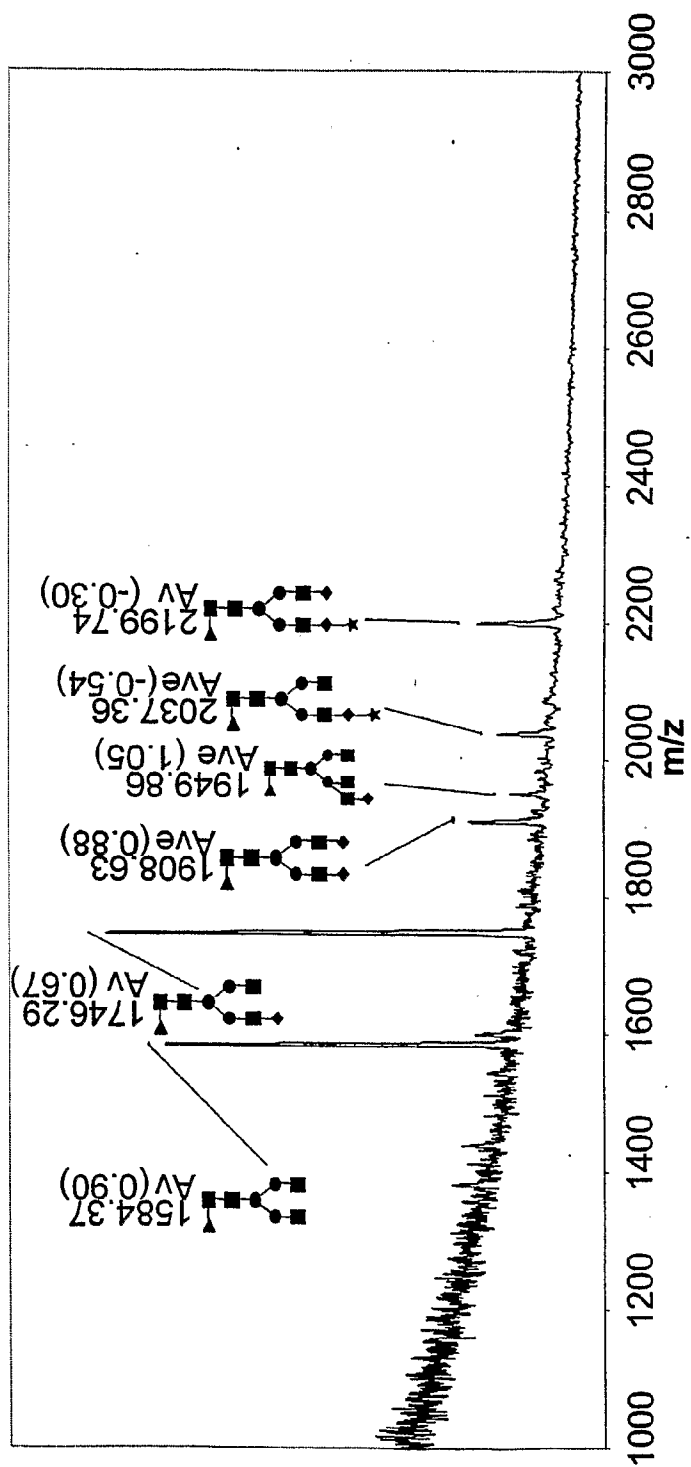


FIG. 98B

348/498

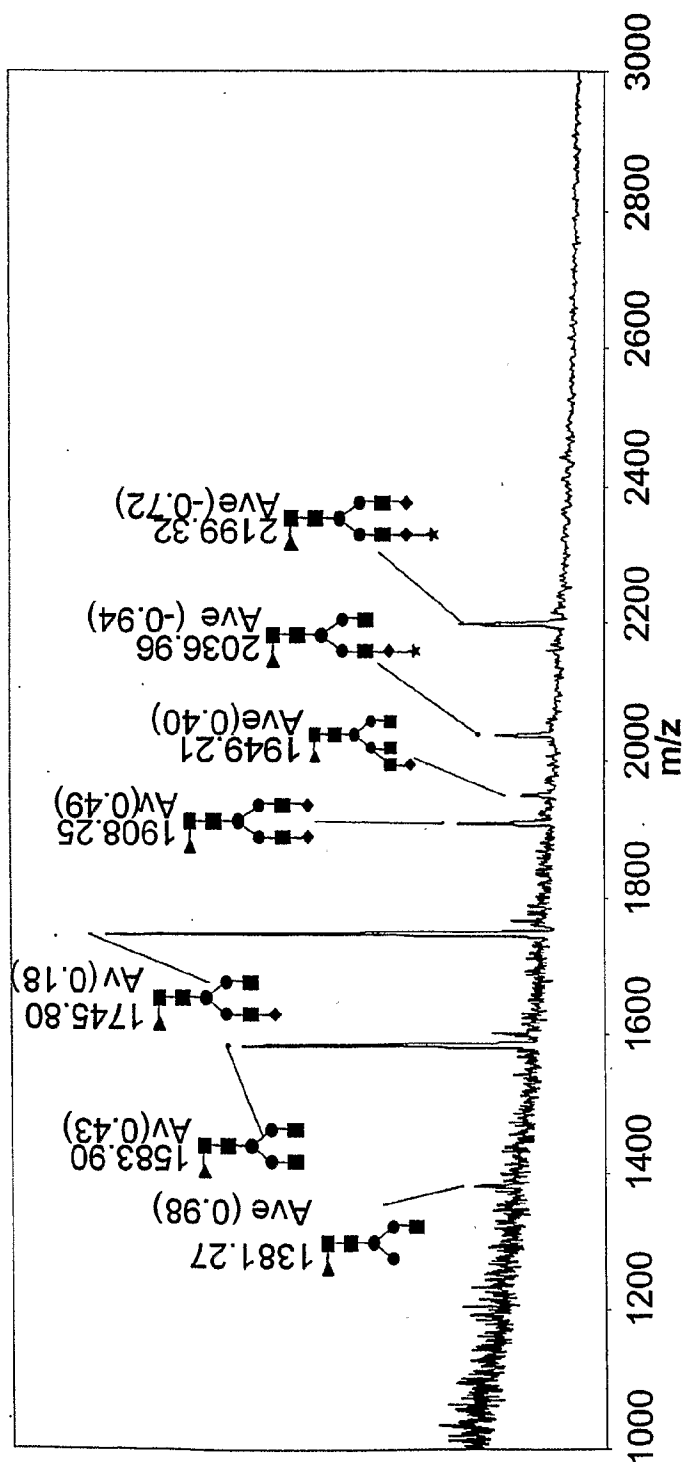


FIG. 98C



349/498

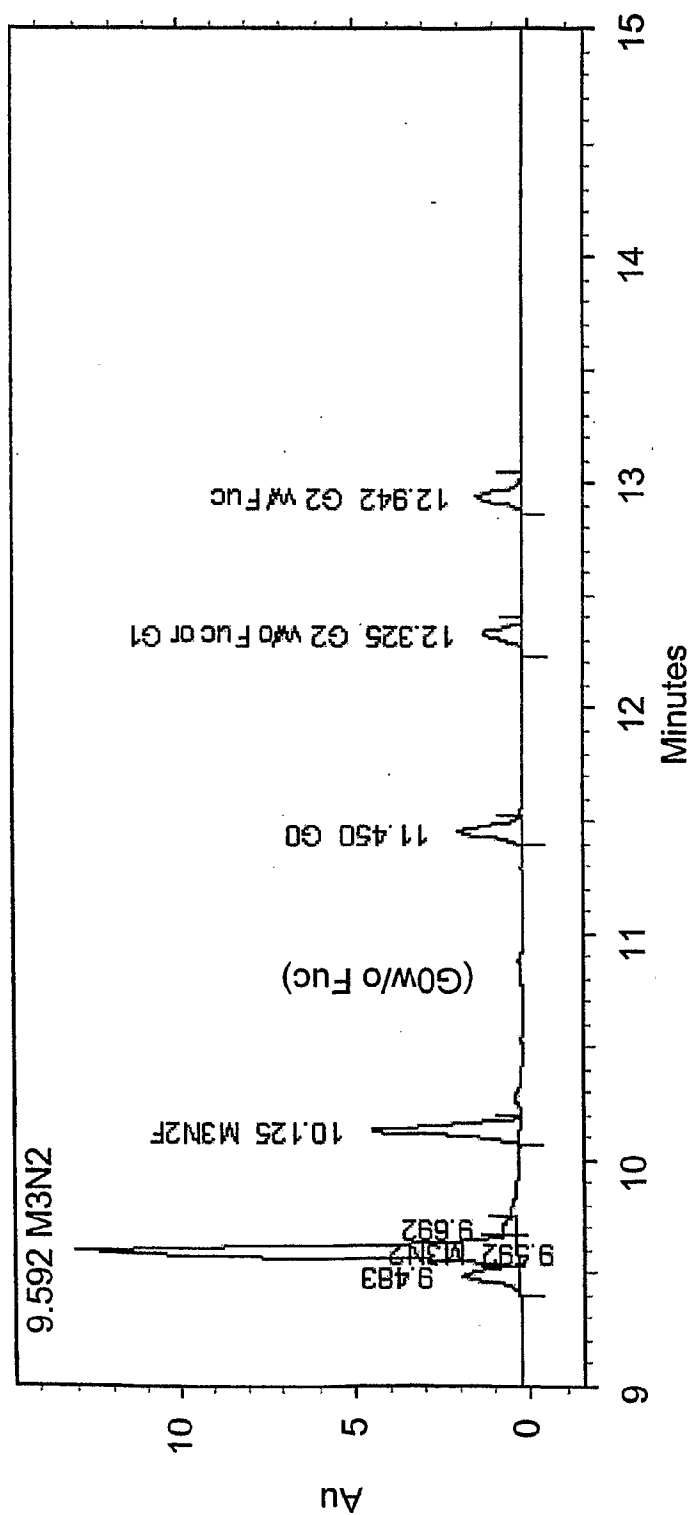


FIG. 99A

350/498

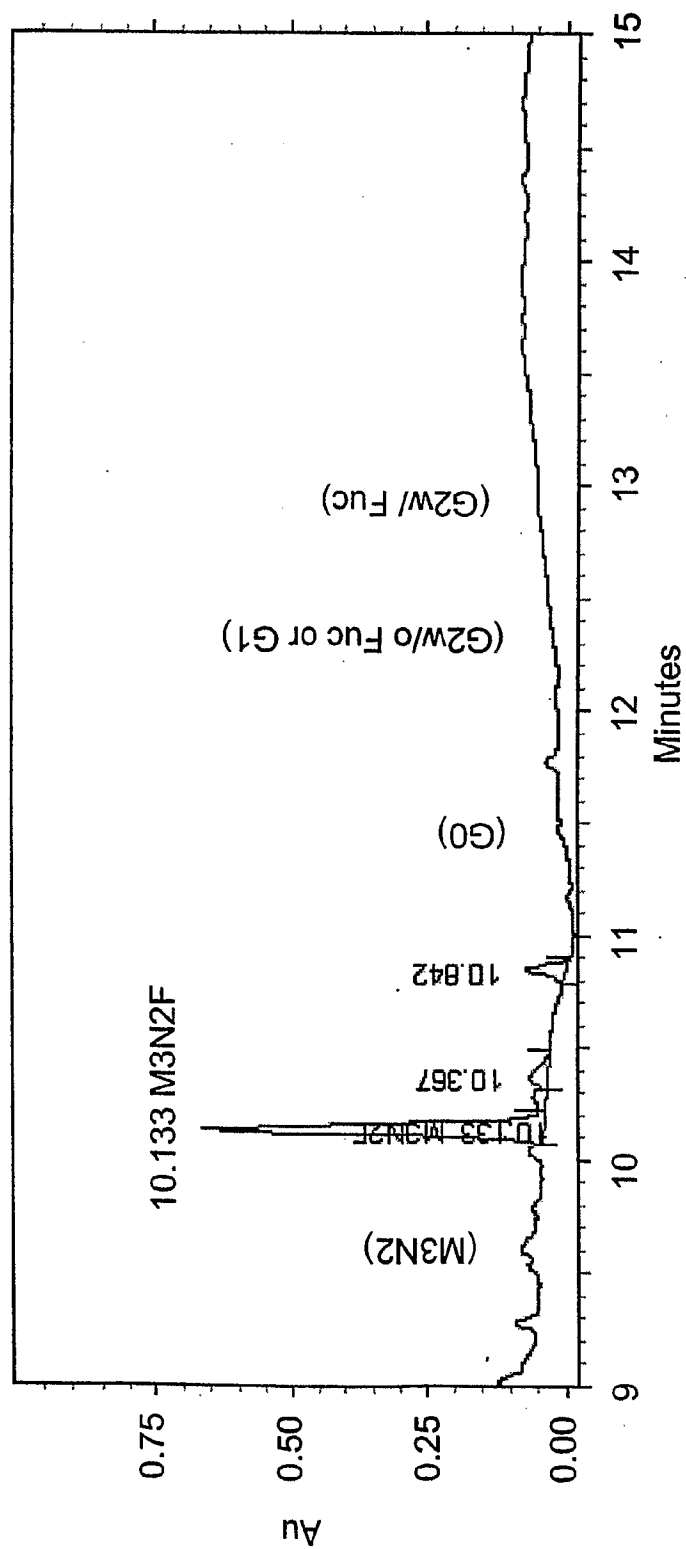


FIG. 99B

351/498

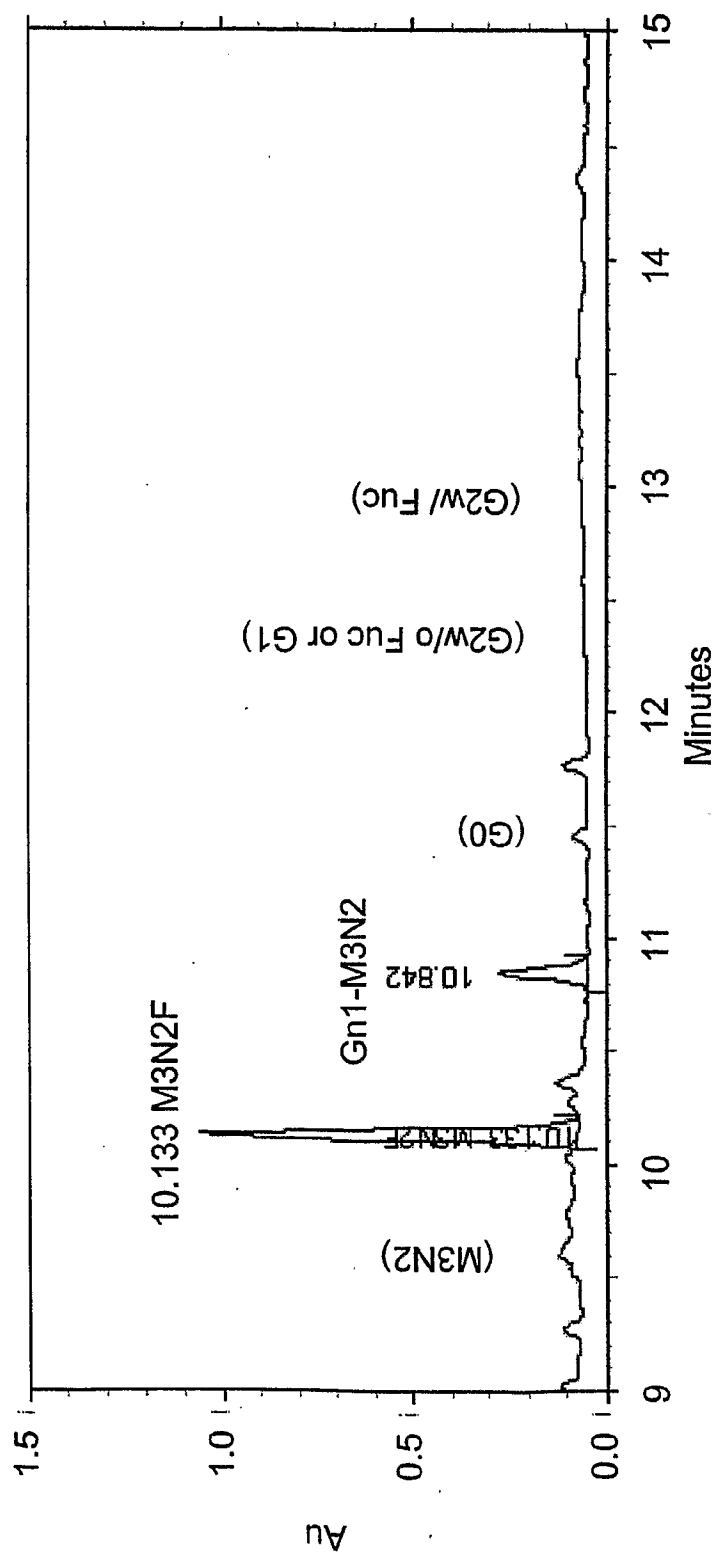


FIG. 99C

352/498

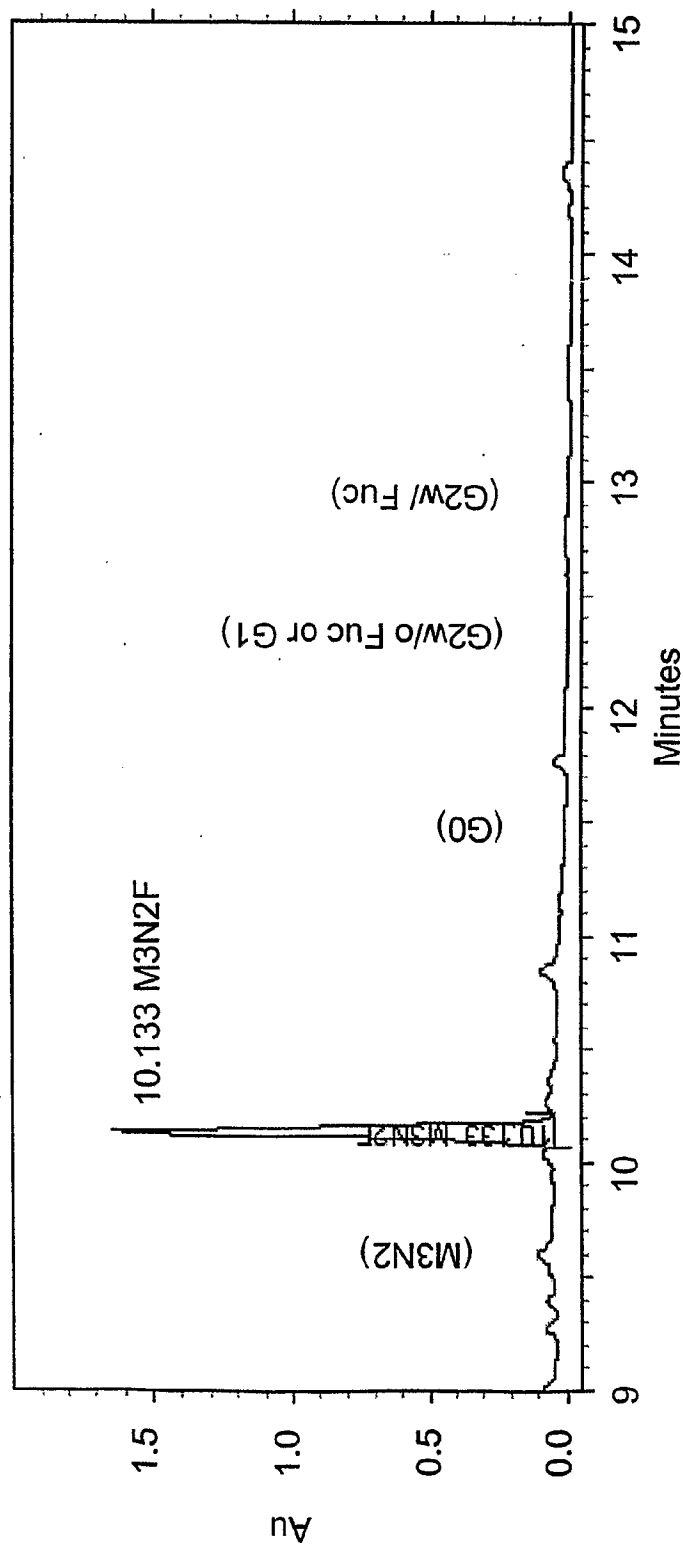


FIG. 99D

353/498

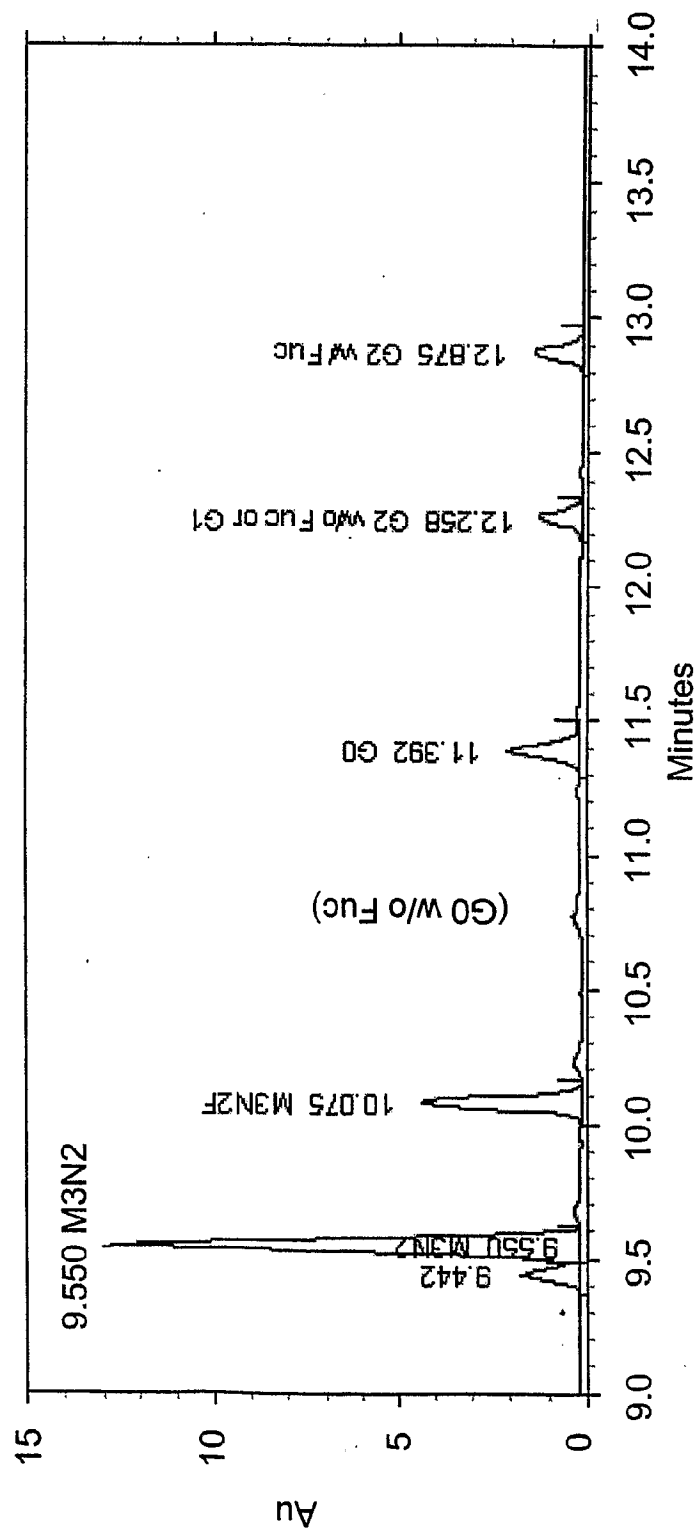


FIG. 100A

354/498

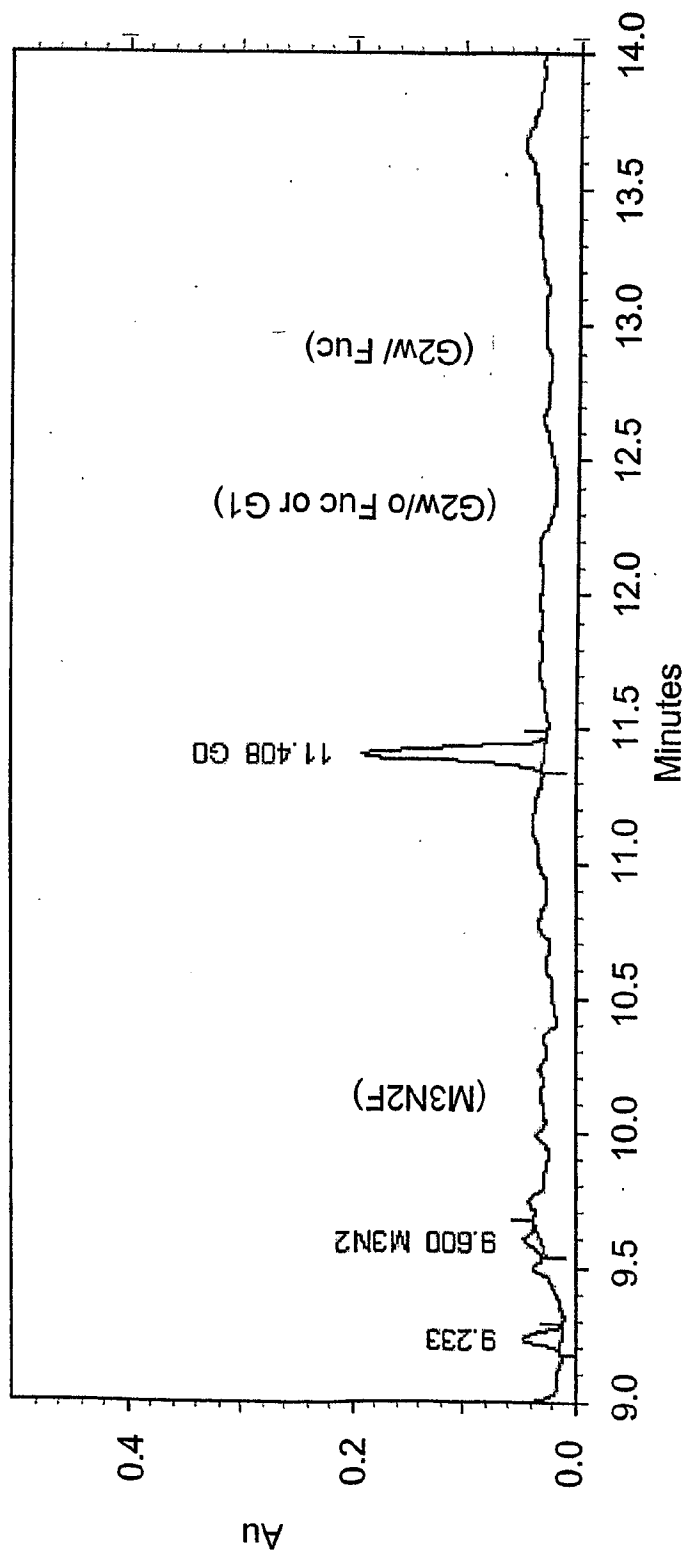


FIG. 100B

355/498

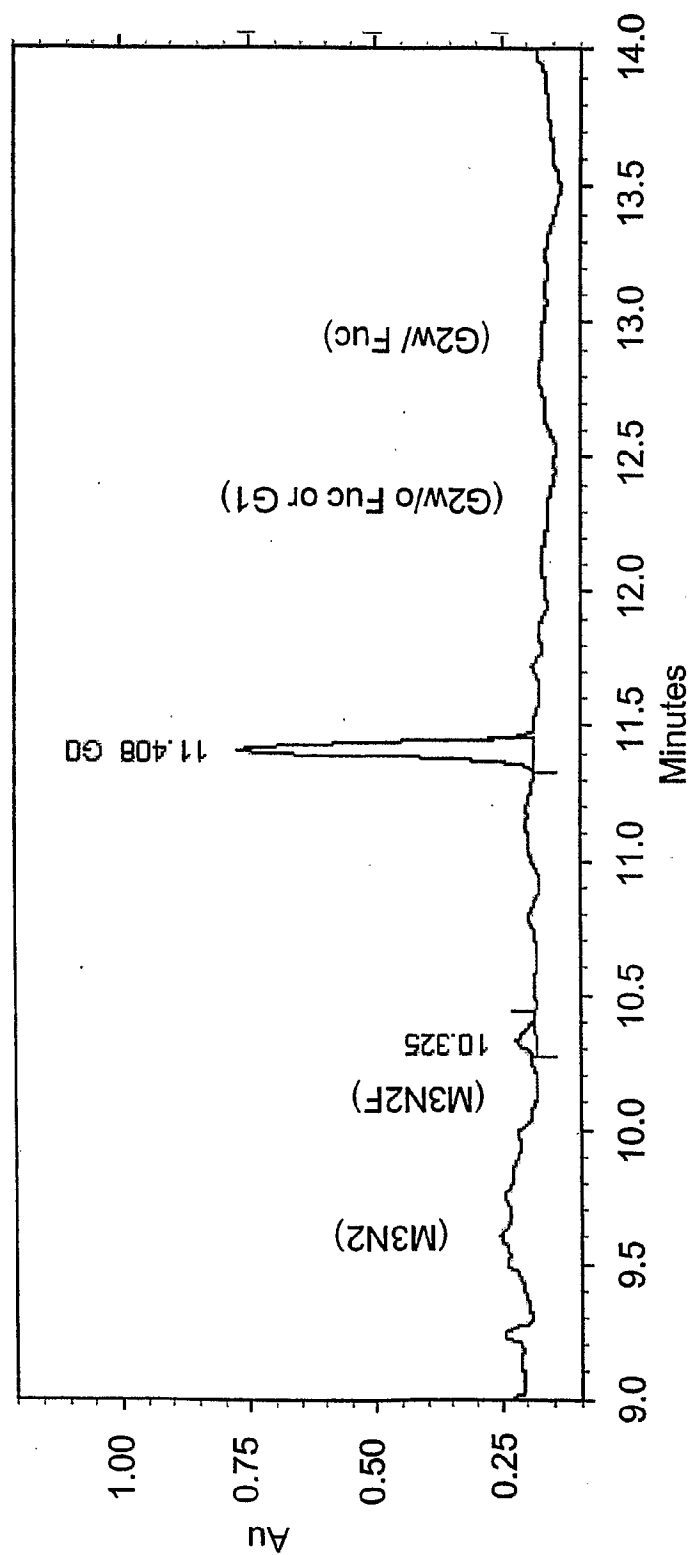


FIG. 100C

356/498

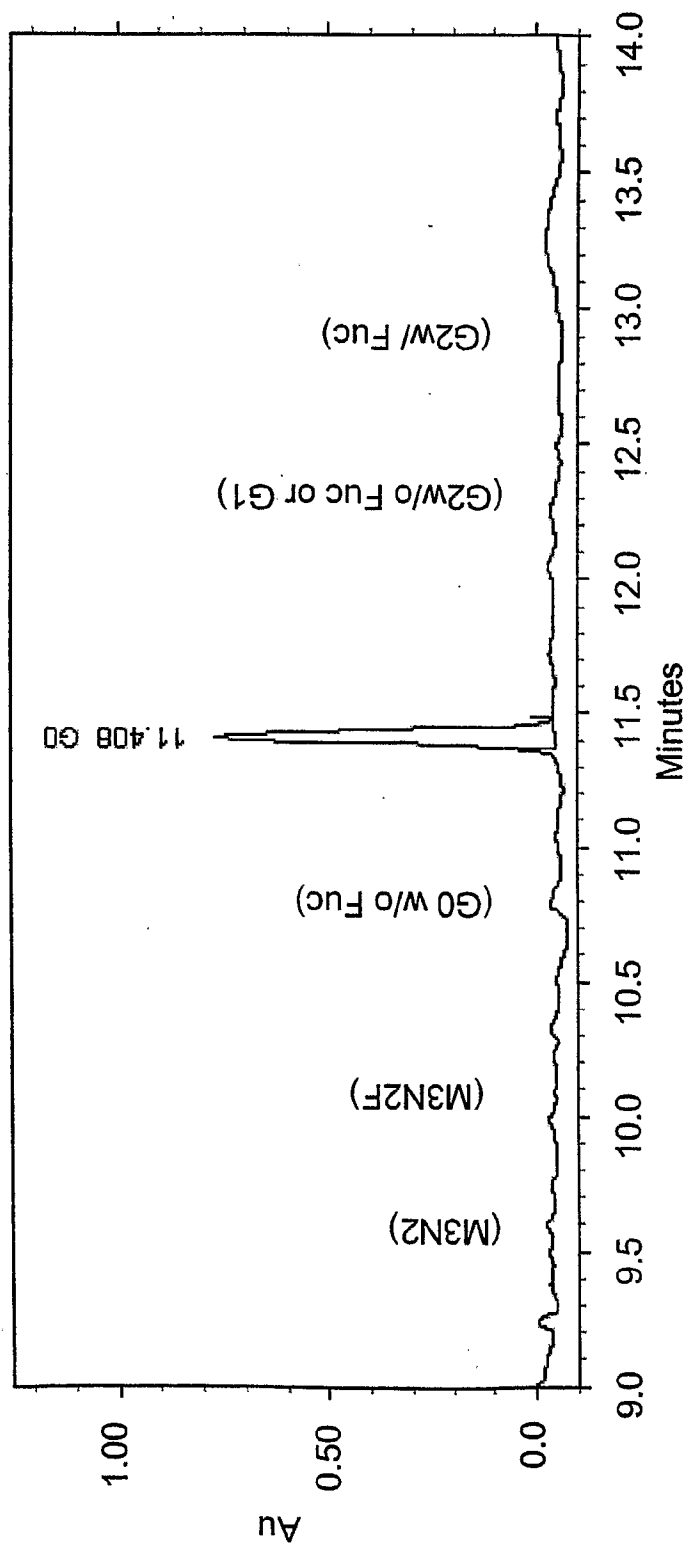


FIG. 100D



357/498

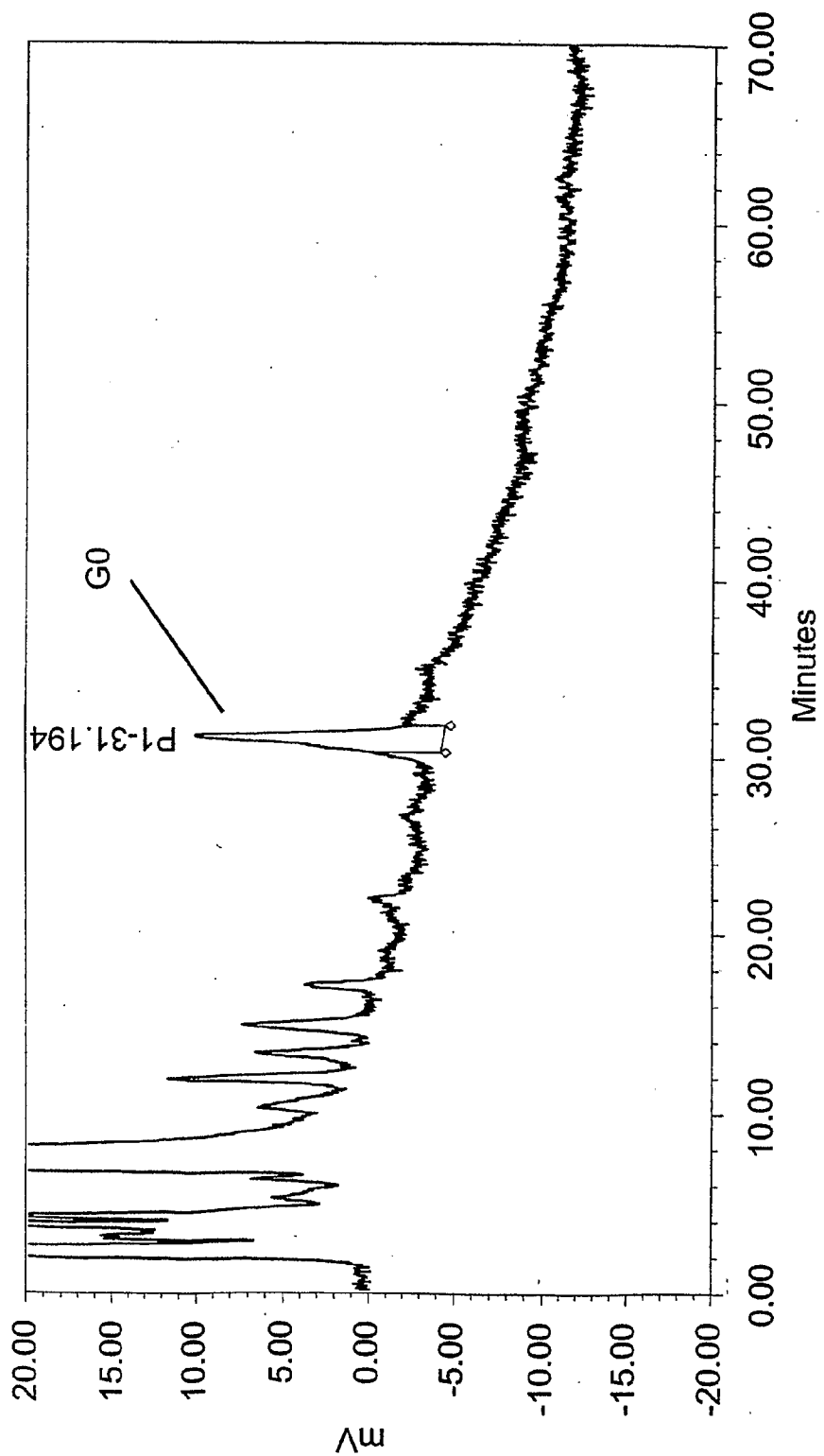


FIG. 101A

358/498

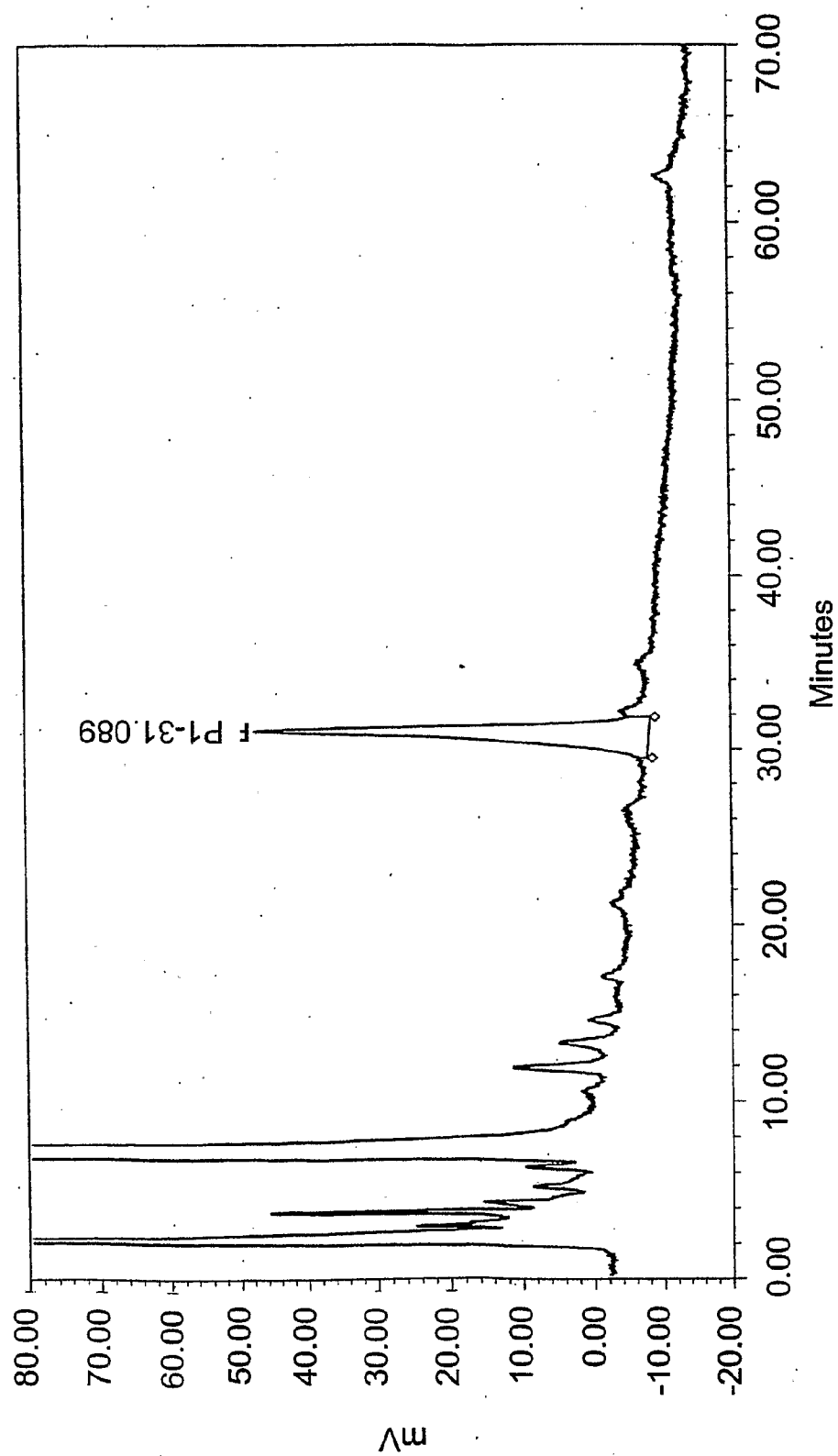


FIG. 101B

359/498

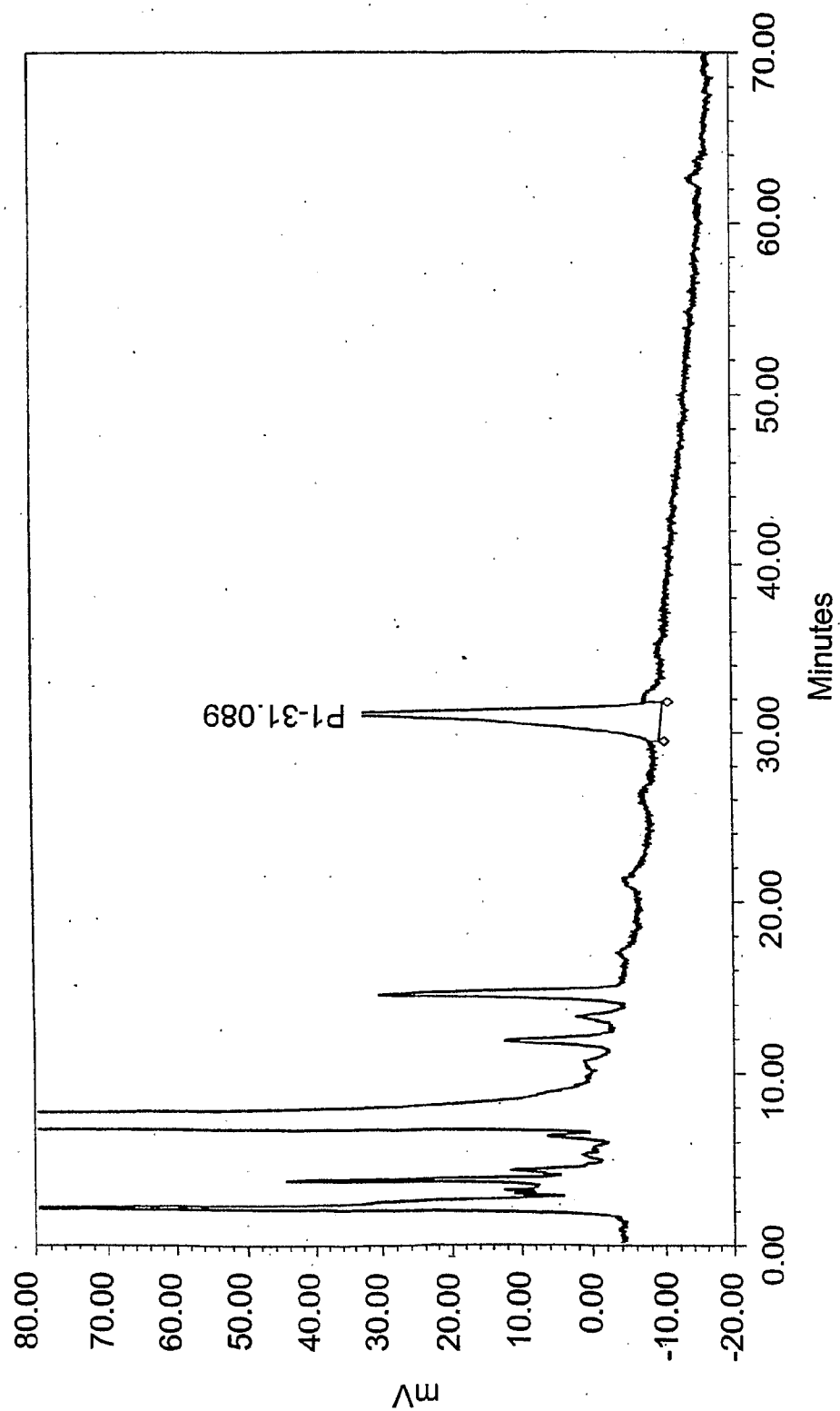


FIG. 101C

360/498

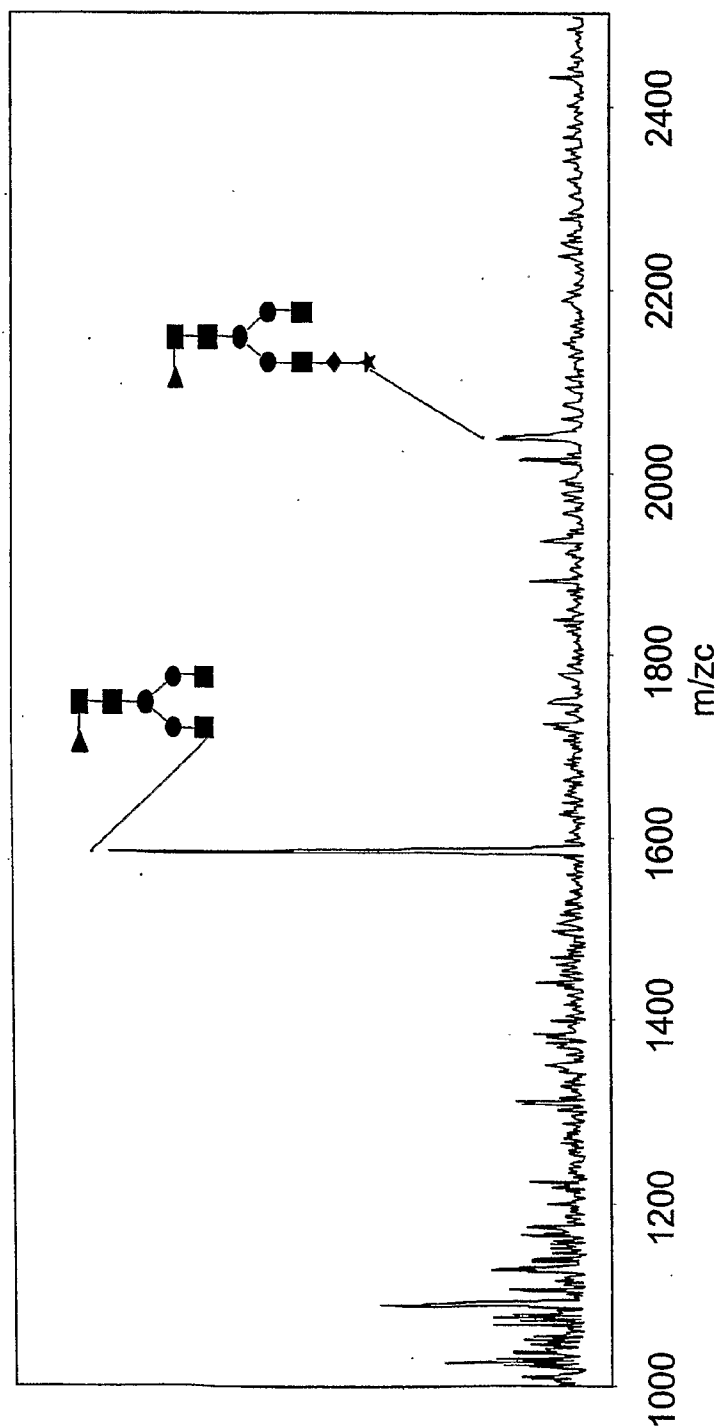


FIG. 102A

361/498

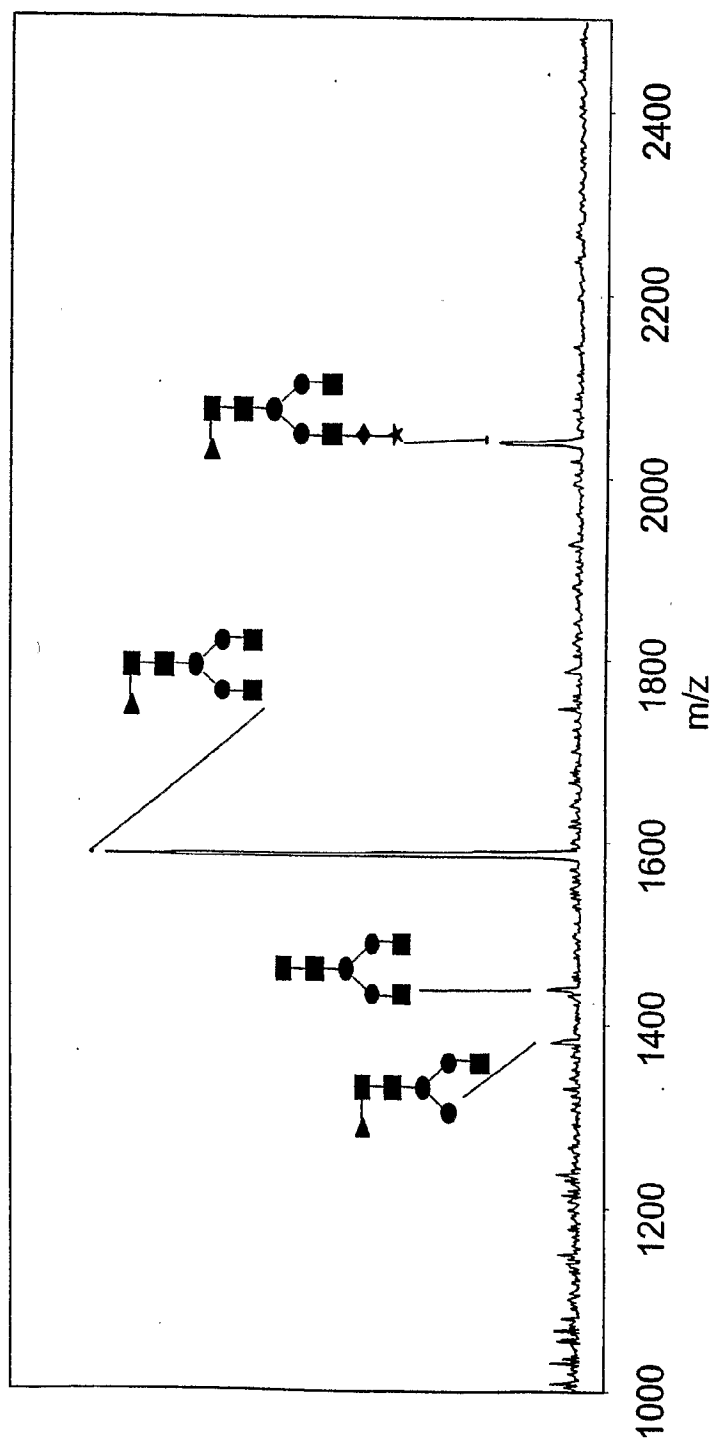


FIG. 102B

362/498

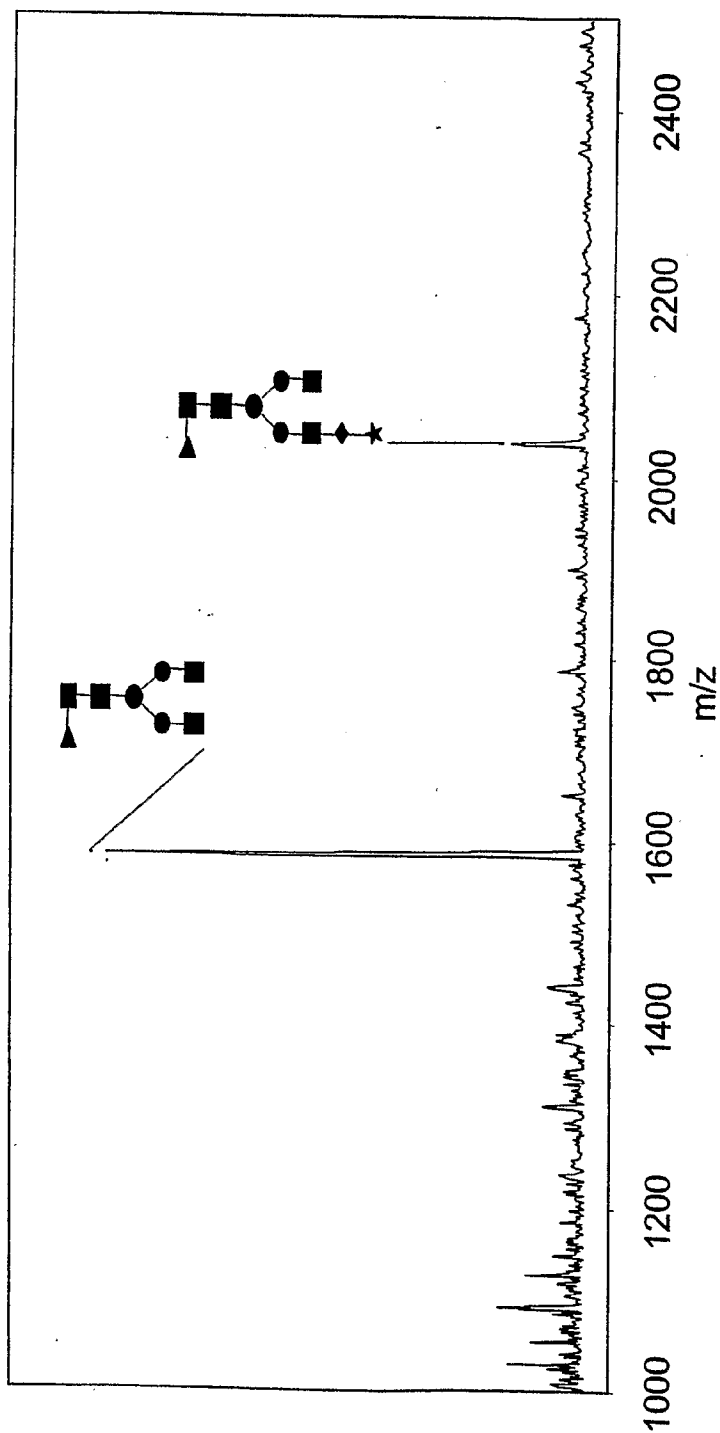


FIG. 102C

363/498

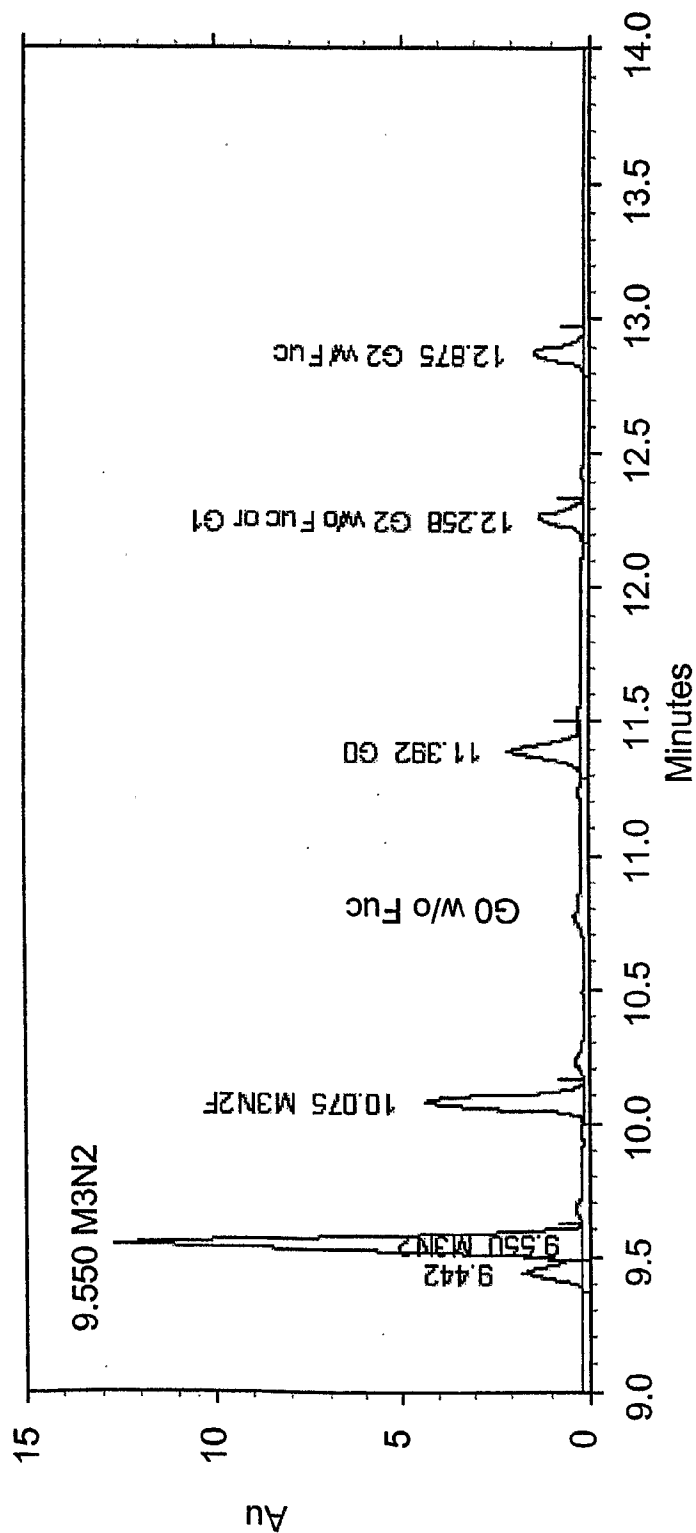


FIG. 103A

364/498

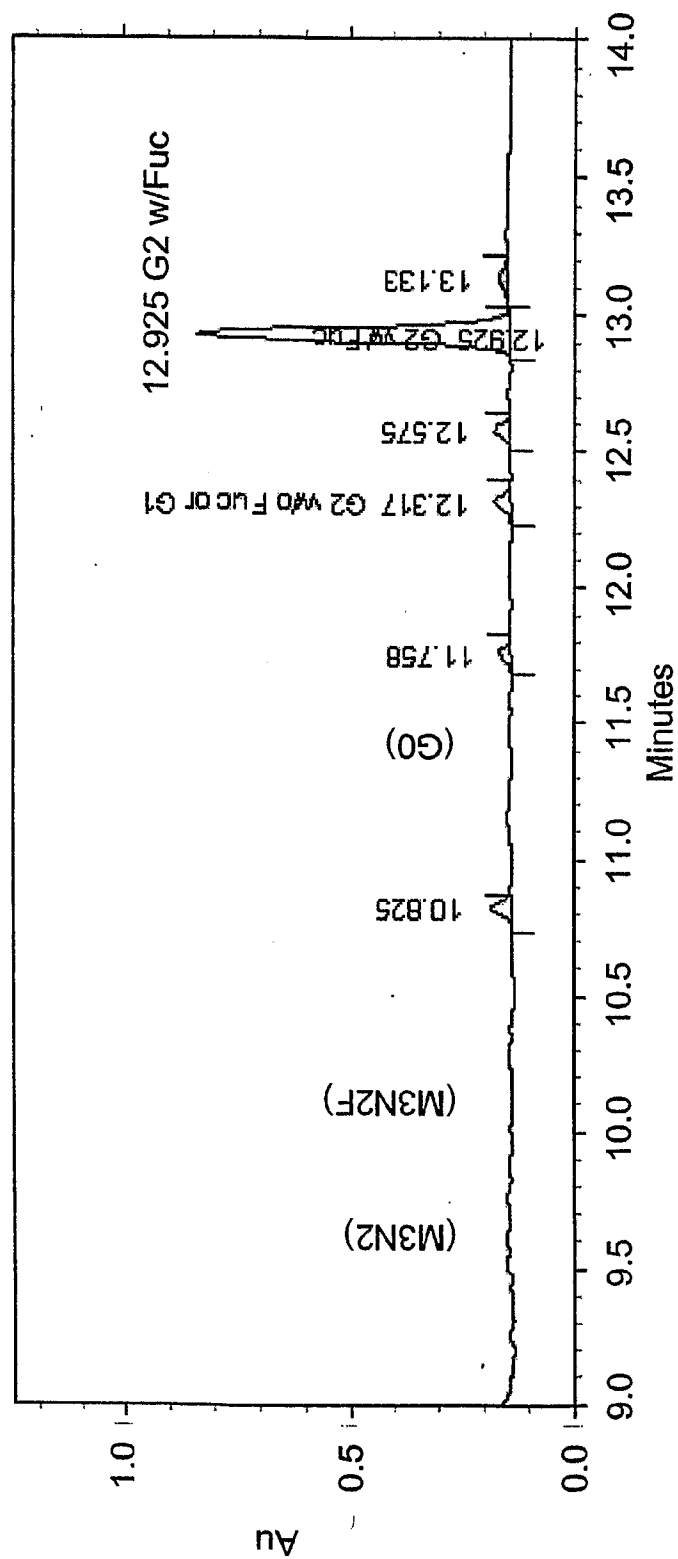


FIG. 103B



365/498

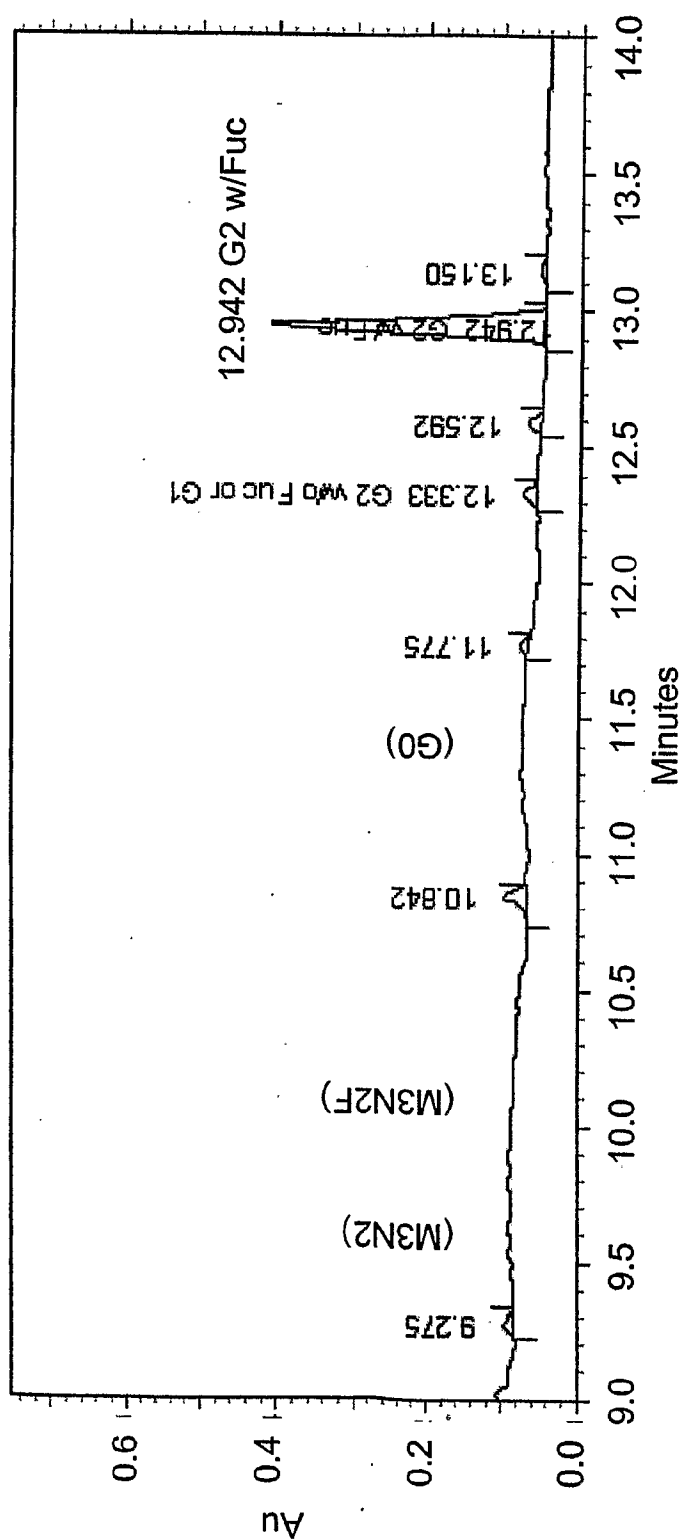


FIG. 103C

366/498

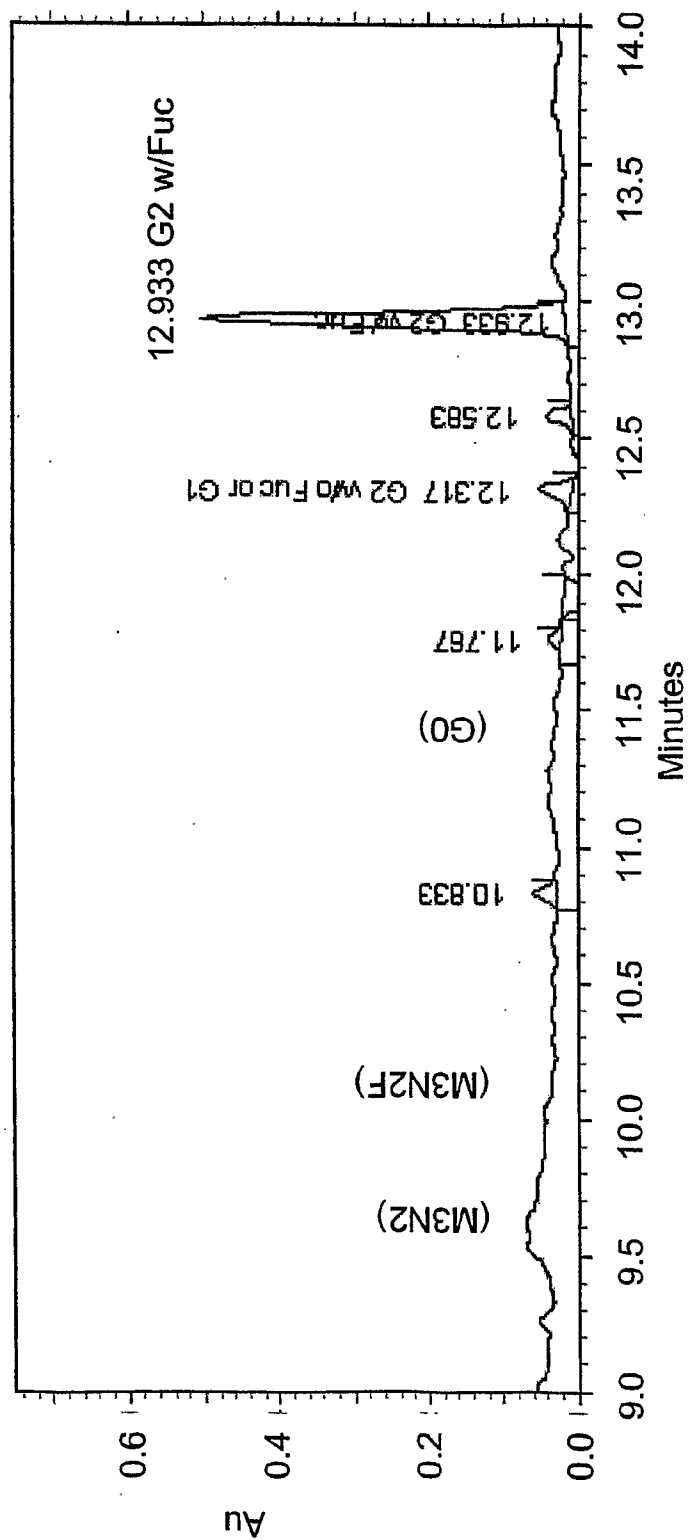


FIG. 103D

367/498

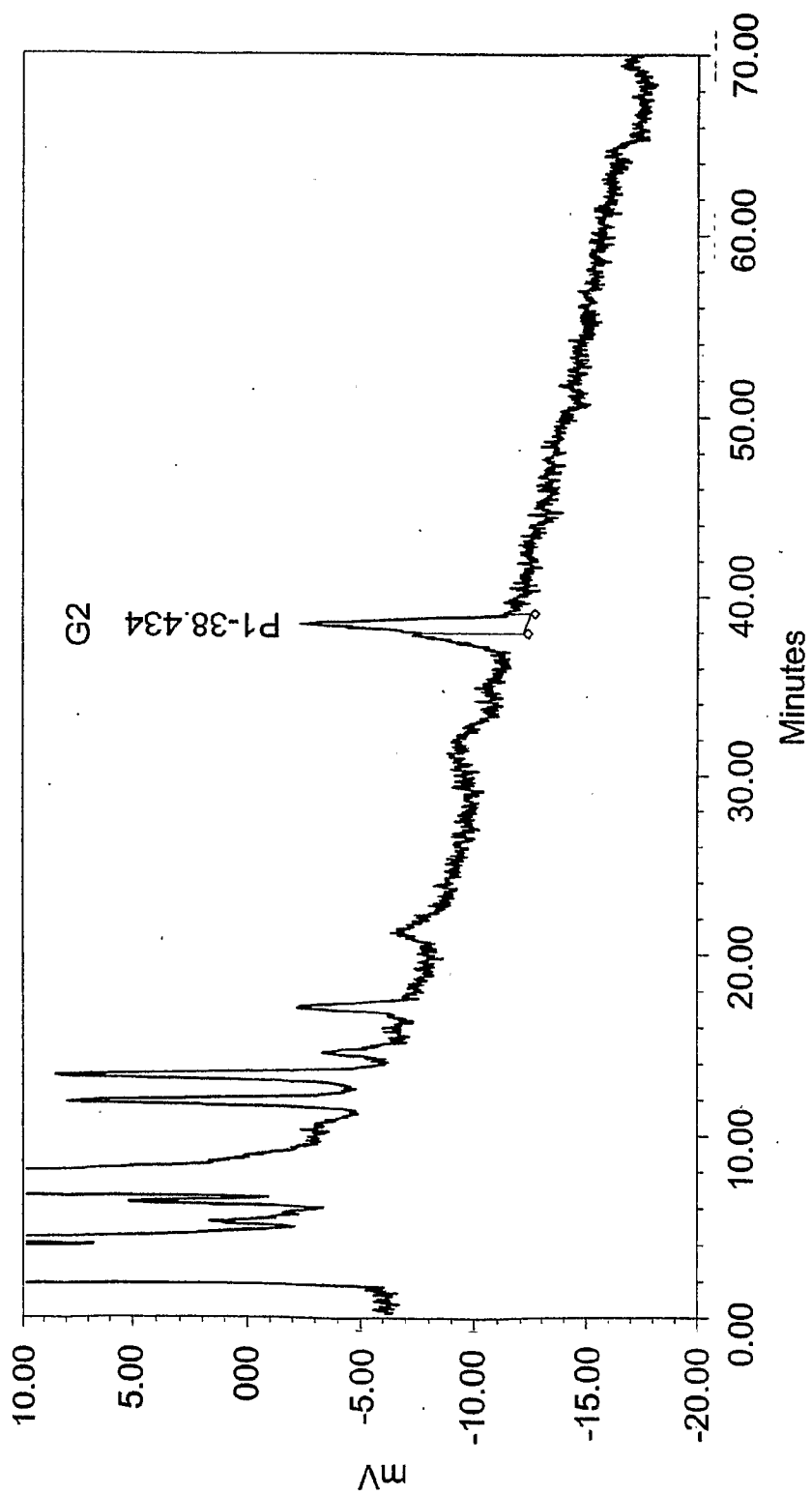


FIG. 104A

368/498

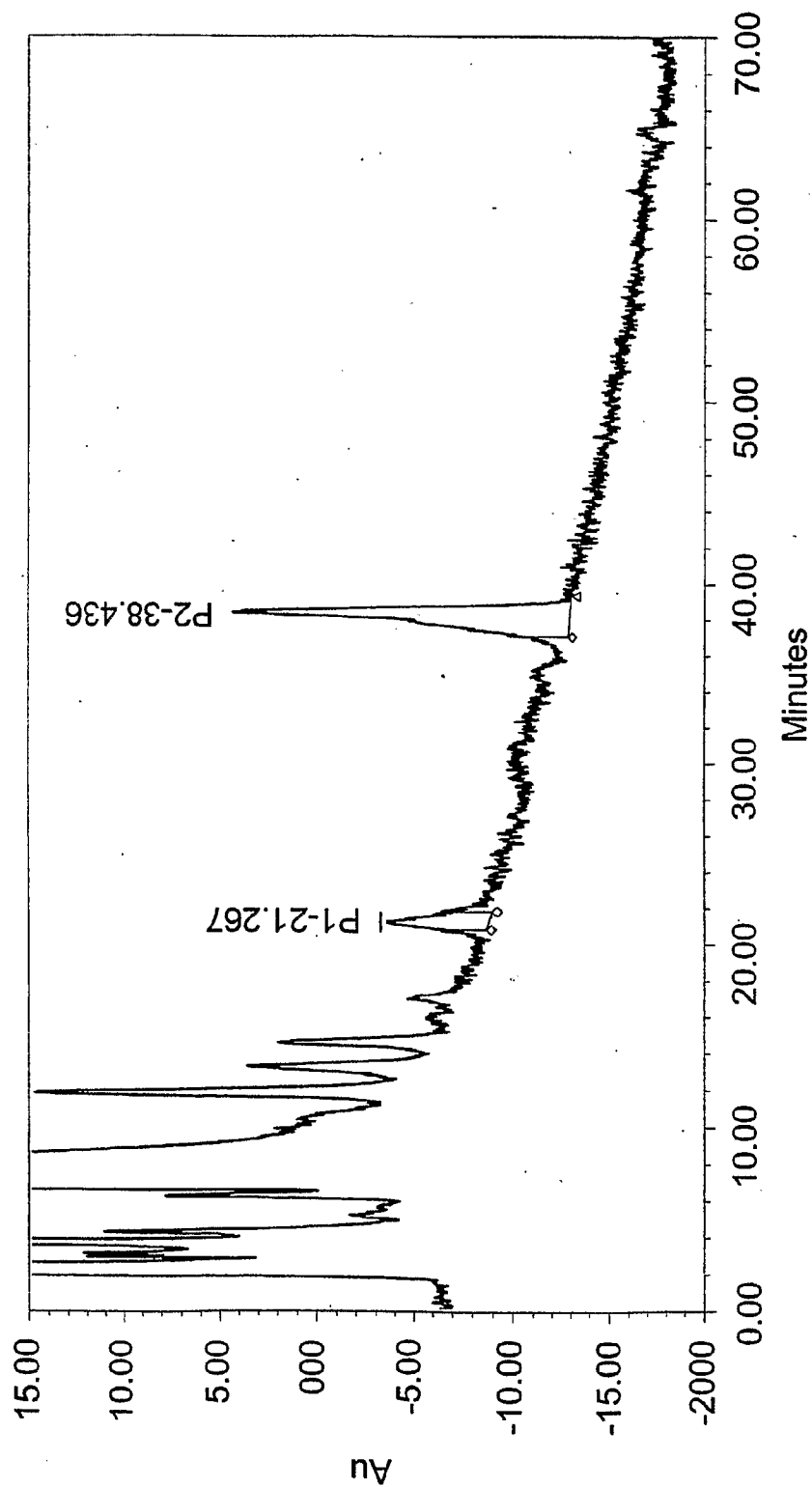


FIG. 104B



370/498

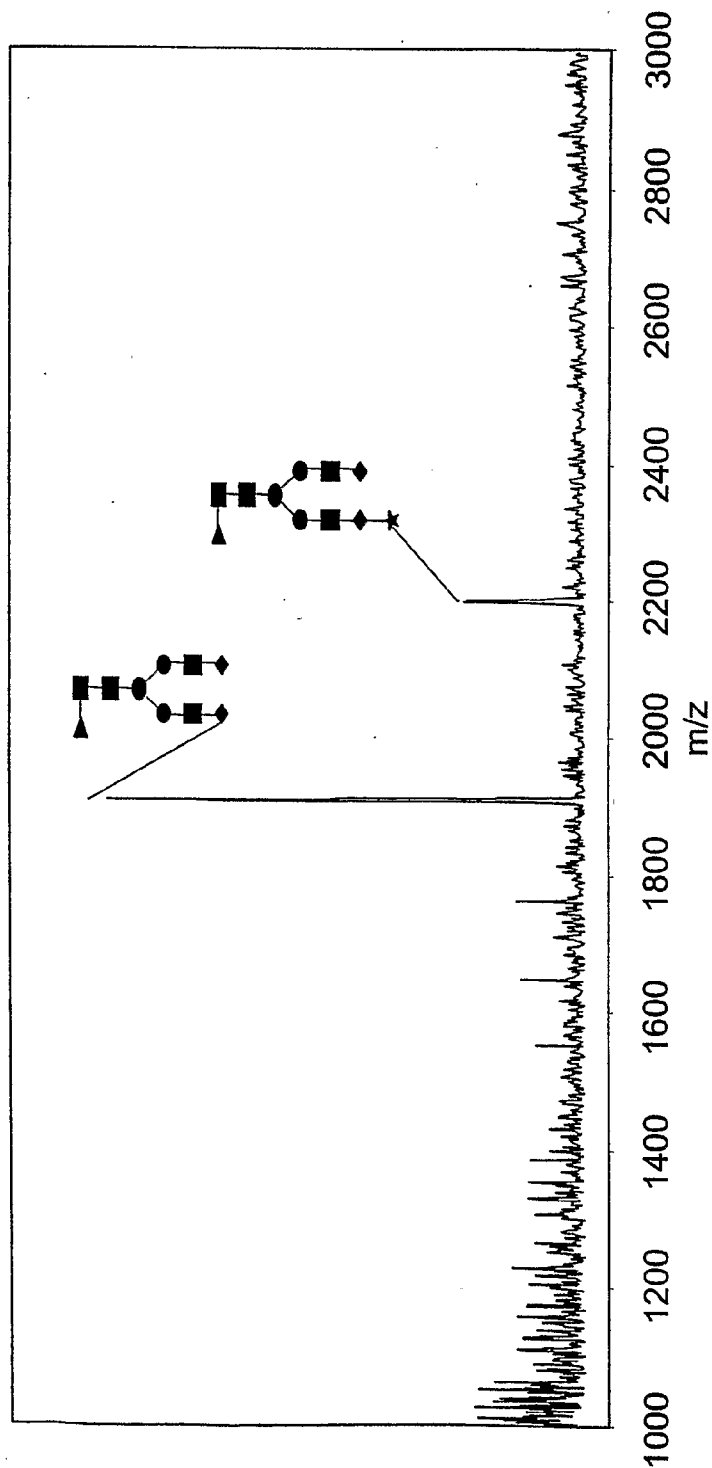


FIG. 105A

371/498

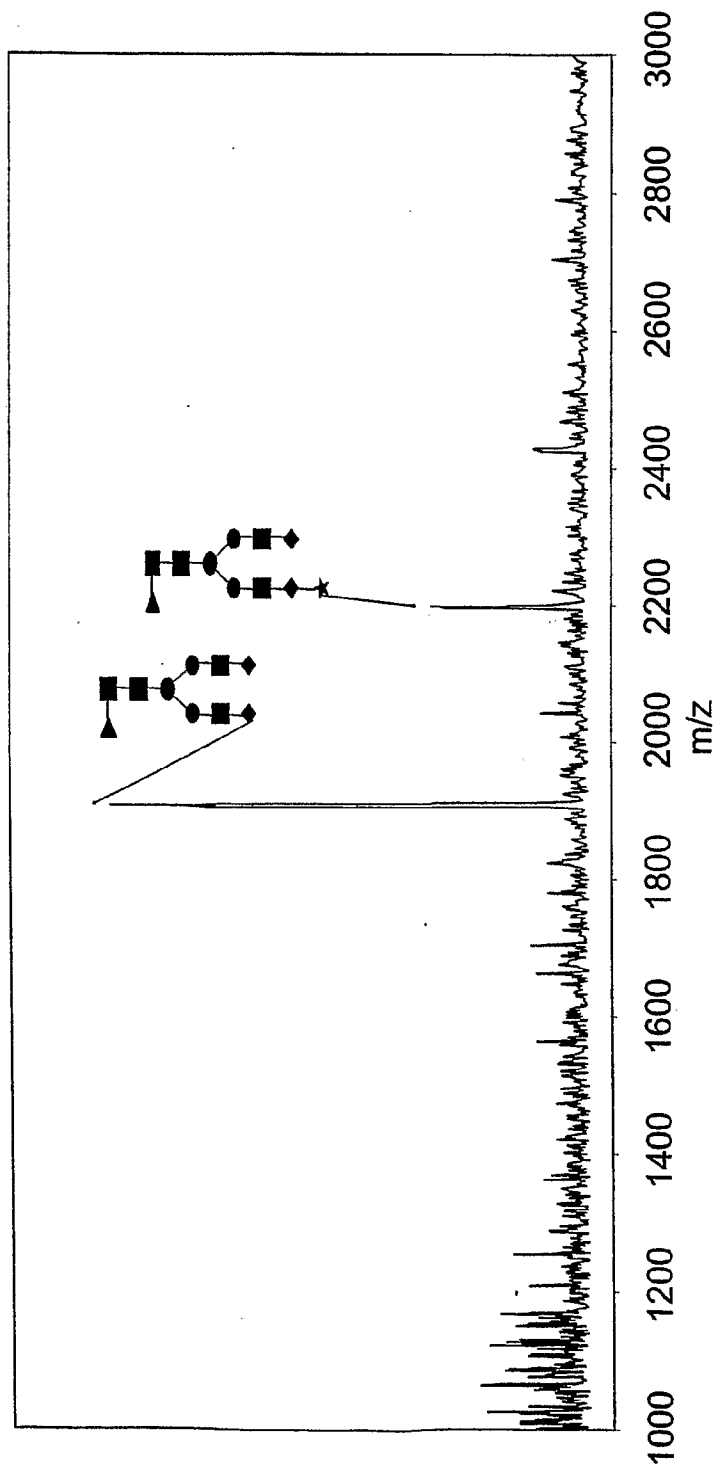


FIG. 105B

372/498

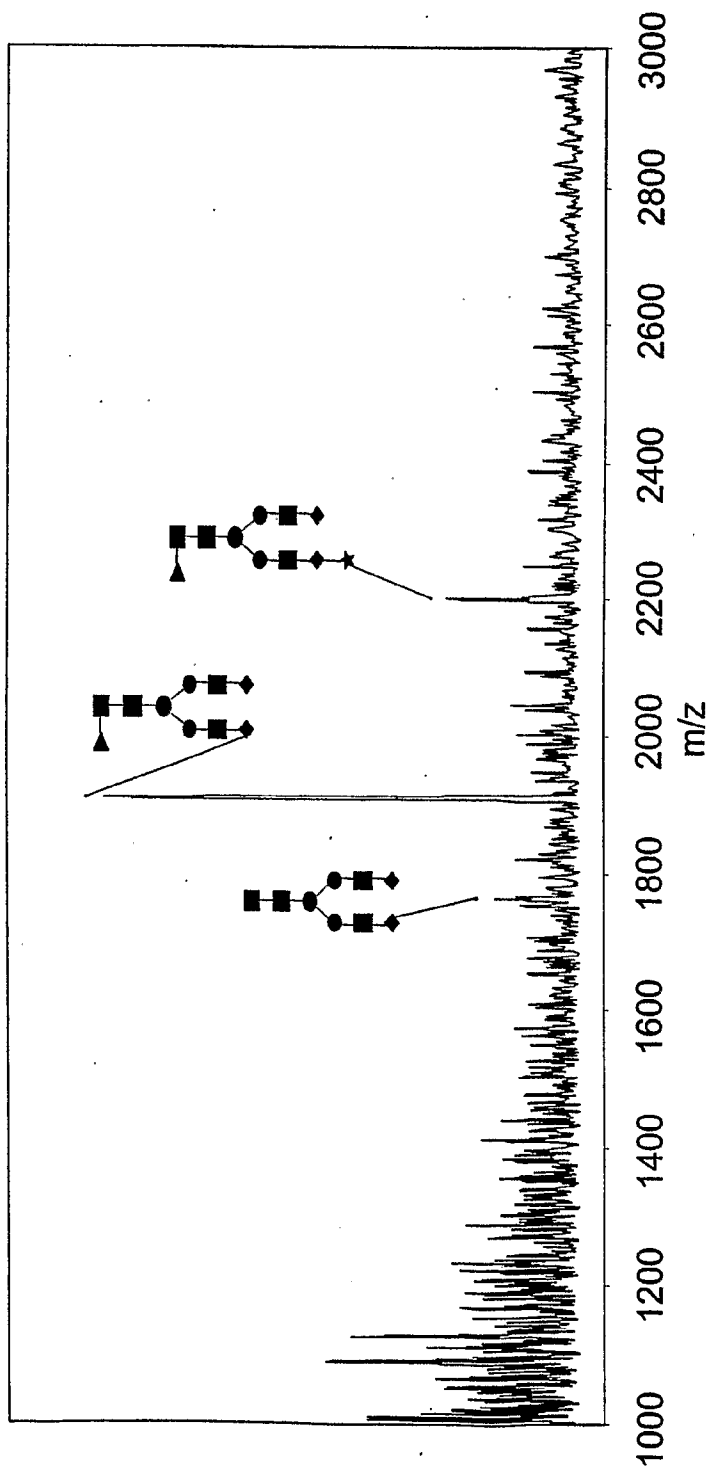


FIG. 105C



373/498

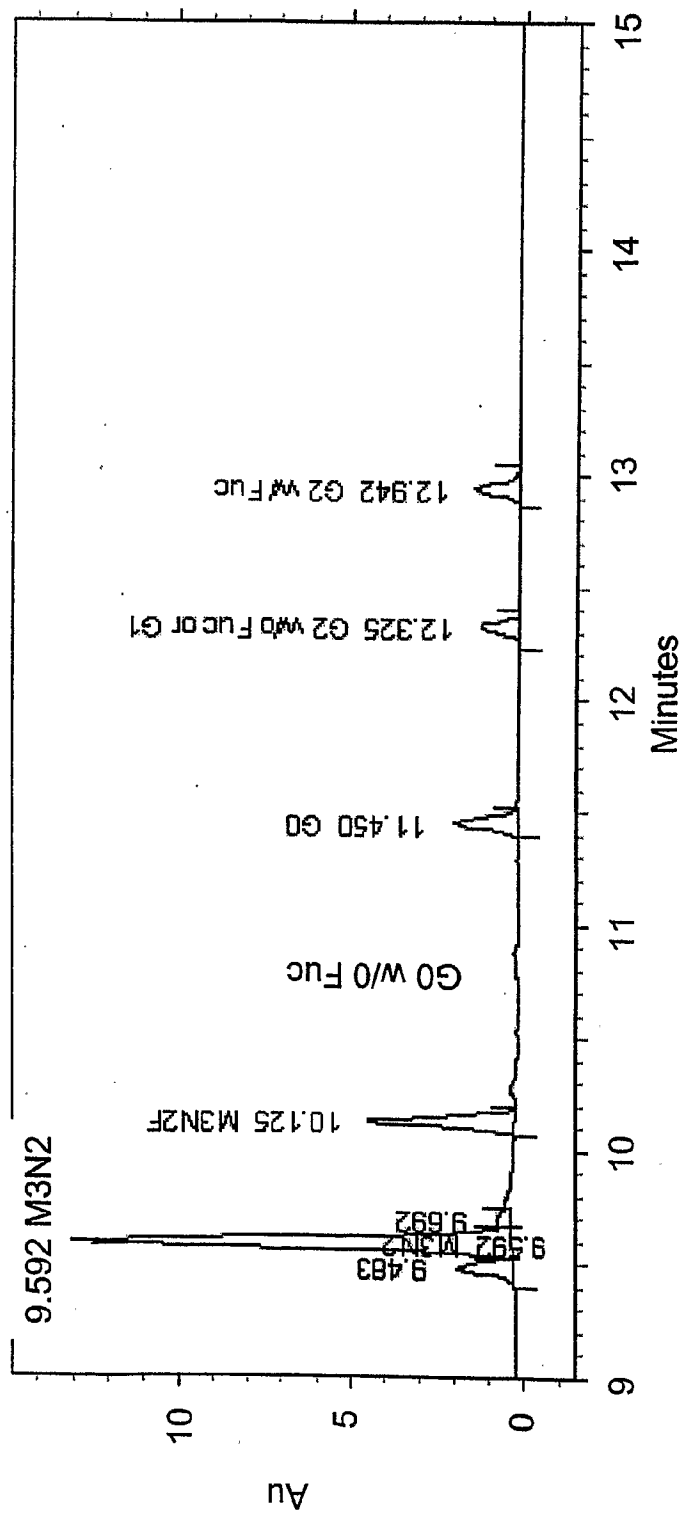


FIG. 106A

374/498

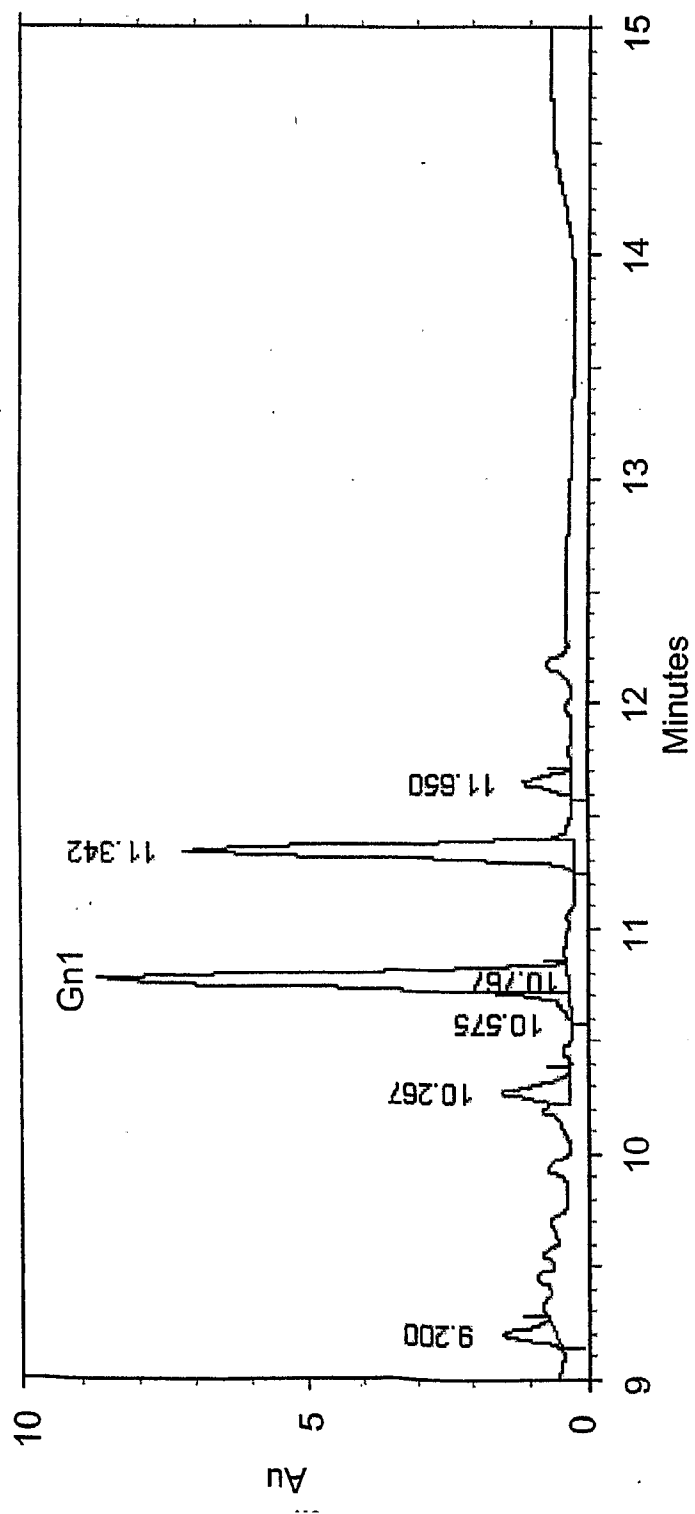


FIG. 106B

375/498

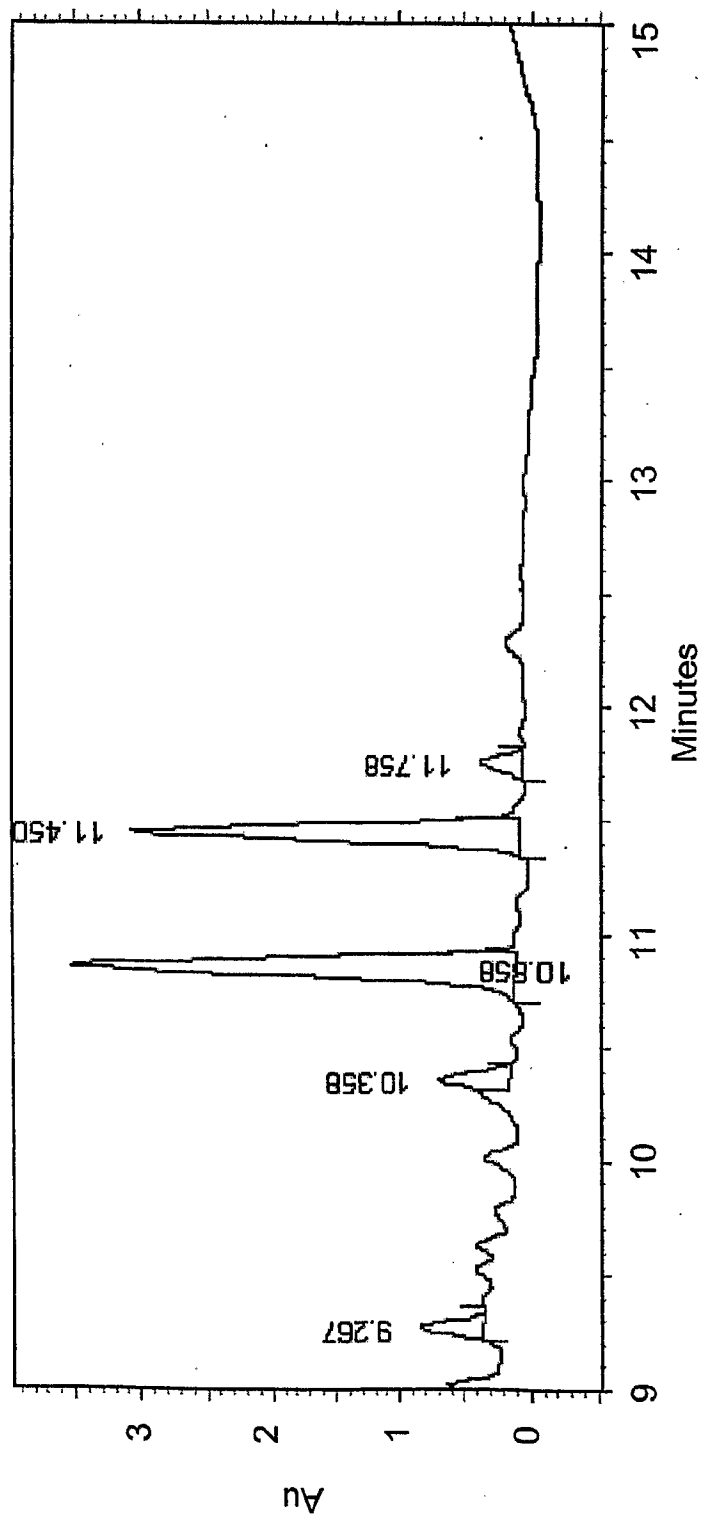


FIG. 106C

376/498

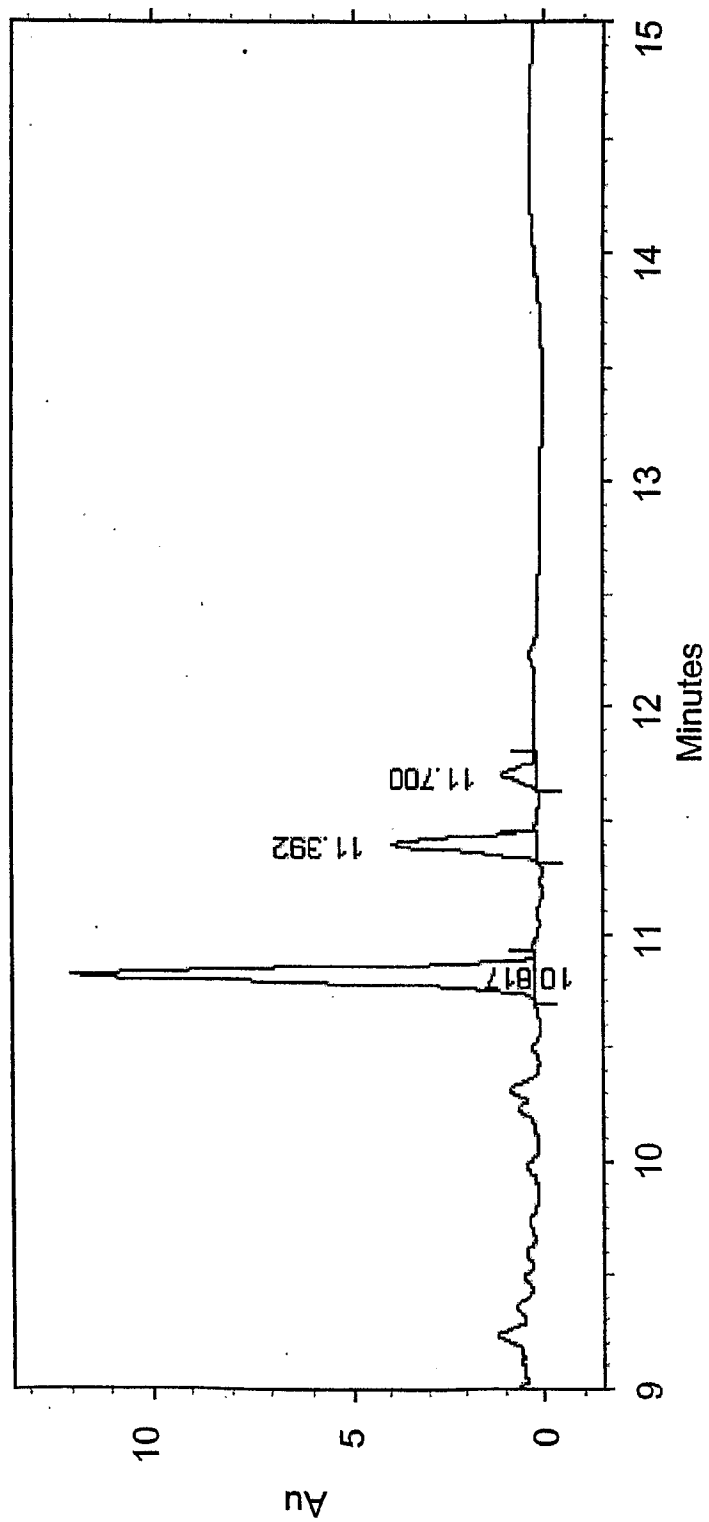


FIG. 106D

377/498

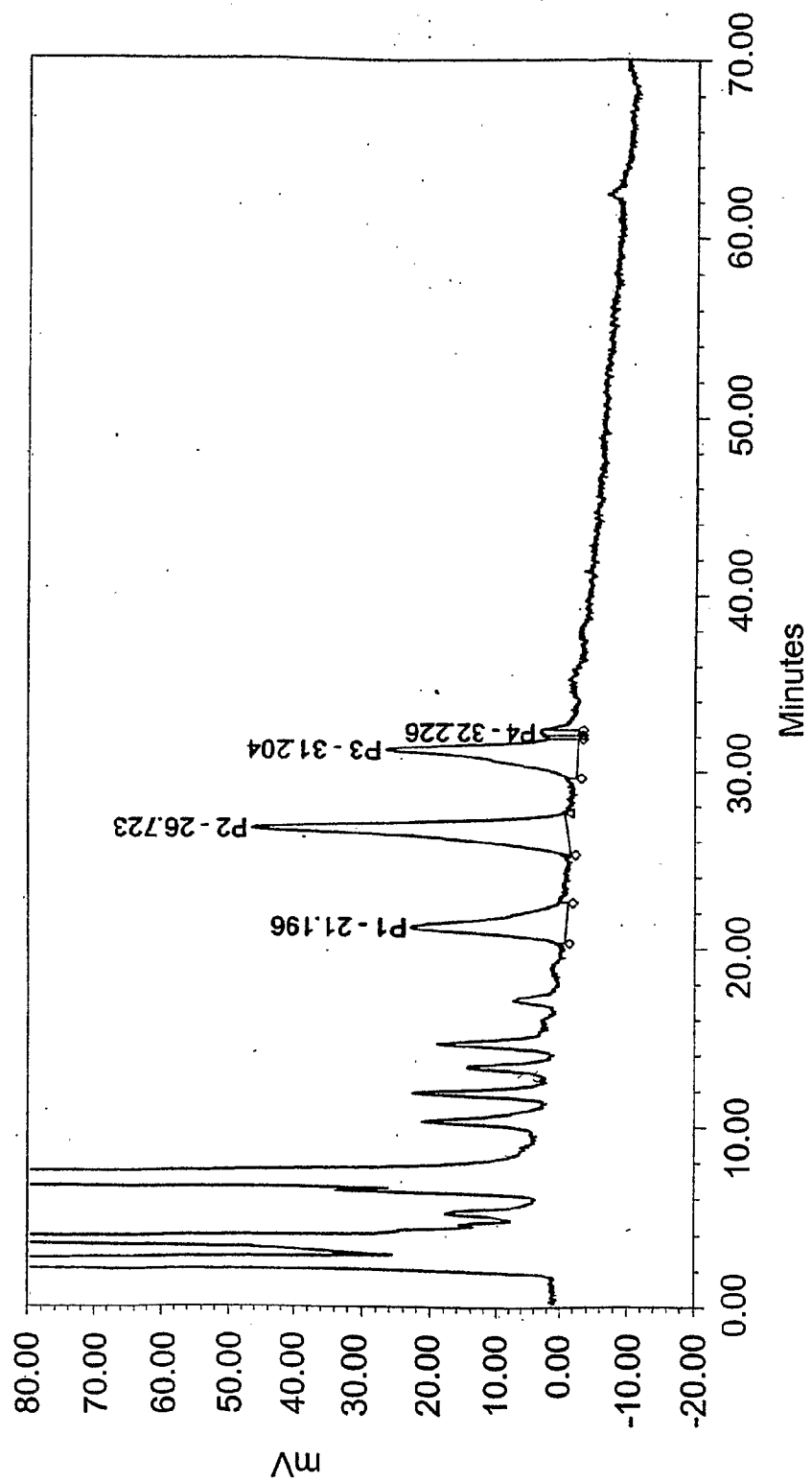


FIG. 107A

378/498

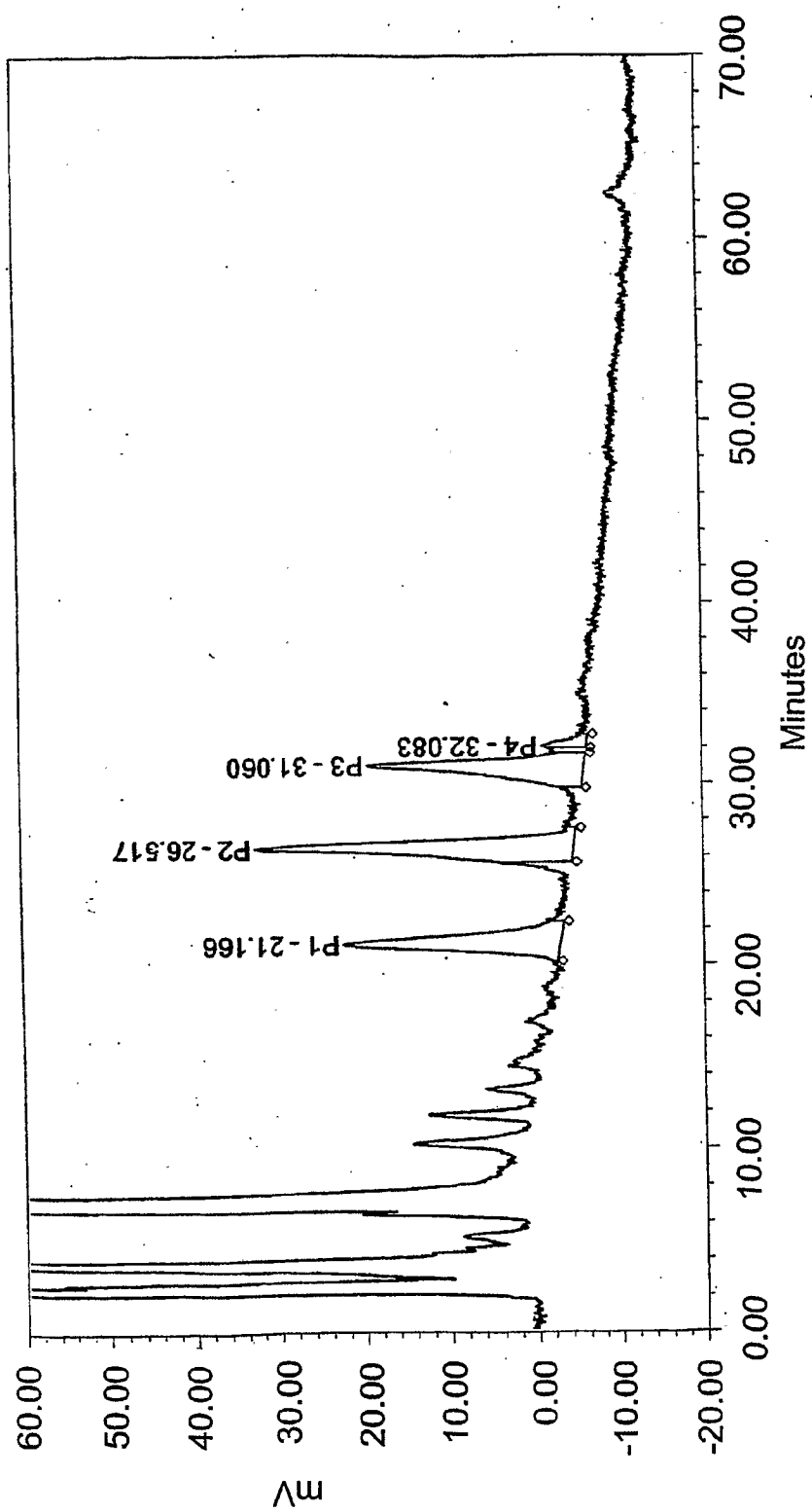


FIG. 107B

379/498

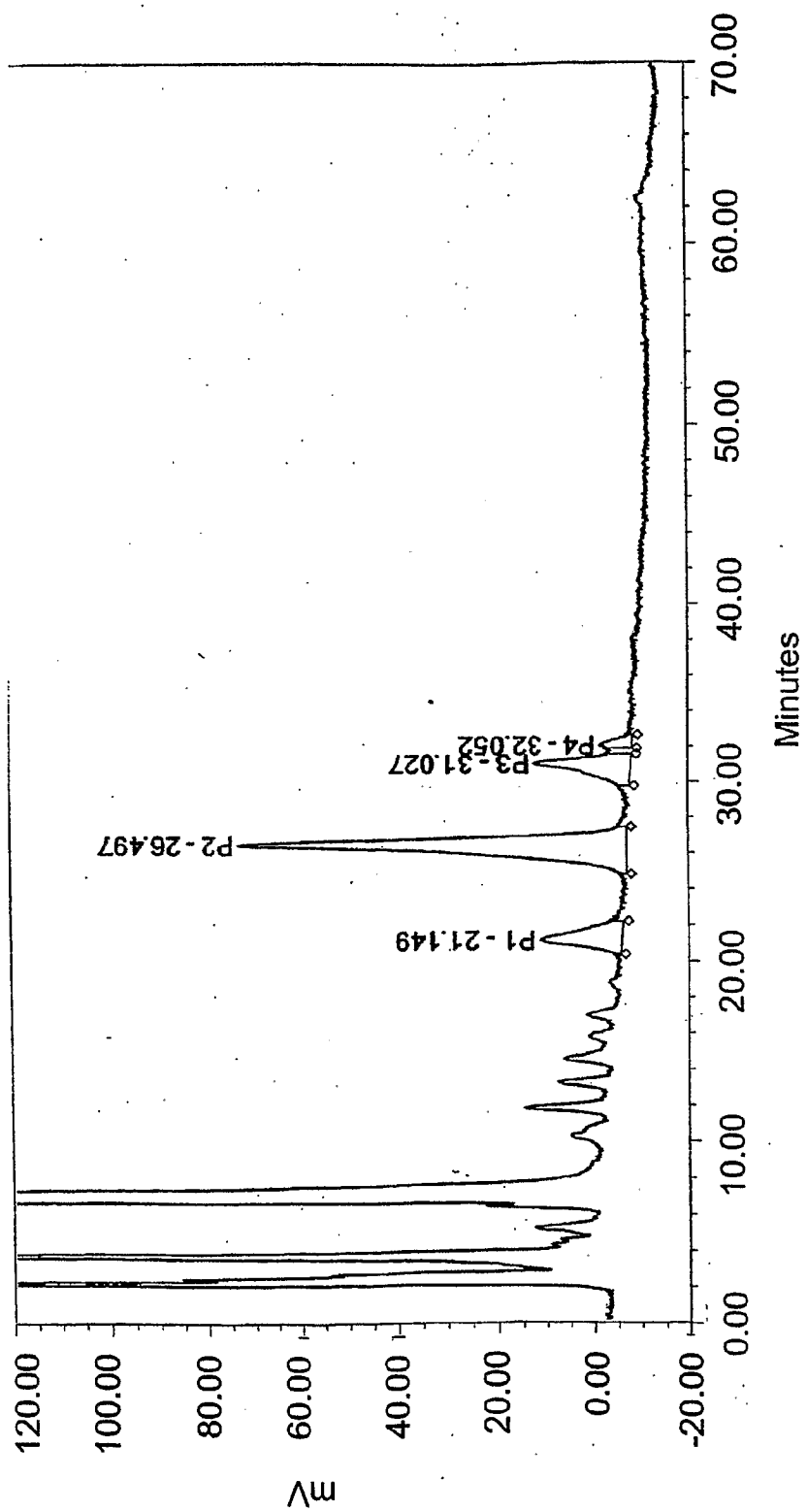


FIG. 107C

380/498

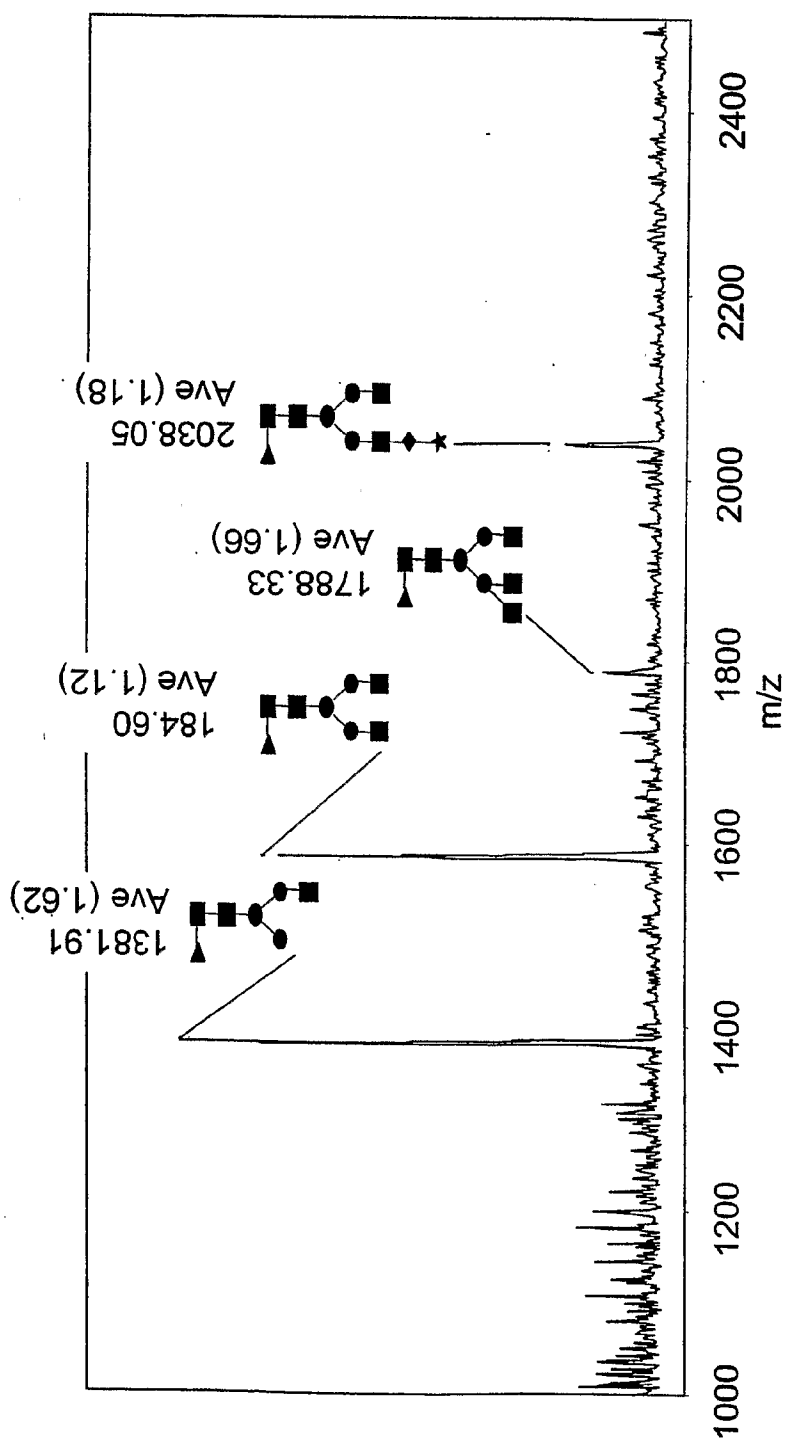


FIG. 108A



381/498

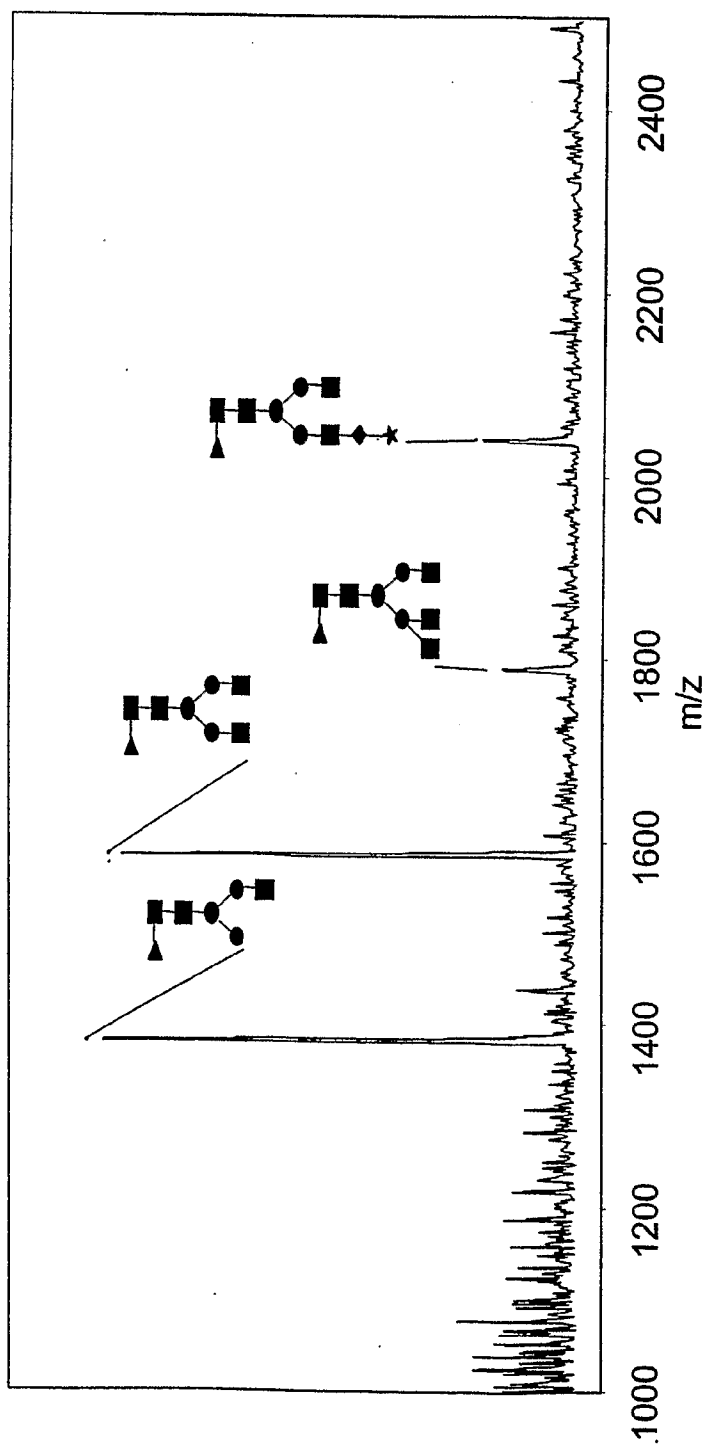


FIG. 108B

382/498

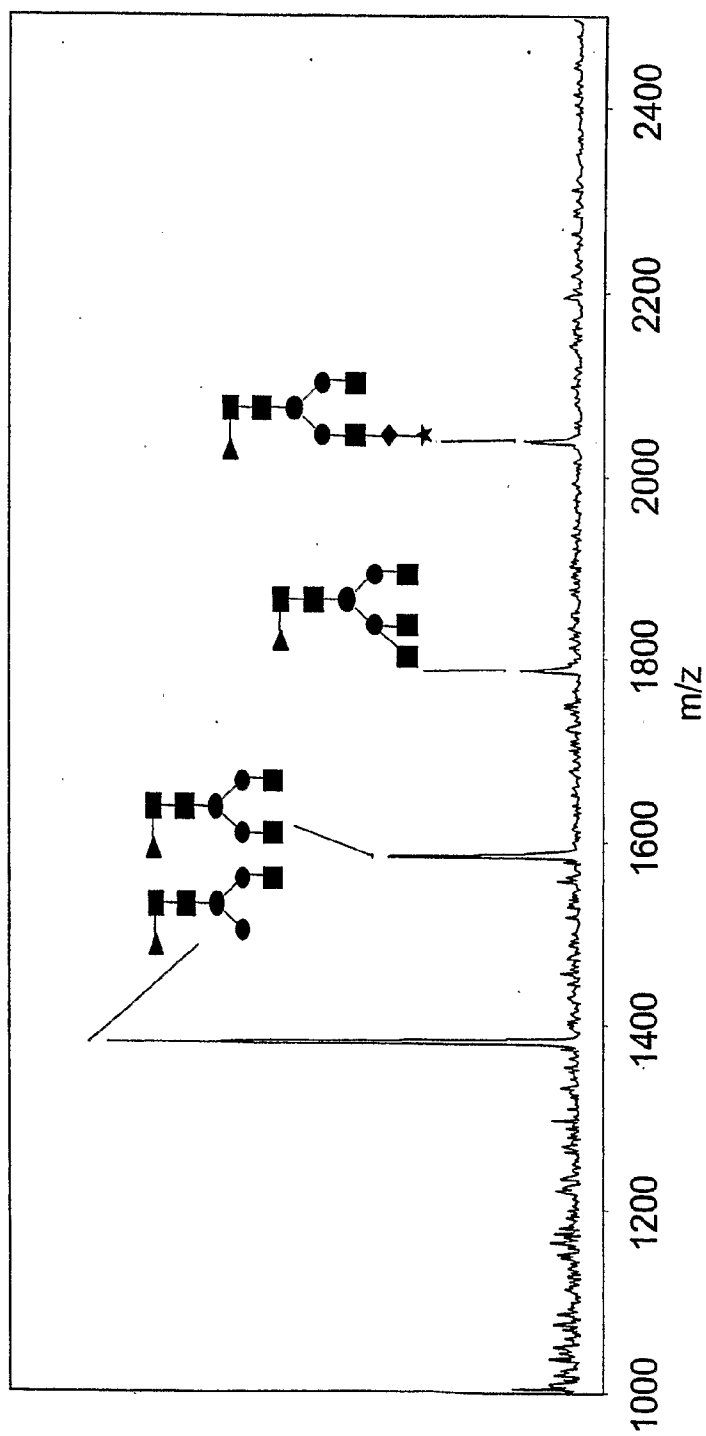


FIG. 108C

383/498

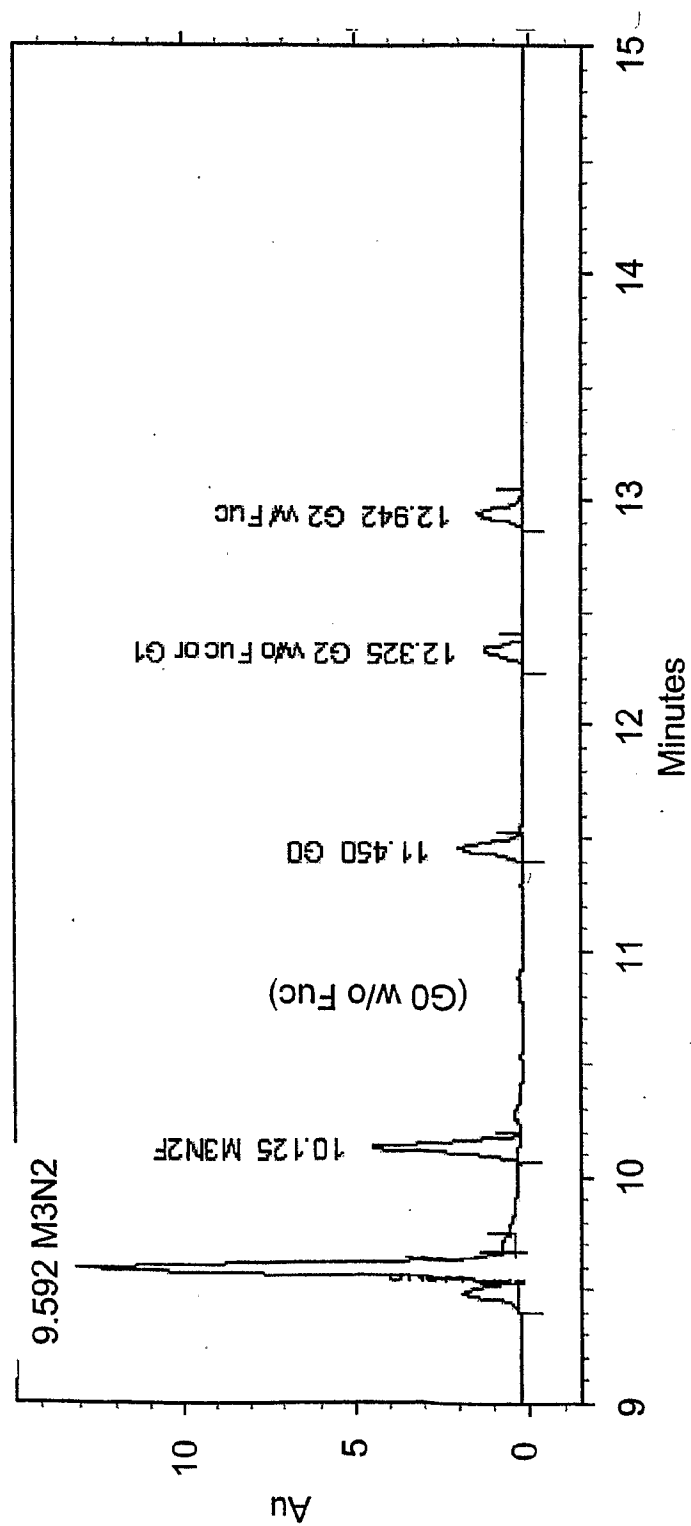


FIG. 109A

384/498

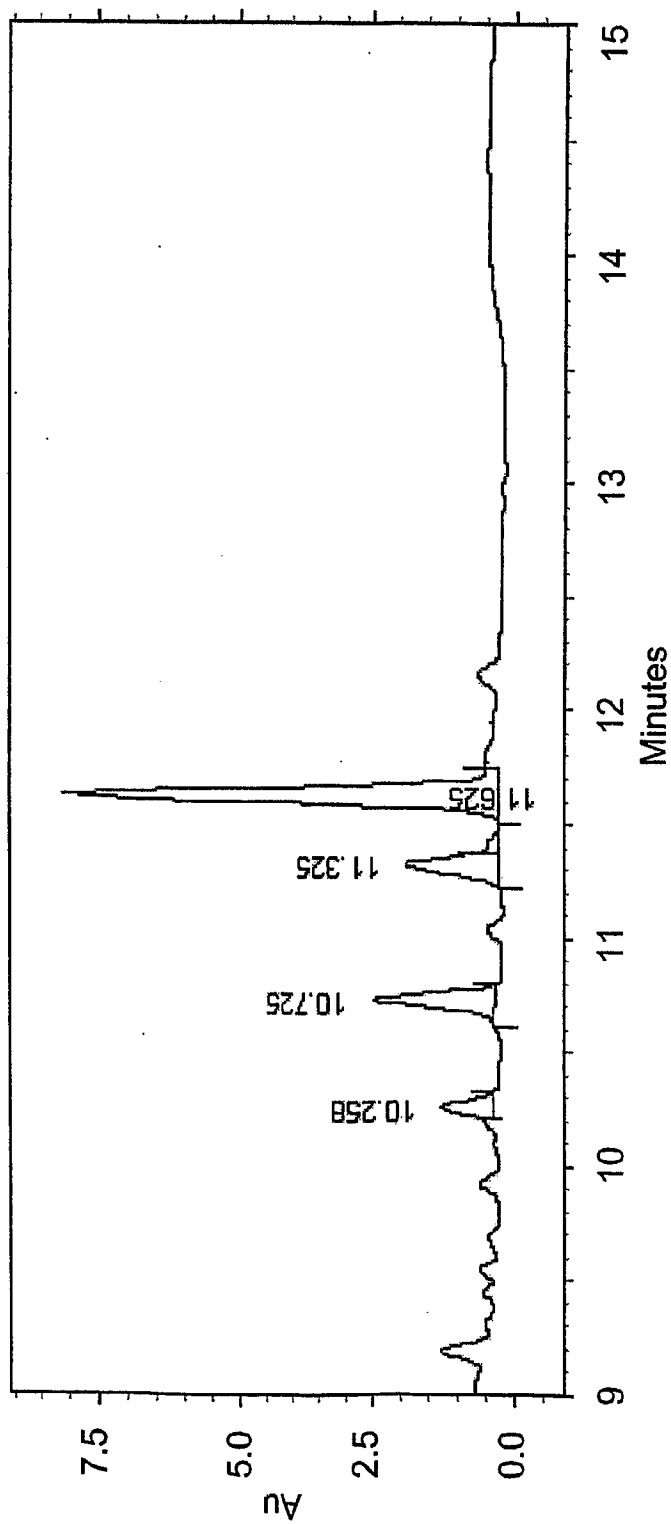


FIG. 109B

385/498

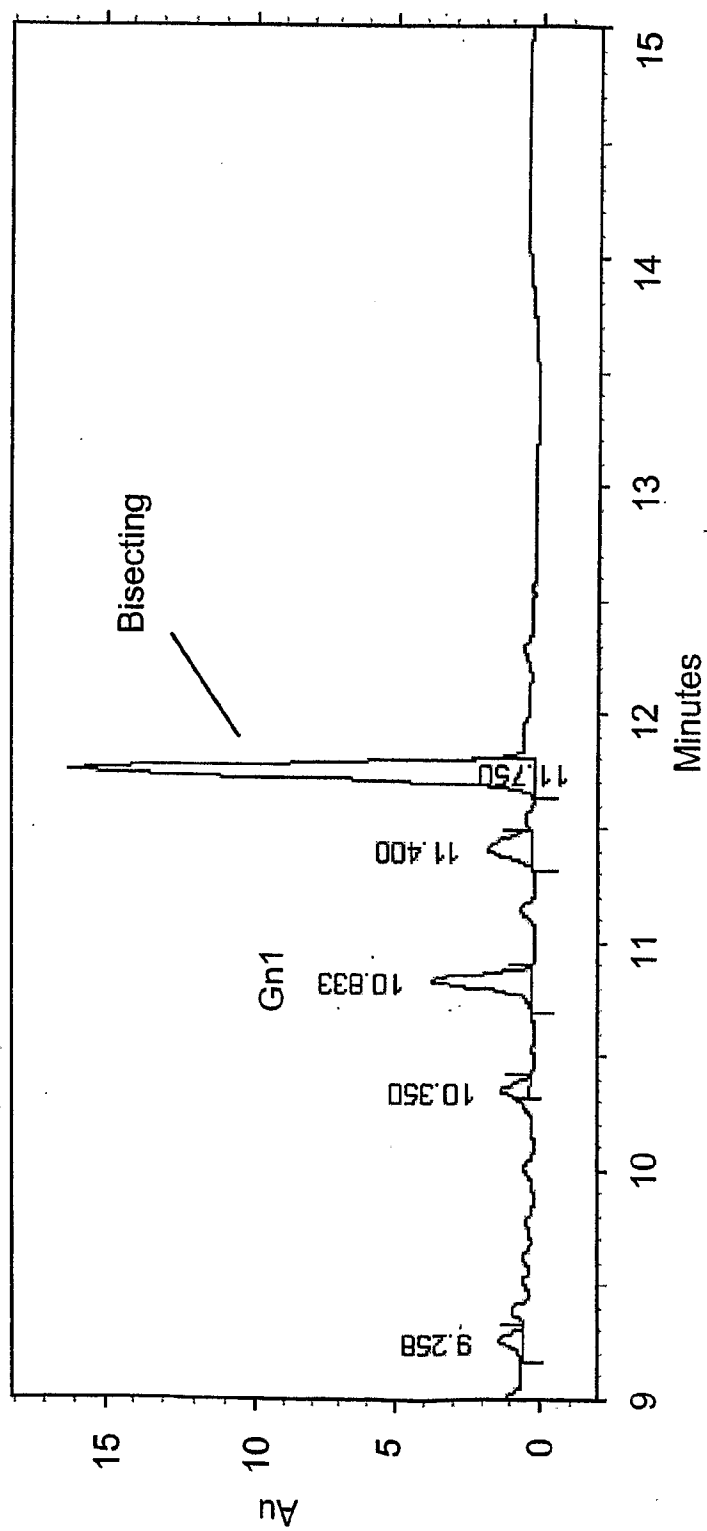


FIG. 109C

386/498

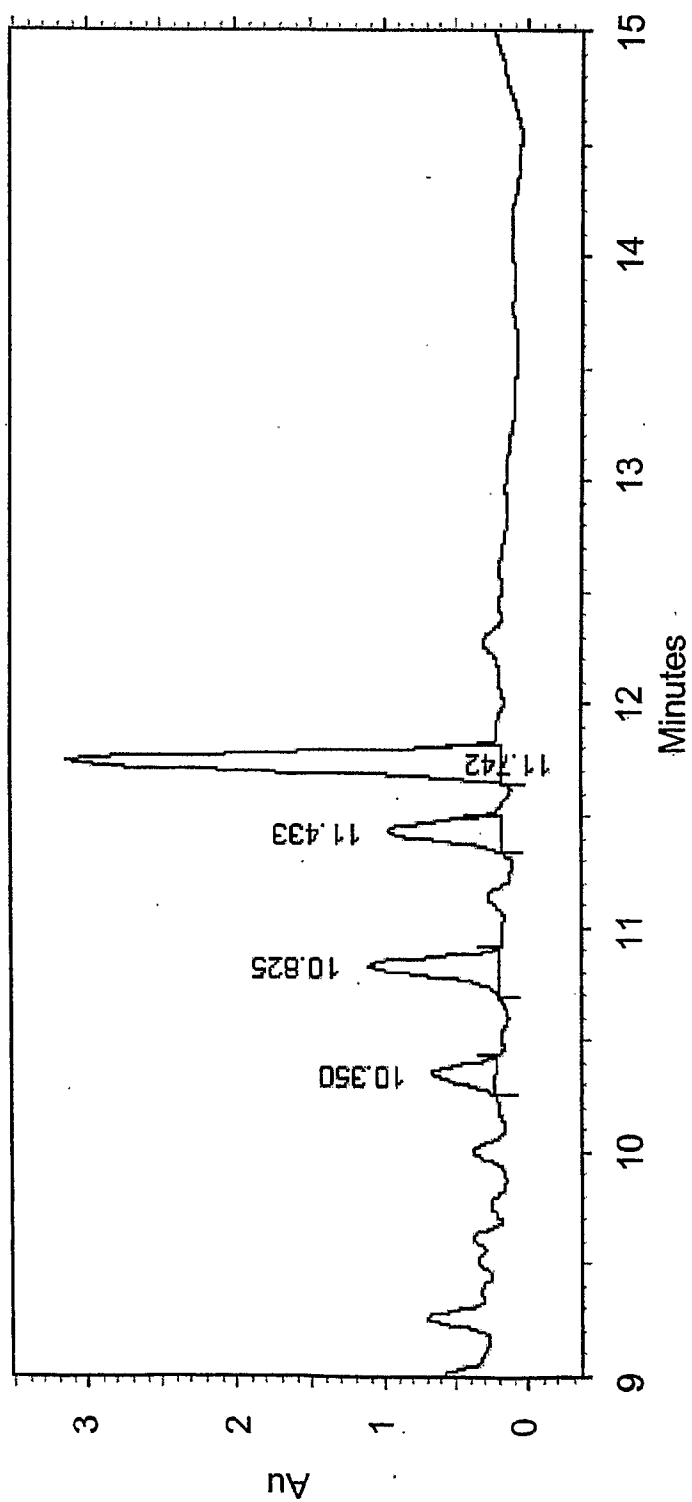


FIG. 109D

387/498

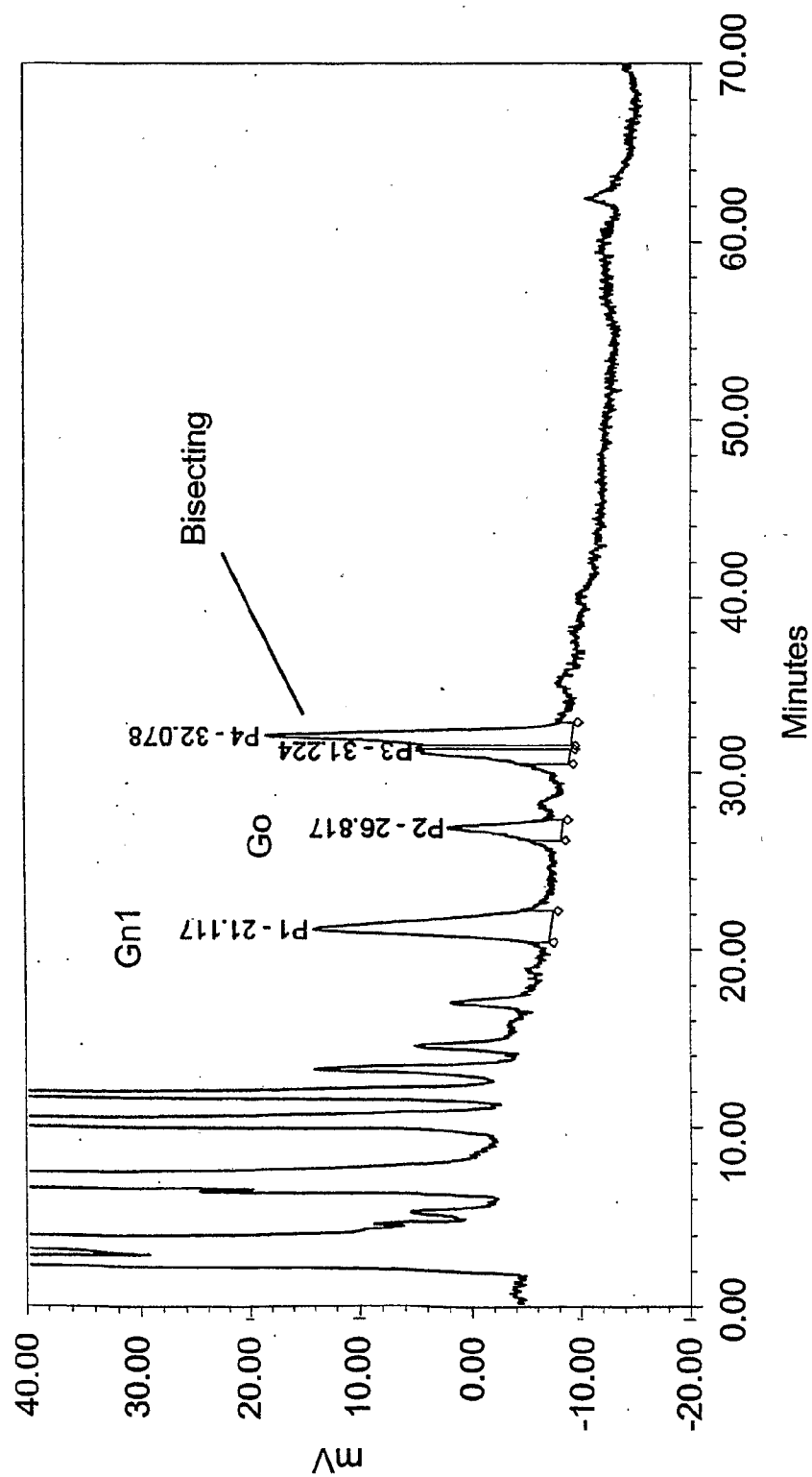


FIG. 110A

388/498

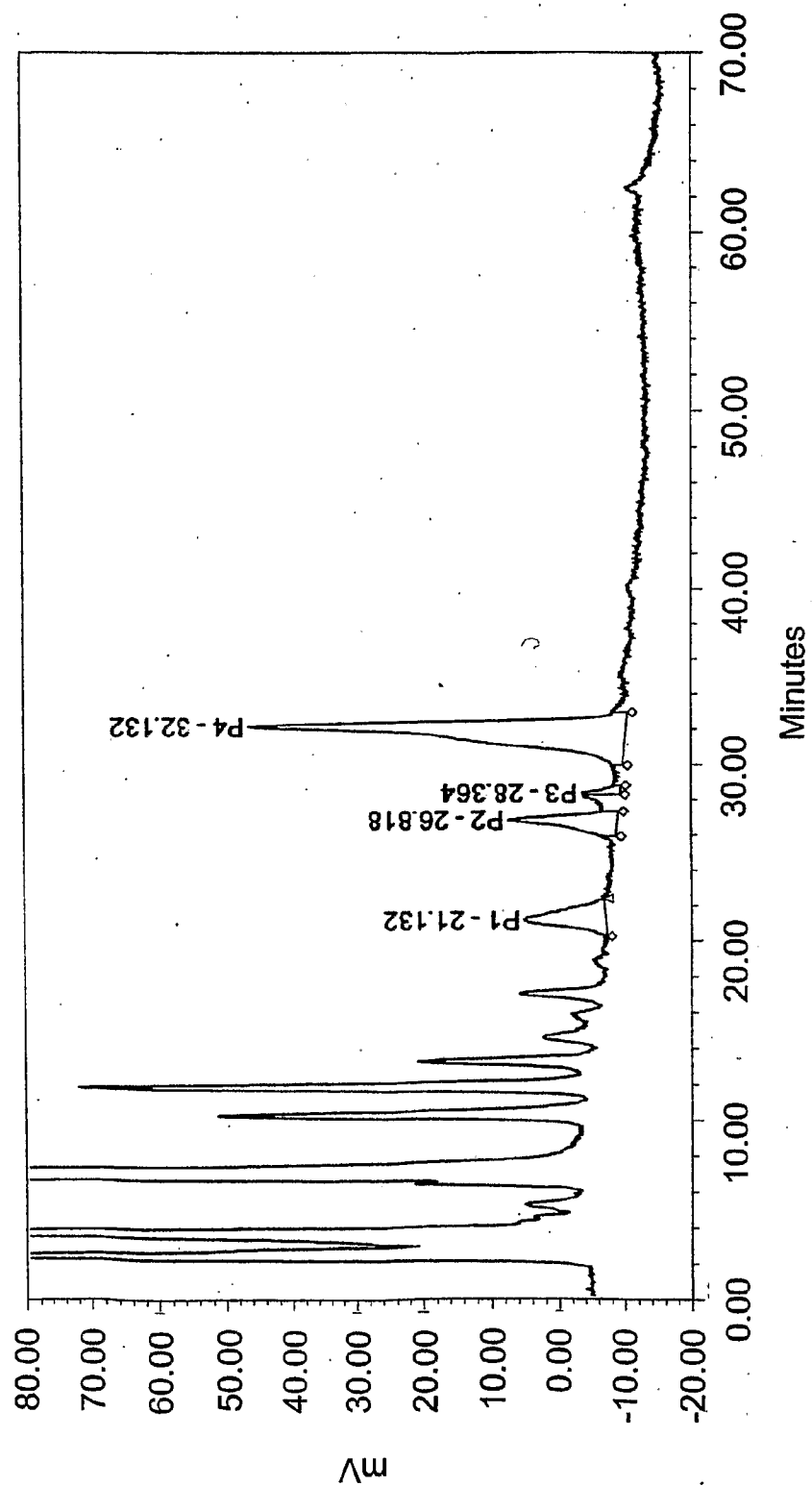


FIG. 110B



389/498

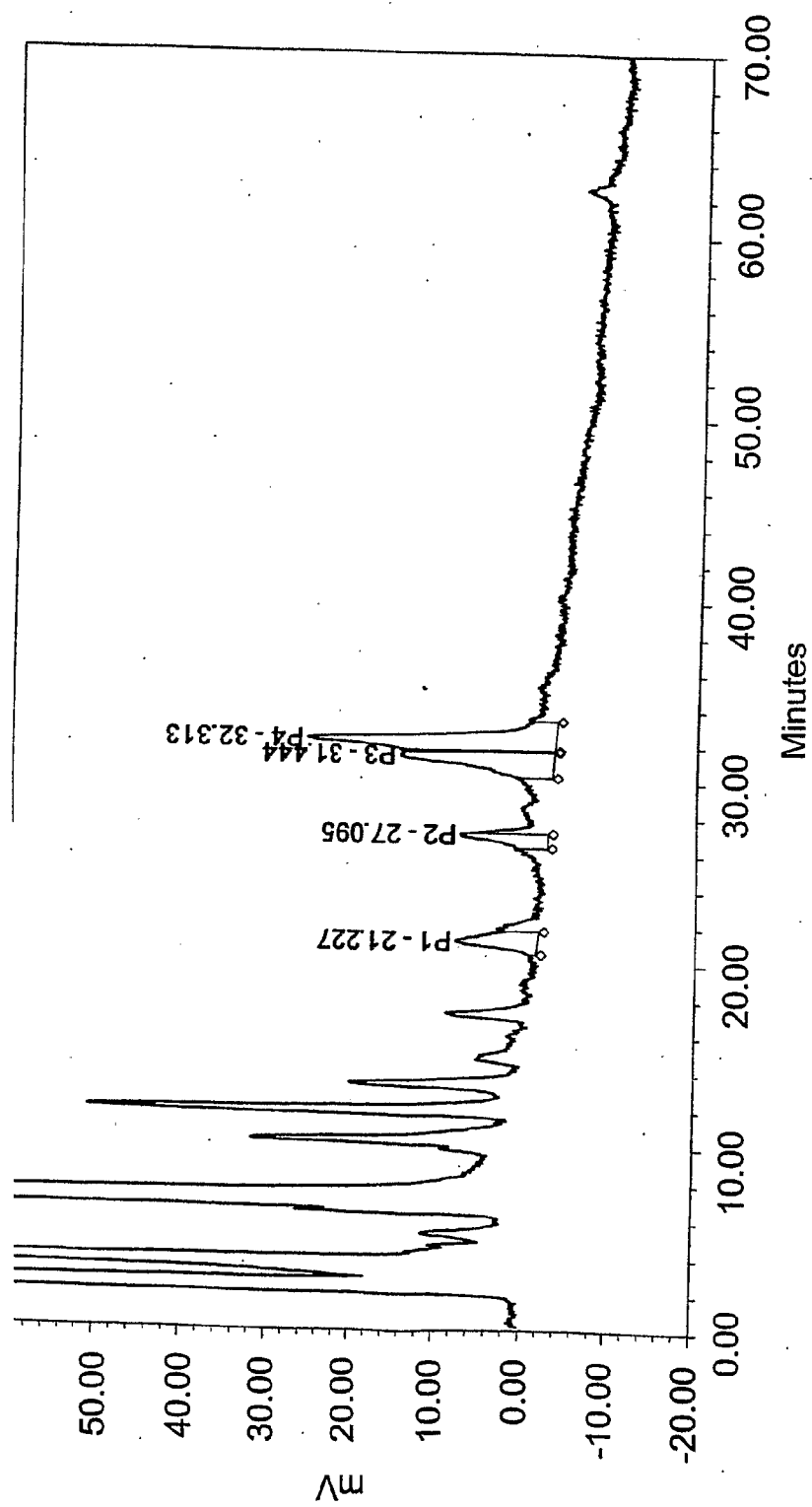


FIG. 110C

390/498

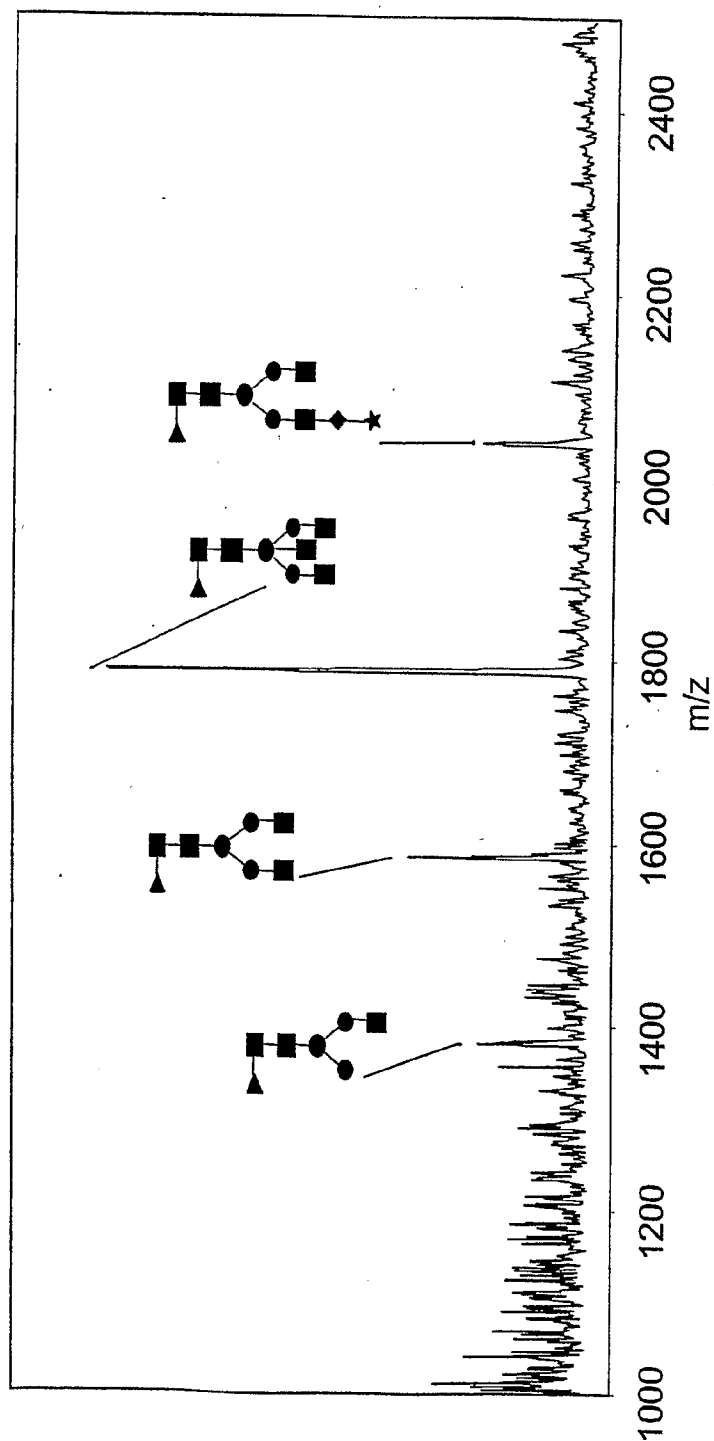


FIG. 111A

391/498

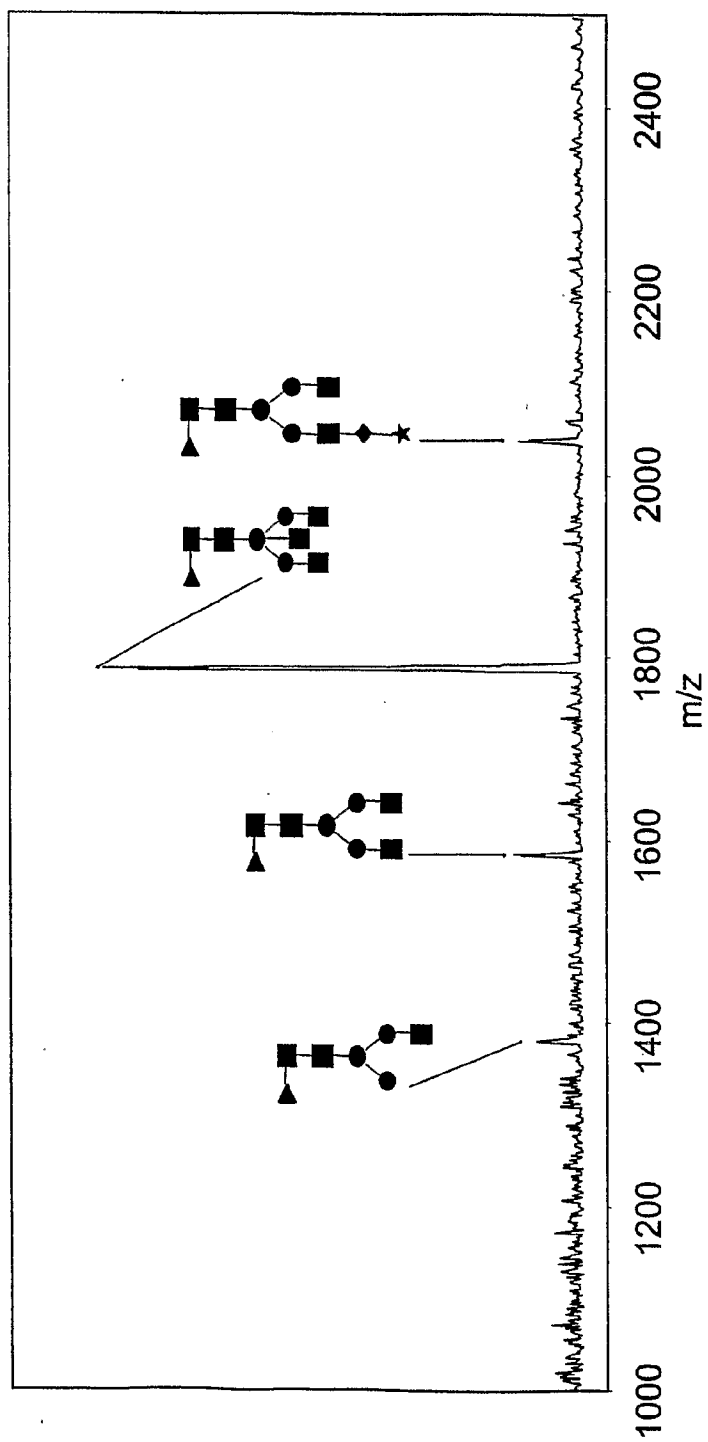


FIG. 111B

392/498

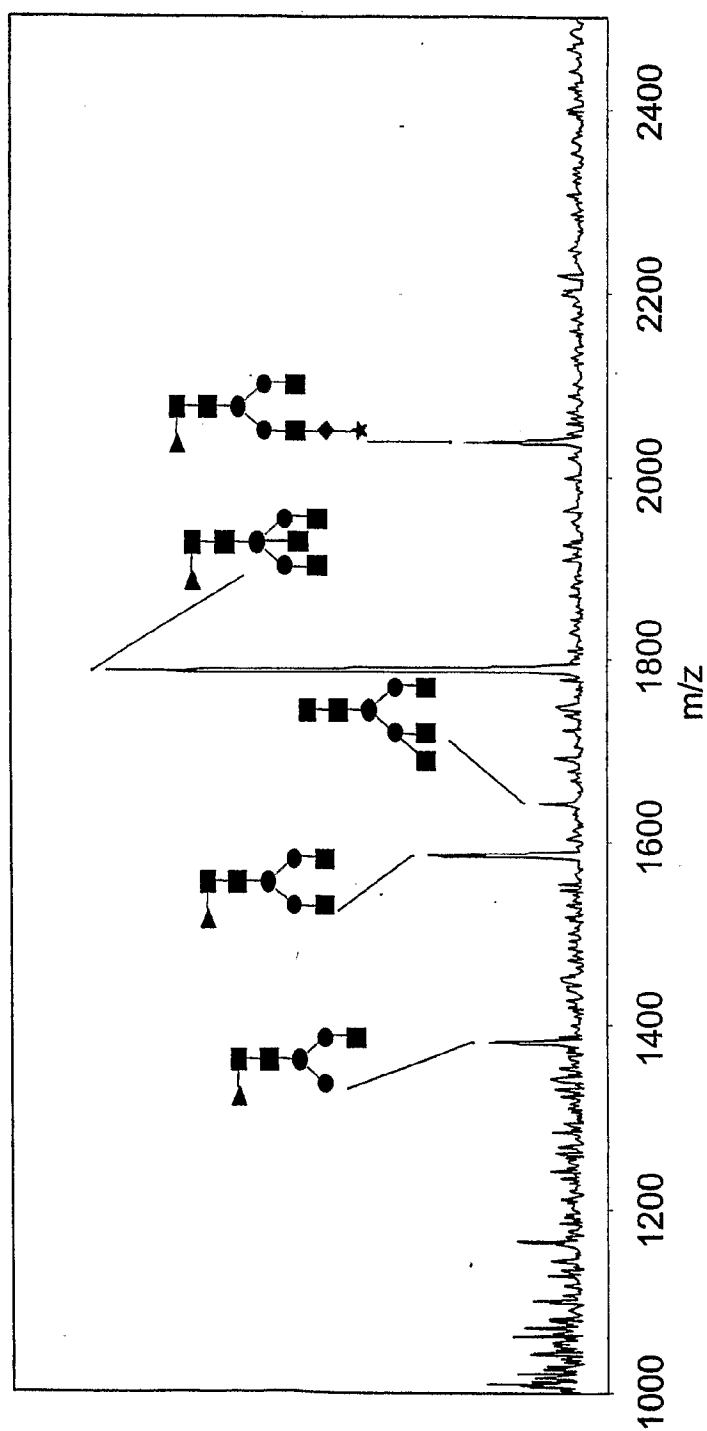


FIG. 111C

393/498

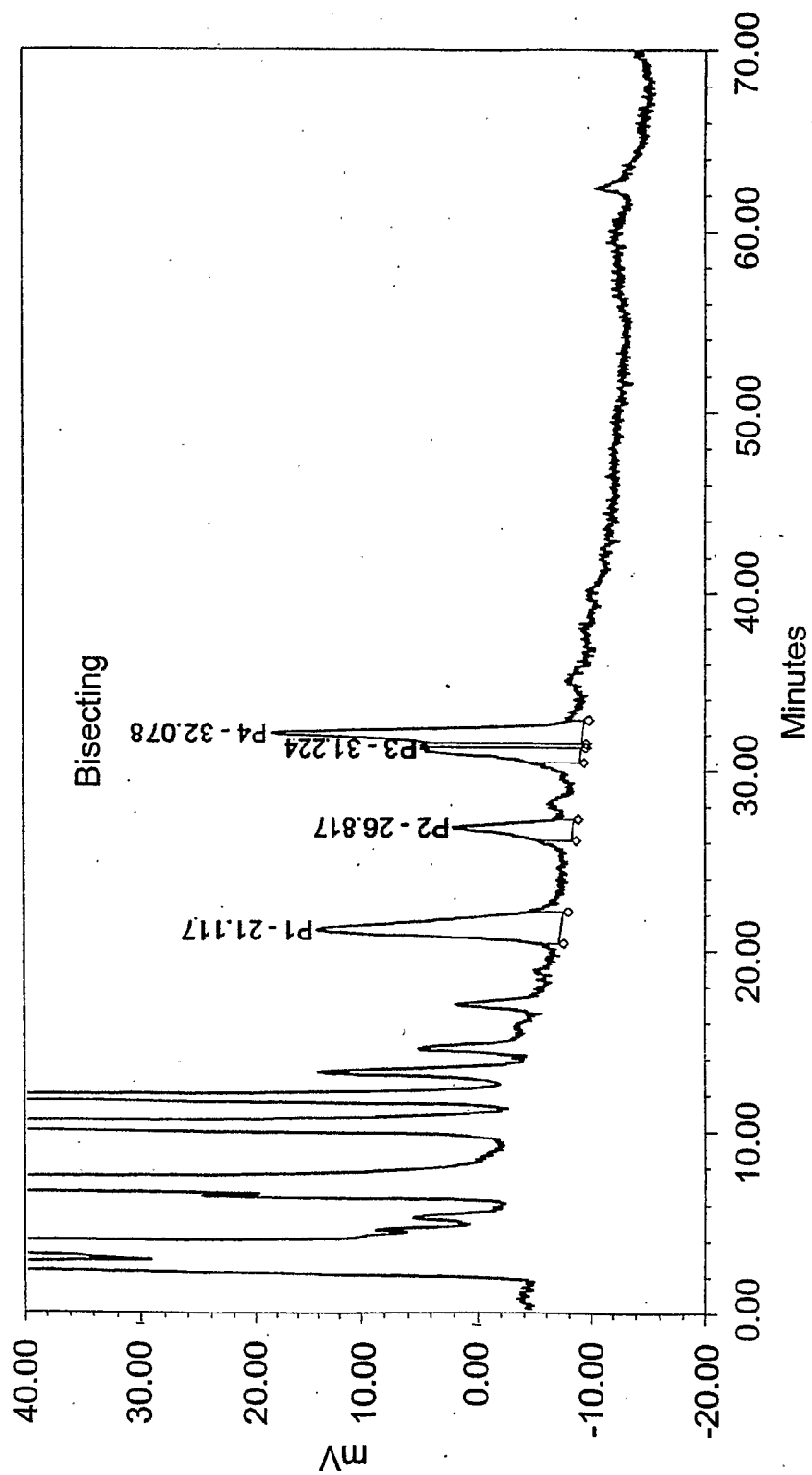


FIG. 112A

394/498

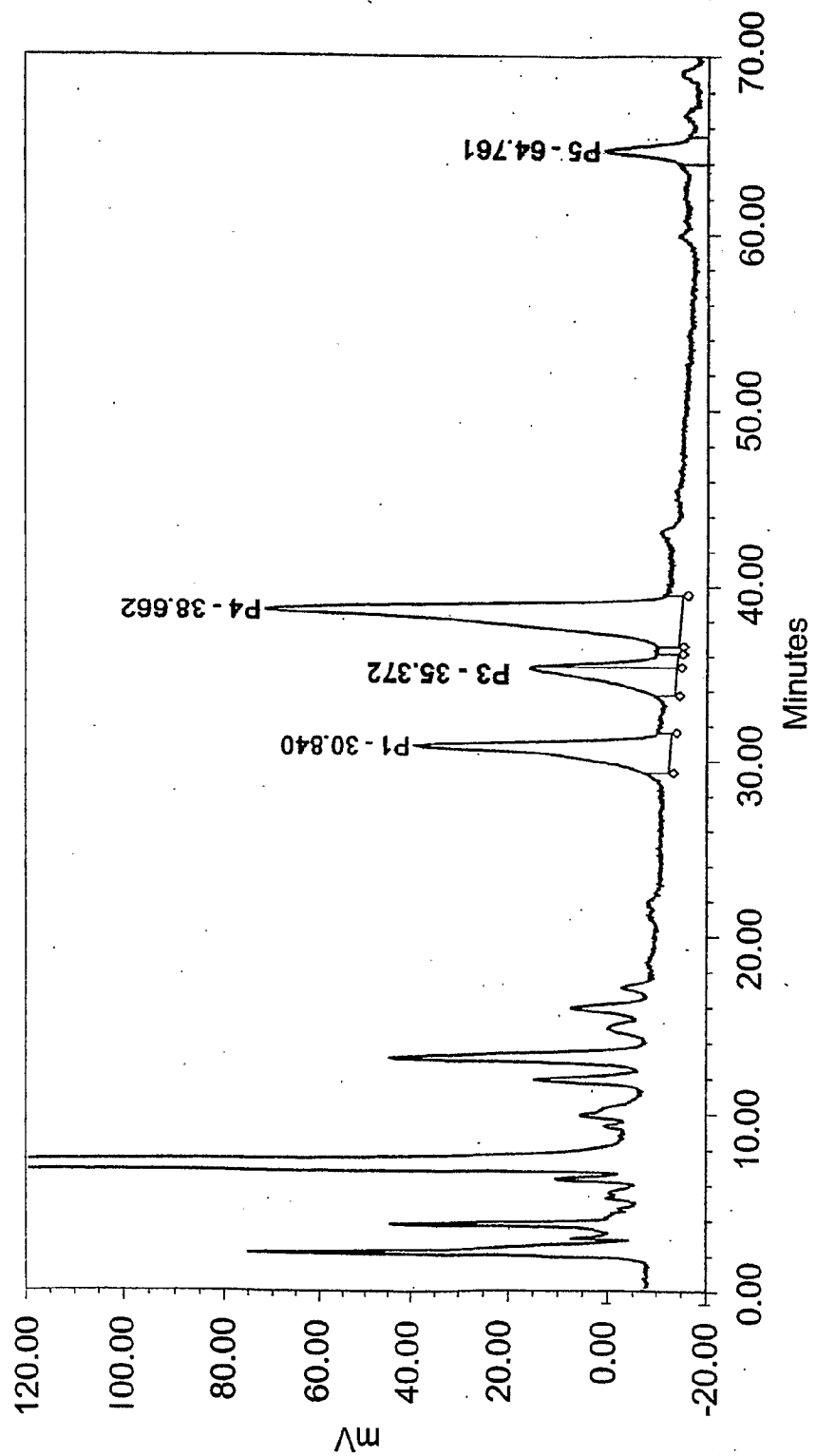


FIG. 112B

395/498

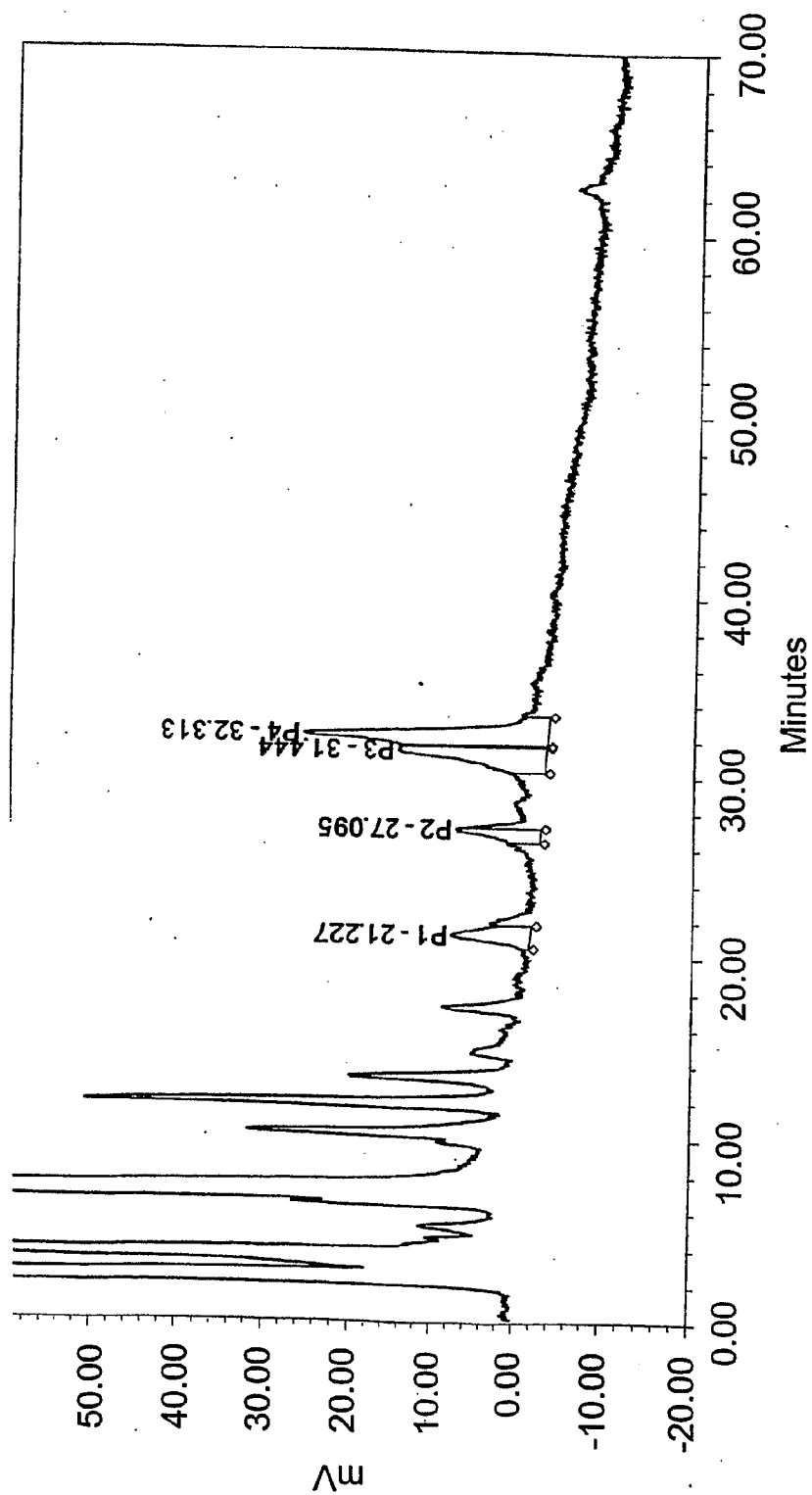


FIG. 112C

396/498

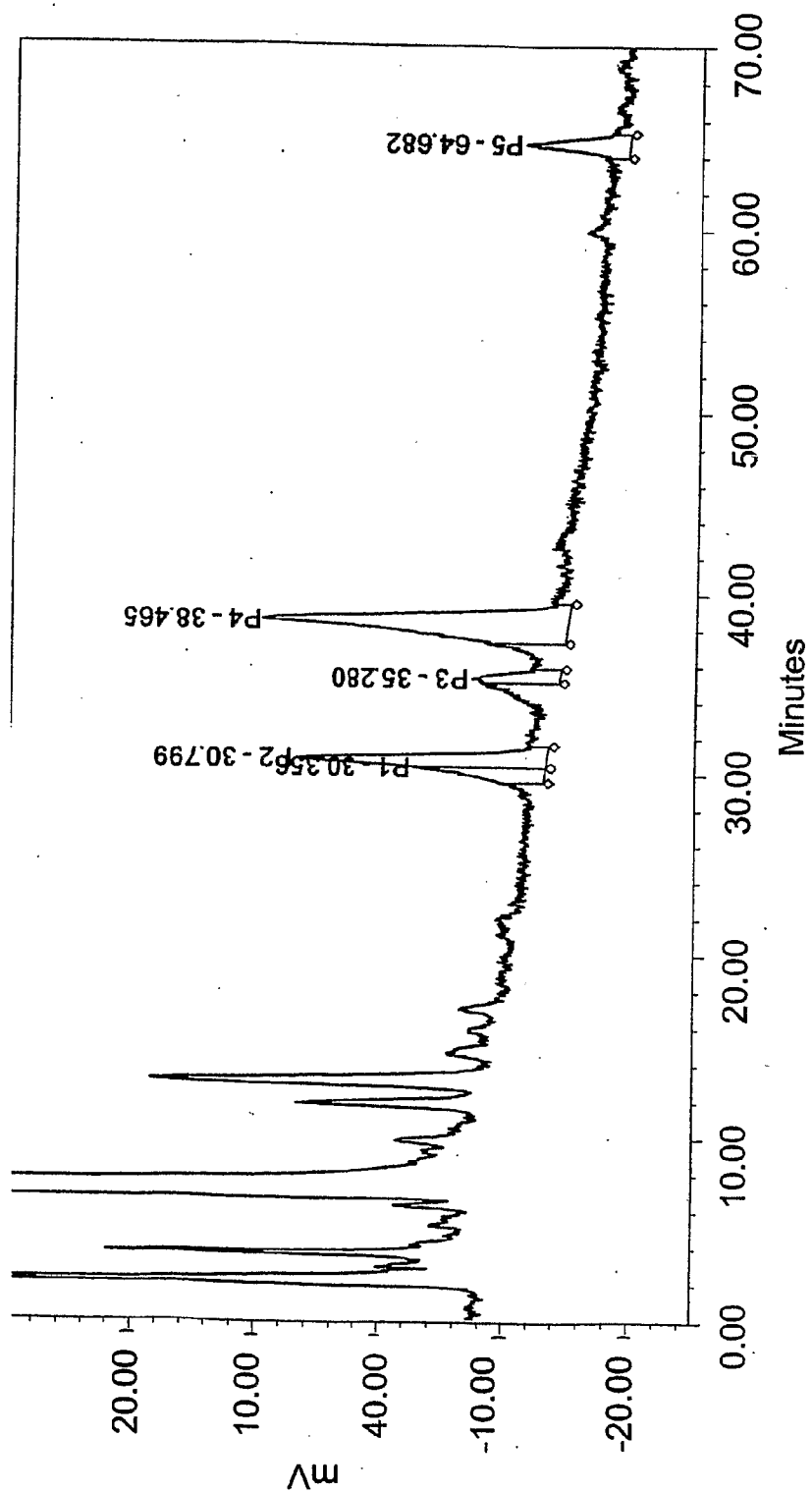


FIG. 112D



397/498

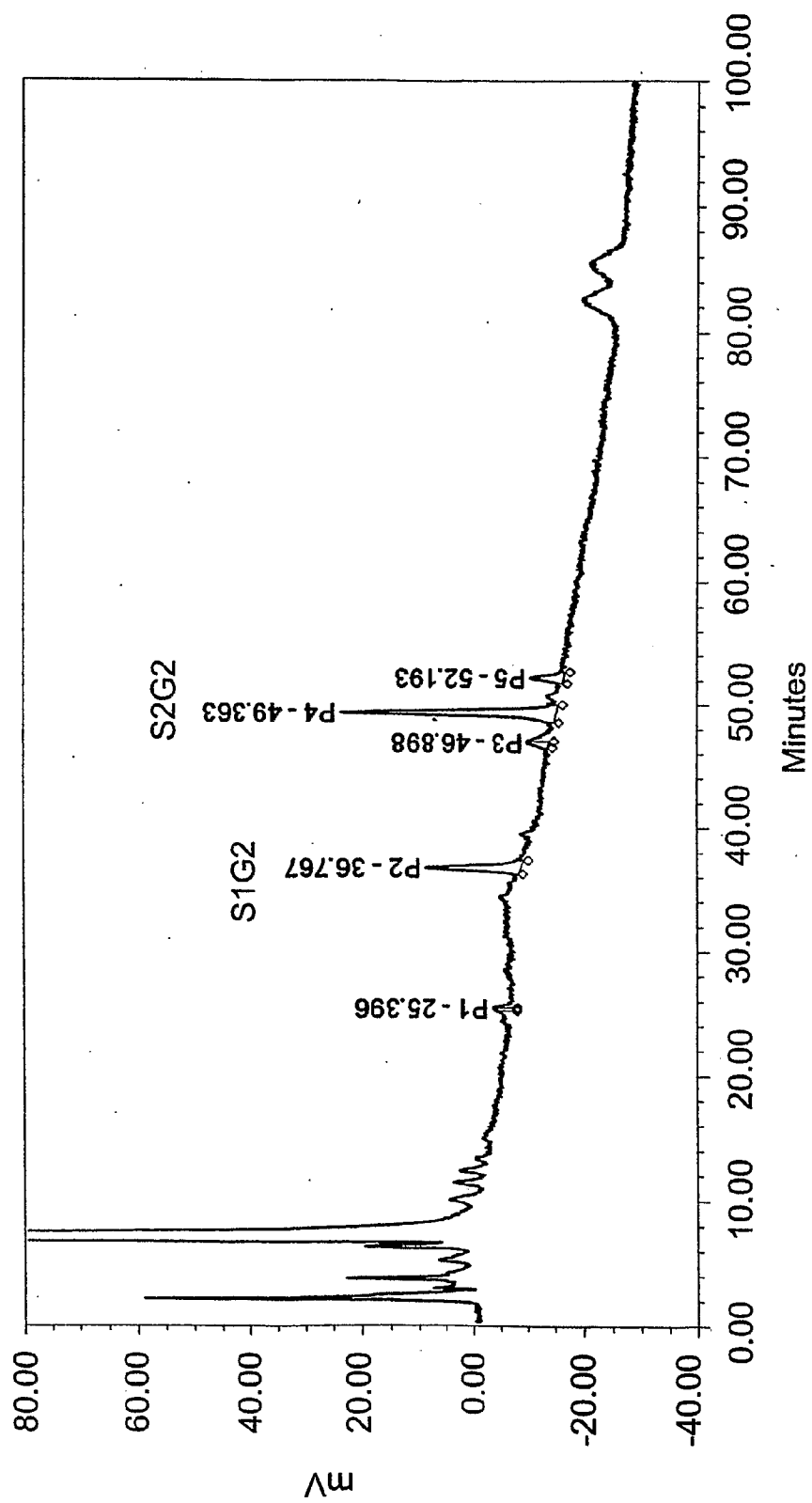


FIG. 113A

398/498

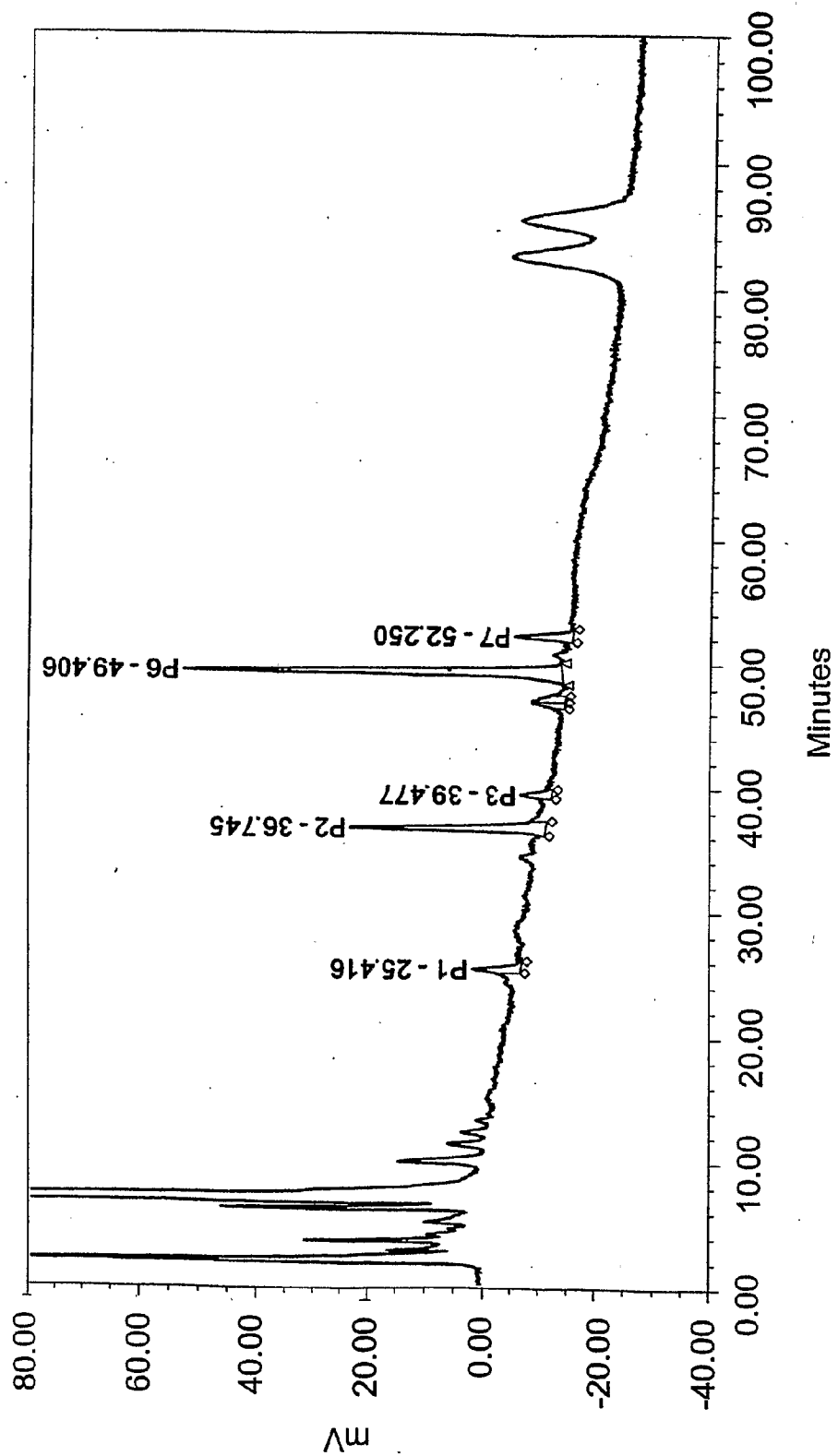
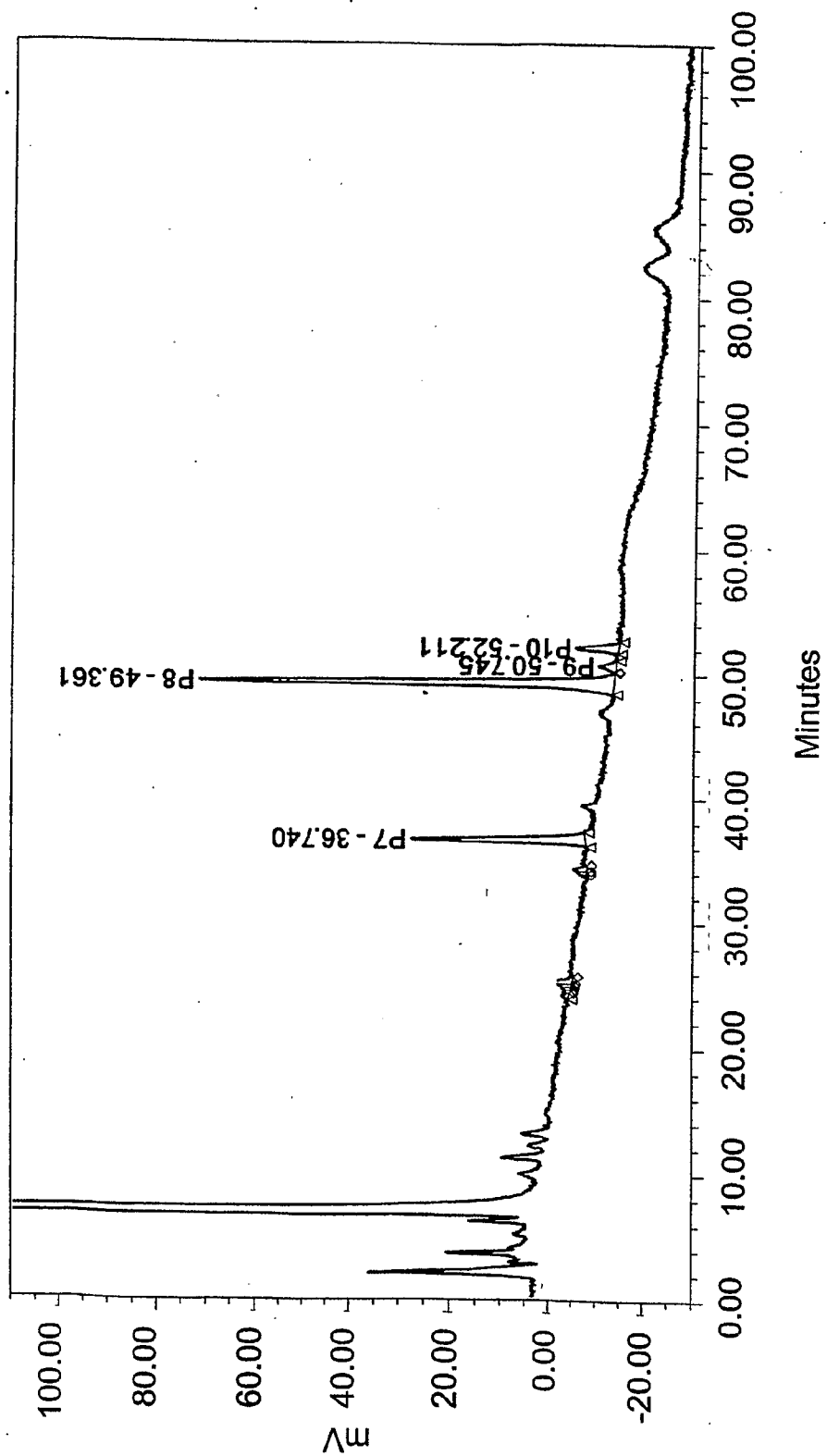


FIG. 113B

399/498



Minutes

FIG. 113C

400/498

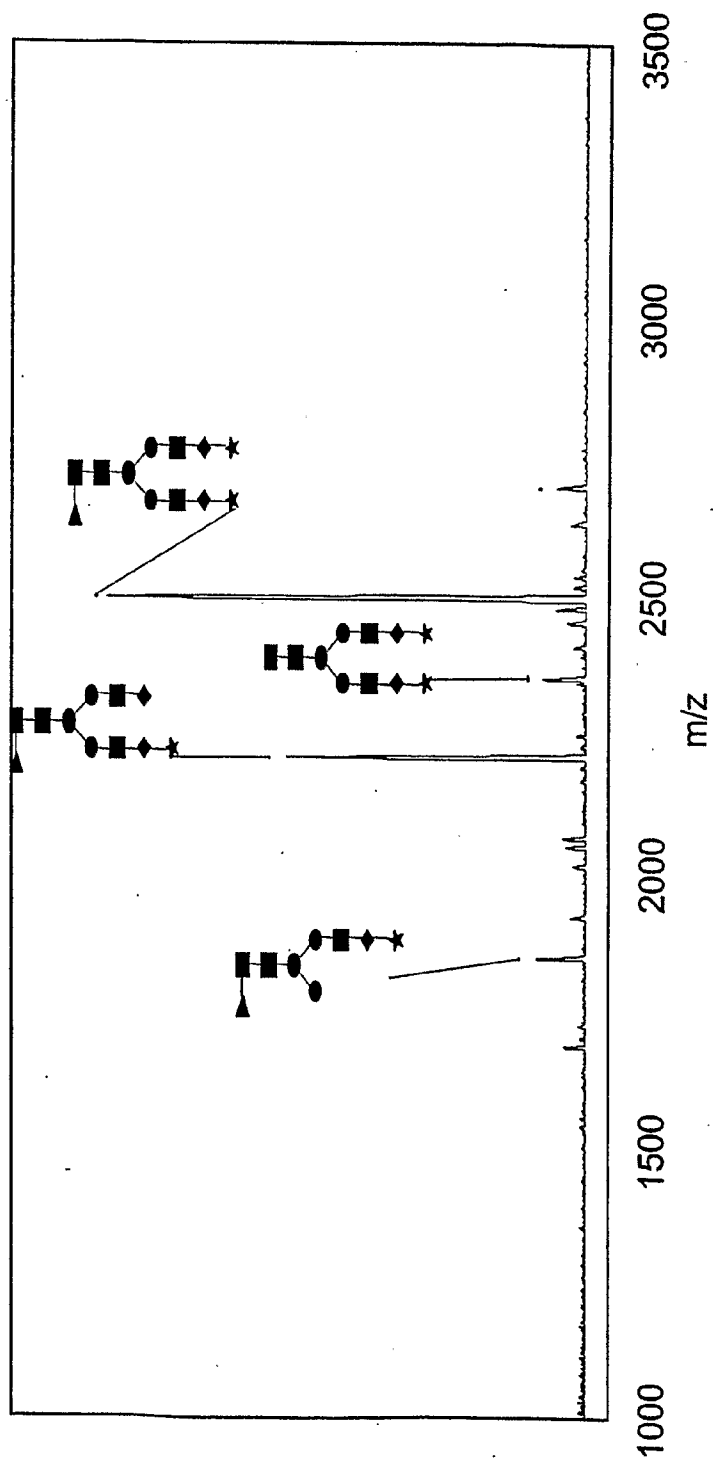


FIG. 114A

401/498

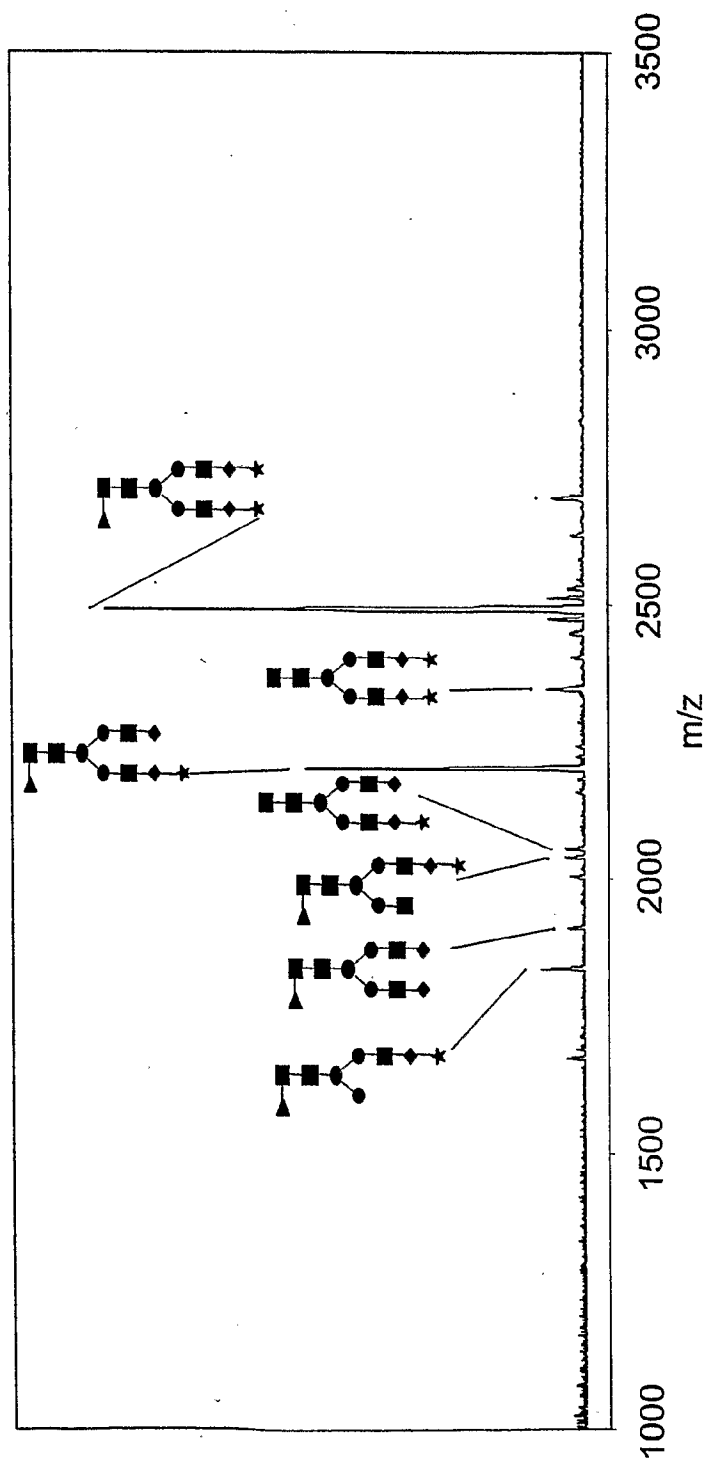


FIG. 114B

402/498

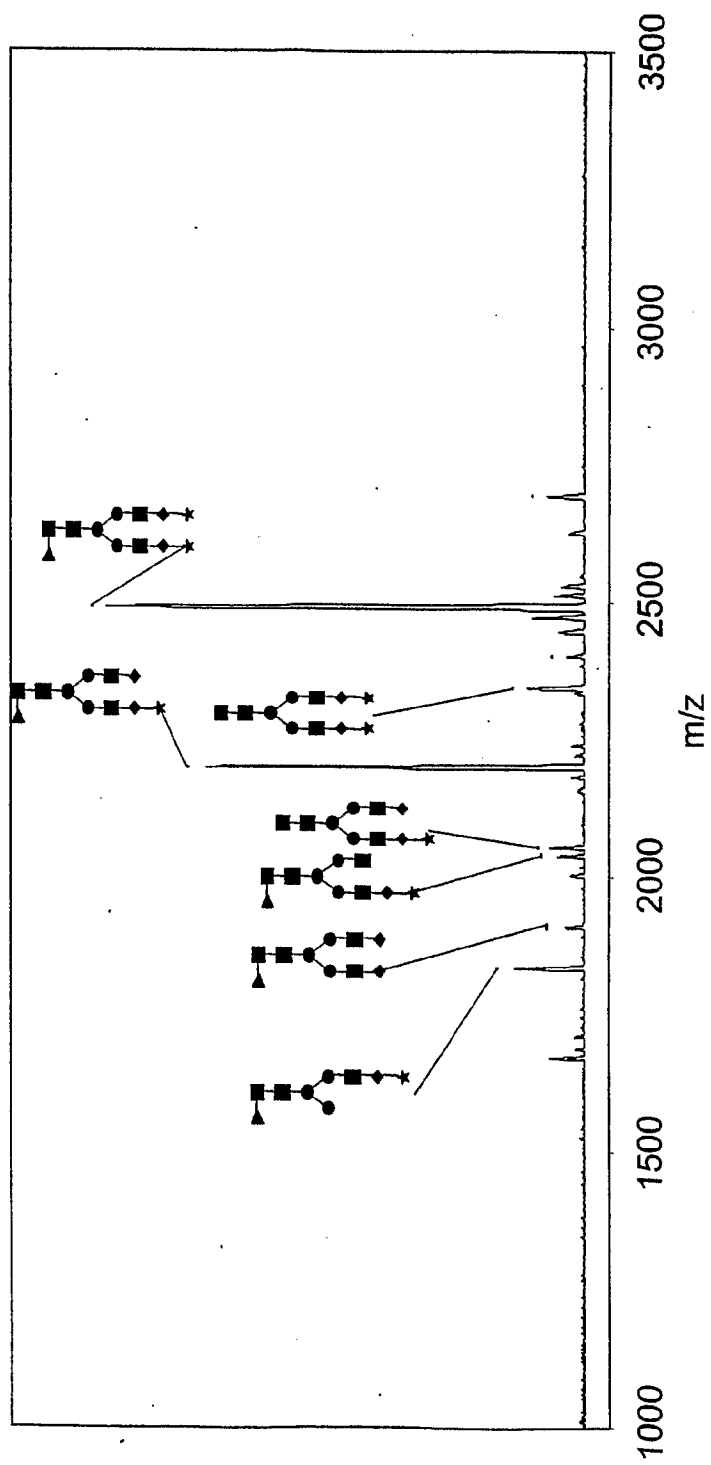


FIG. 114C

403/498

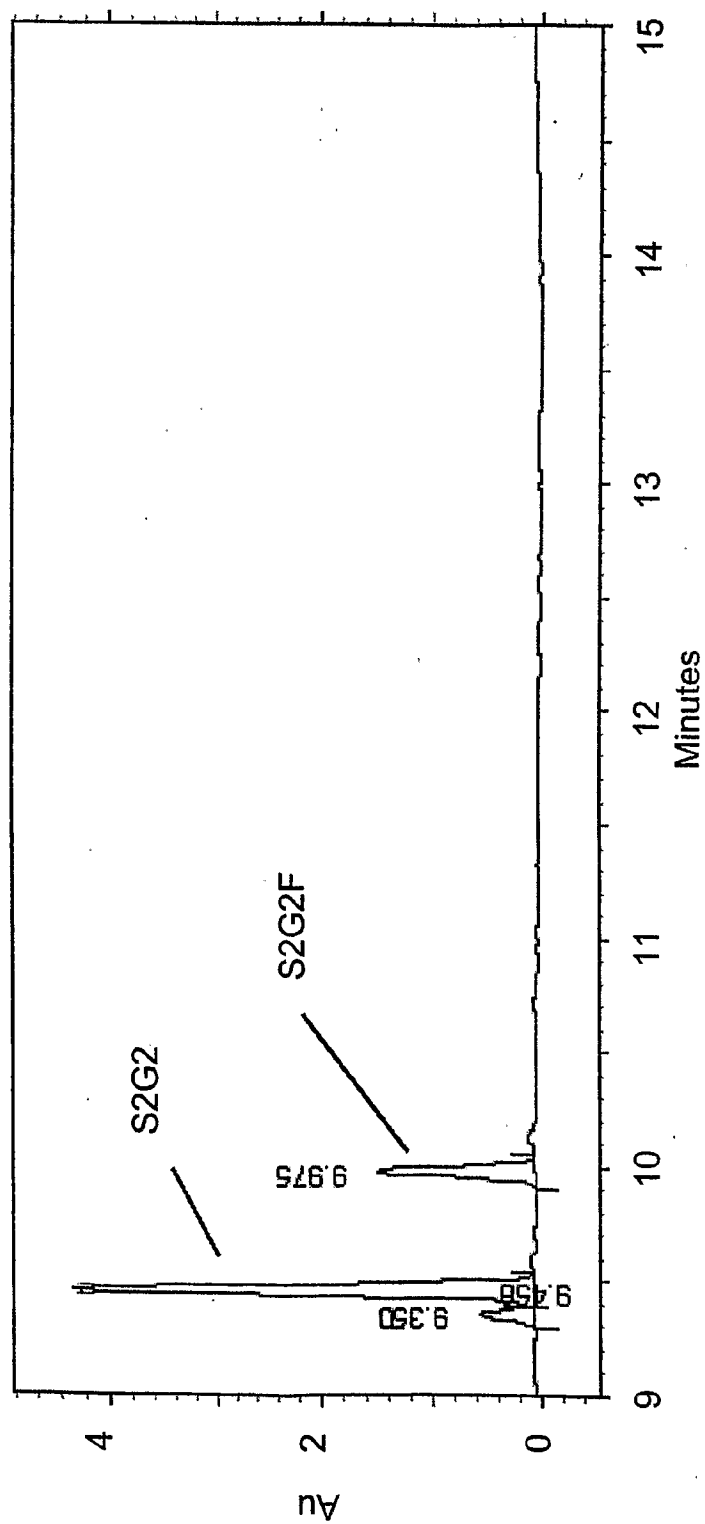


FIG. 115A

404/498

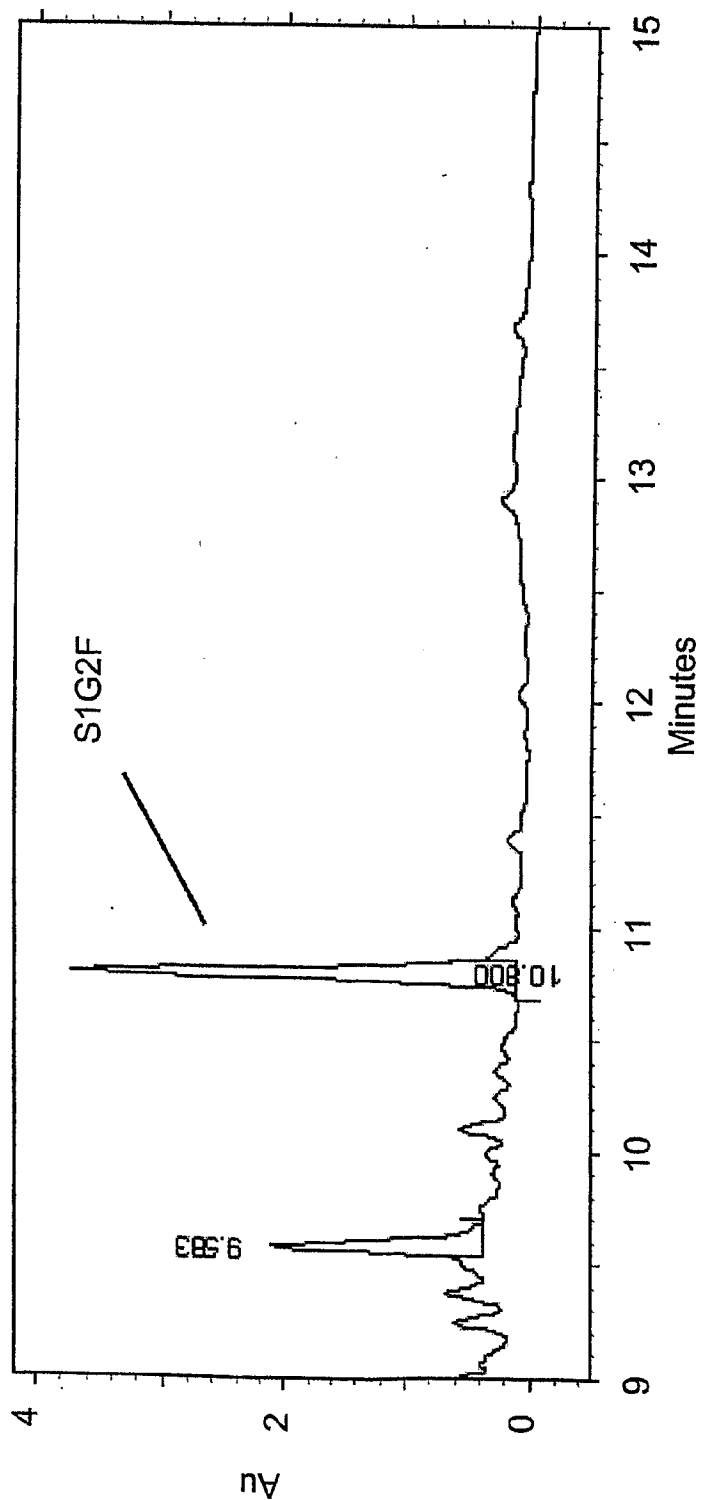


FIG. 115B



405/498

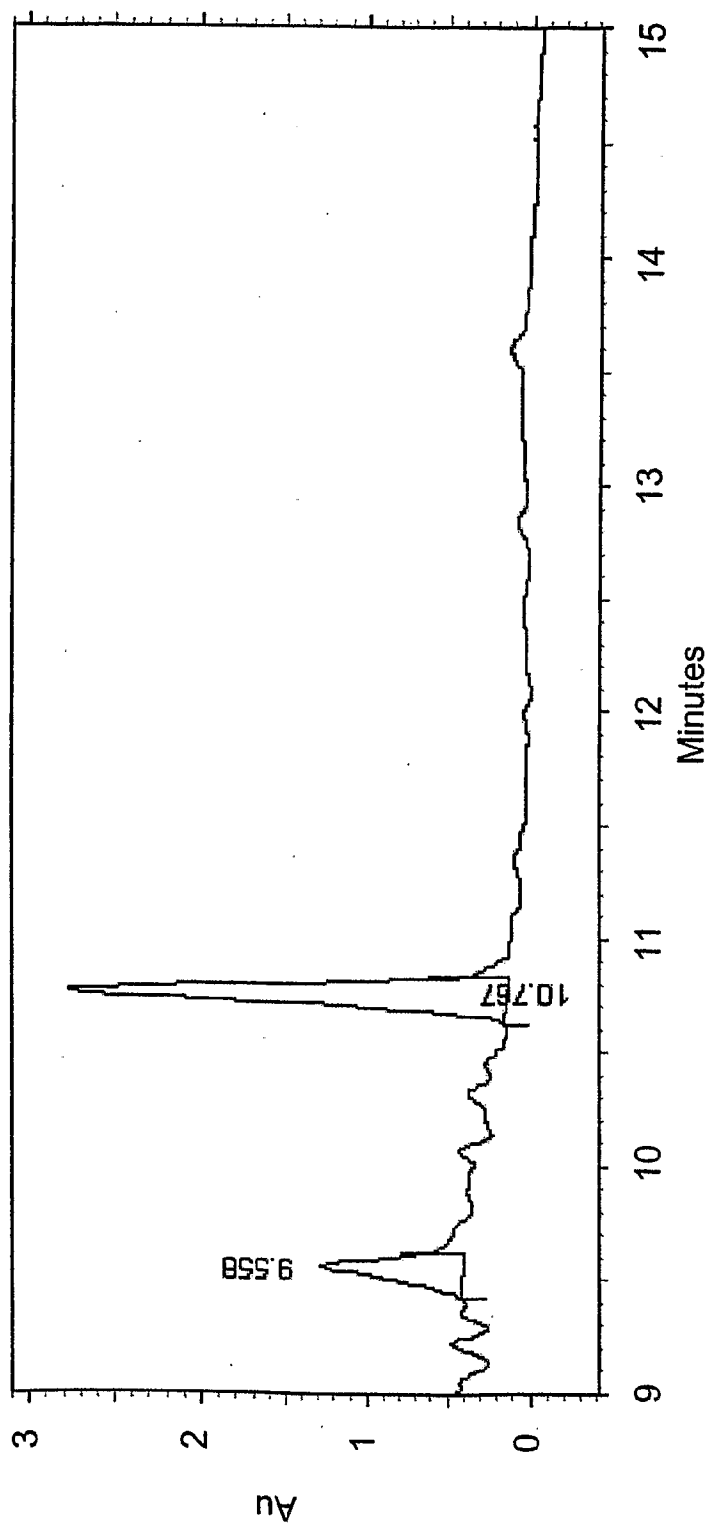


FIG. 115C

406/498

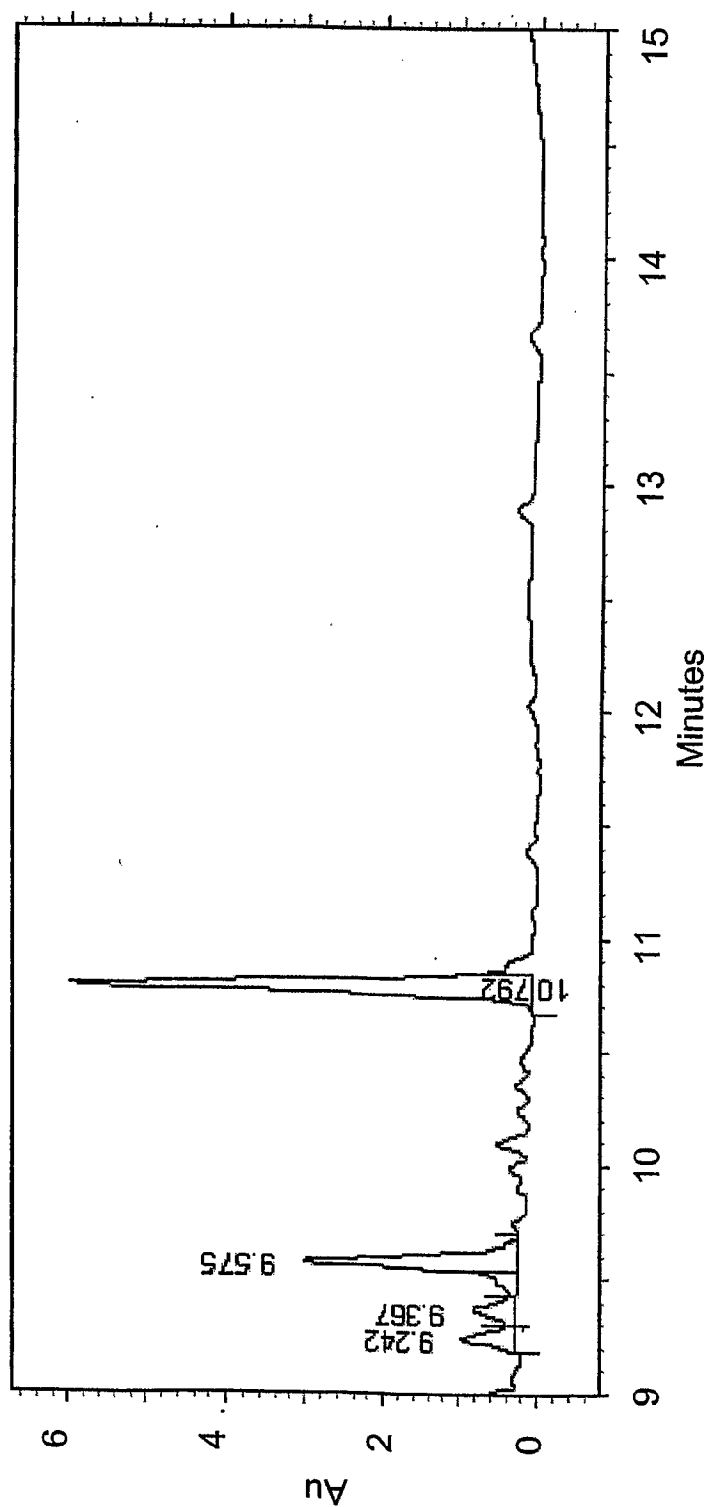


FIG. 115D

407/498

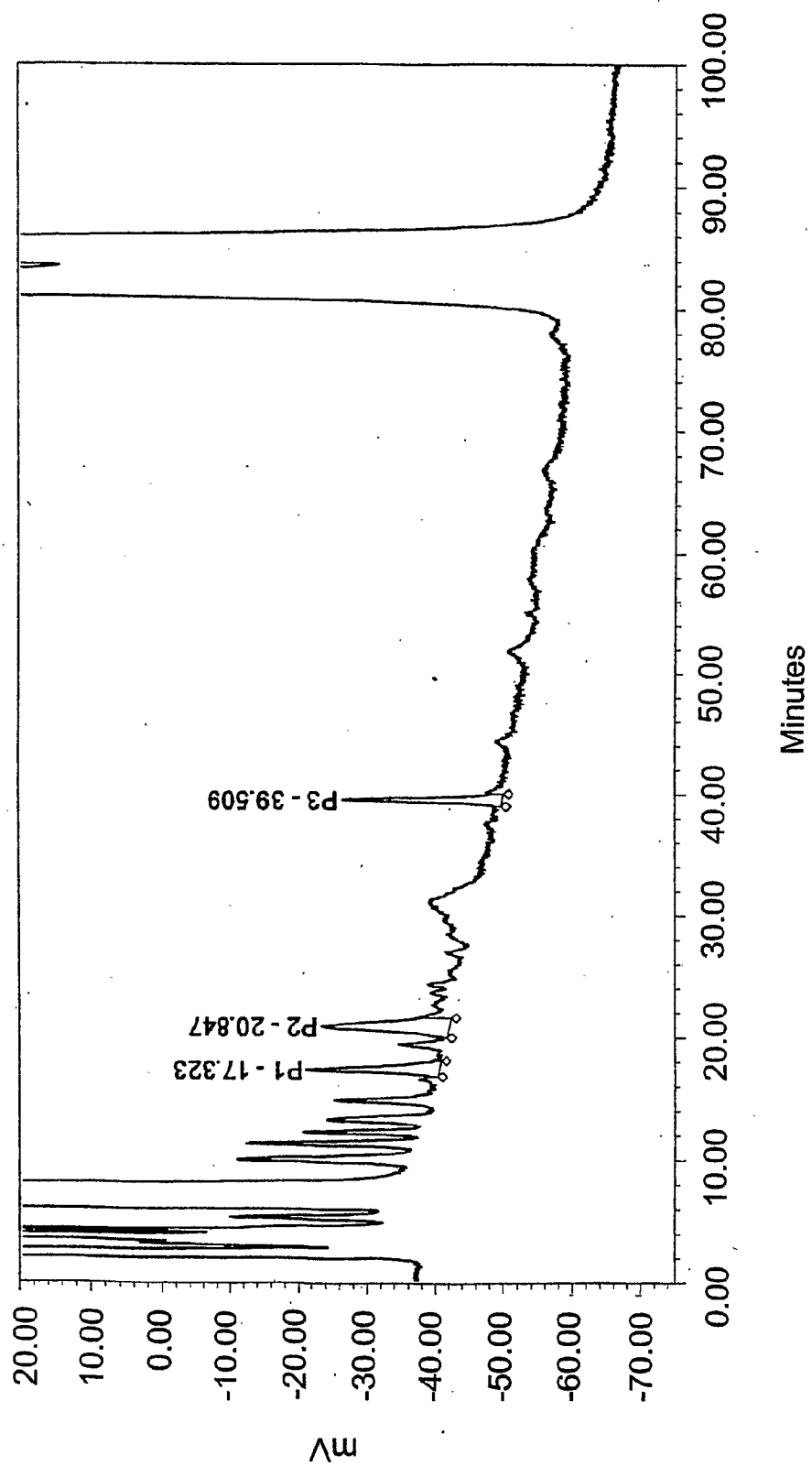


FIG. 116A

408/498

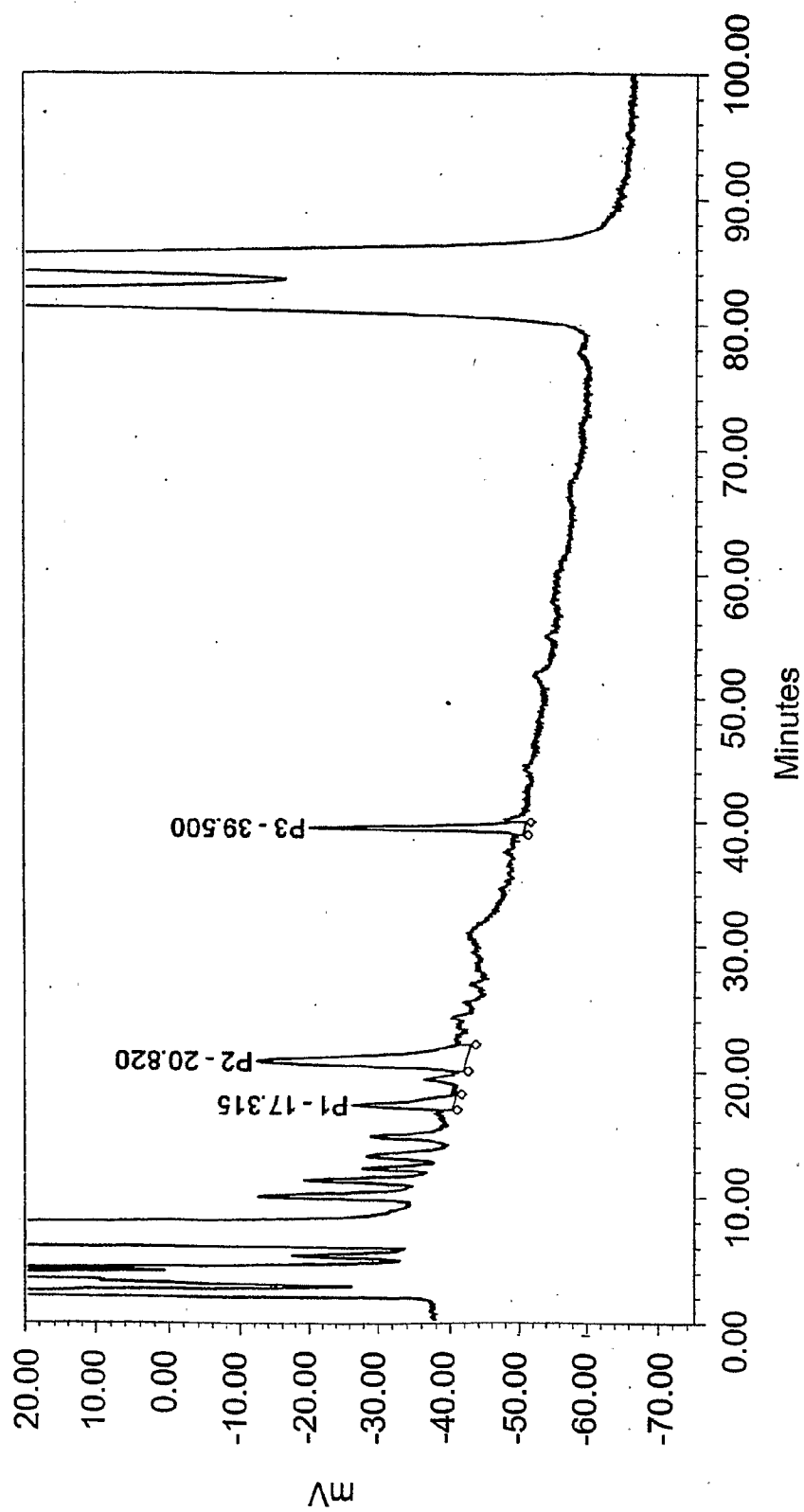


FIG. 116B

409/498

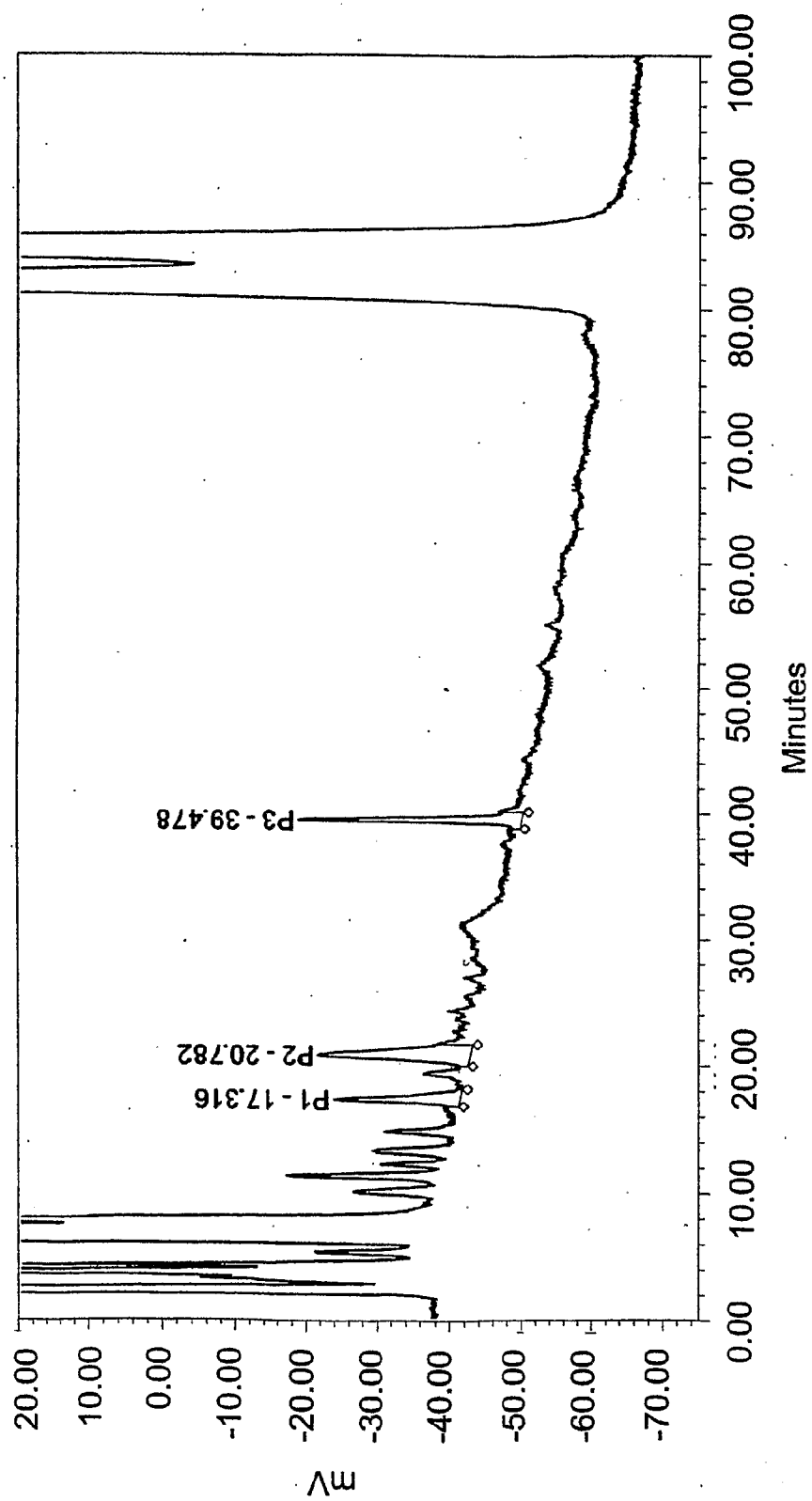


FIG. 116C

410/498

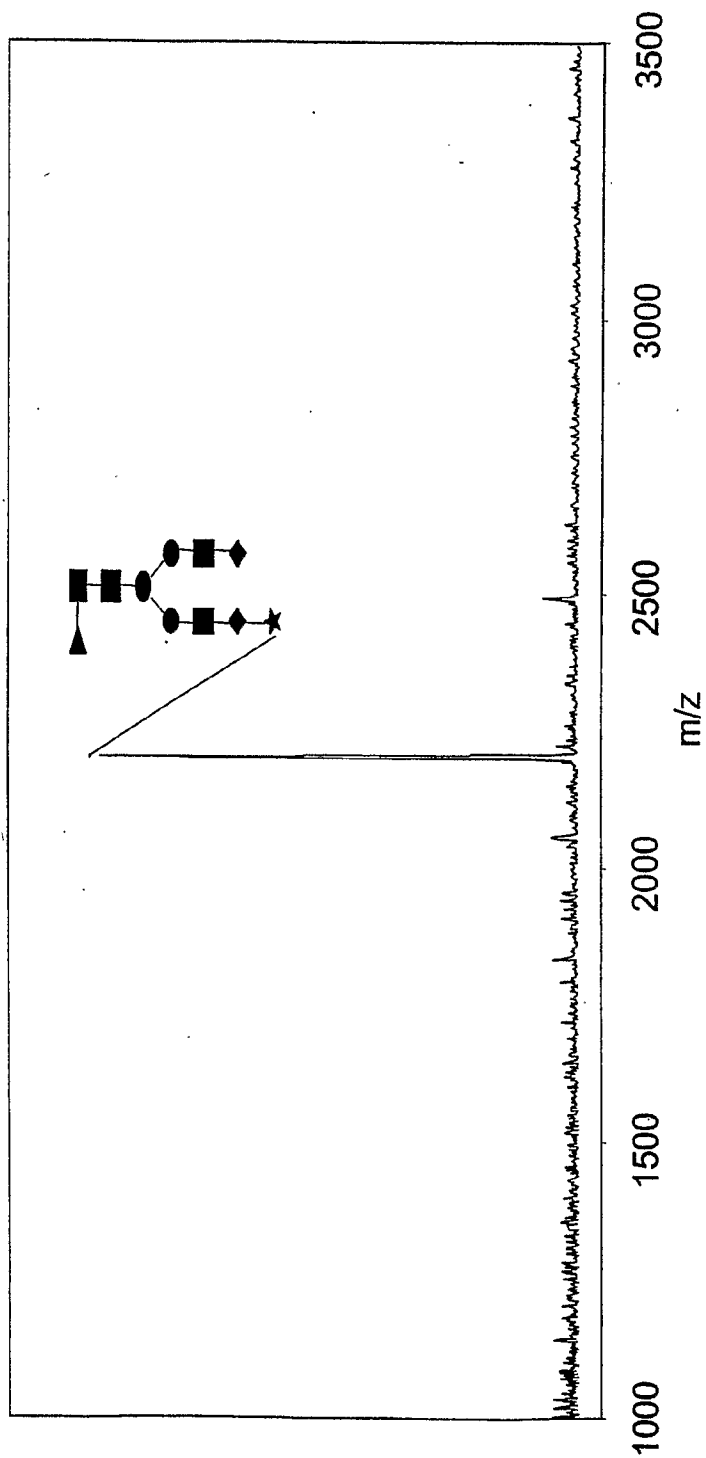


FIG. 117A

411/498

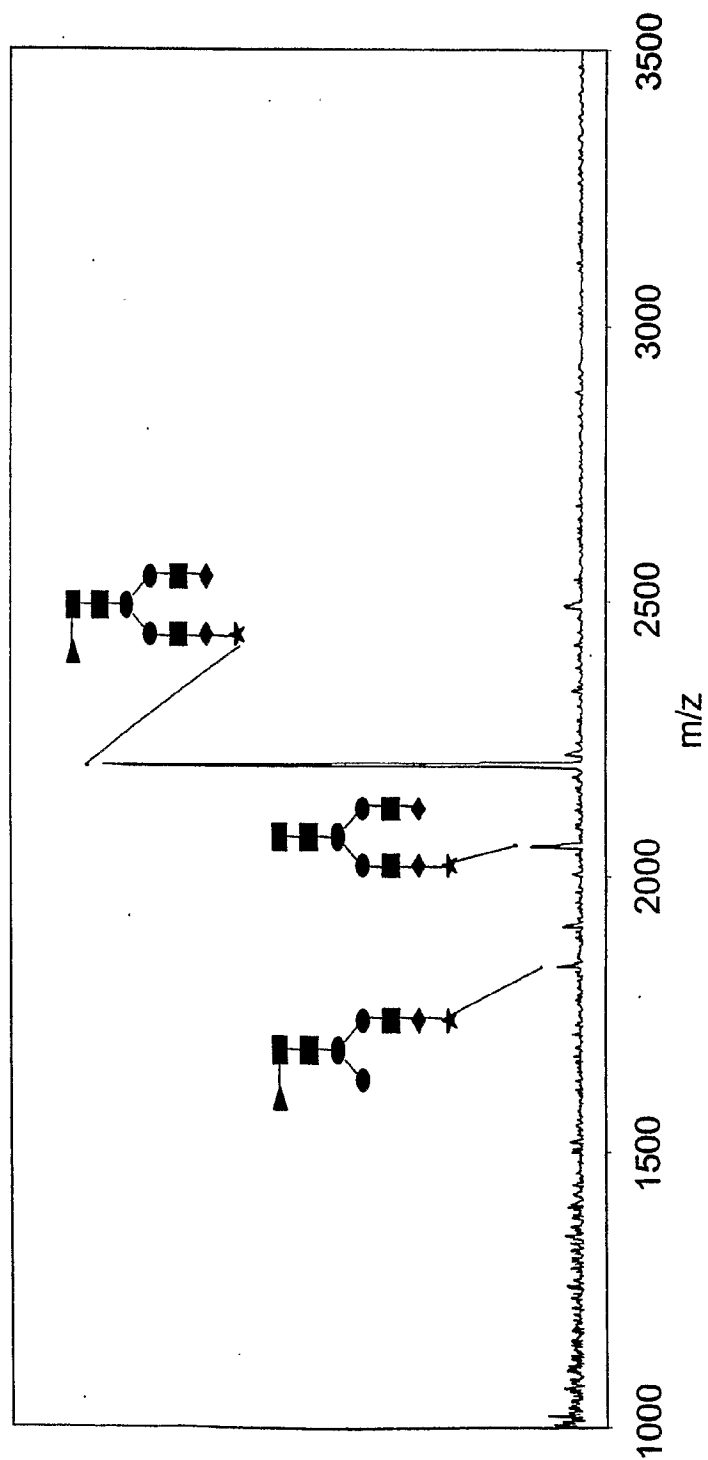


FIG. 117B

412/498

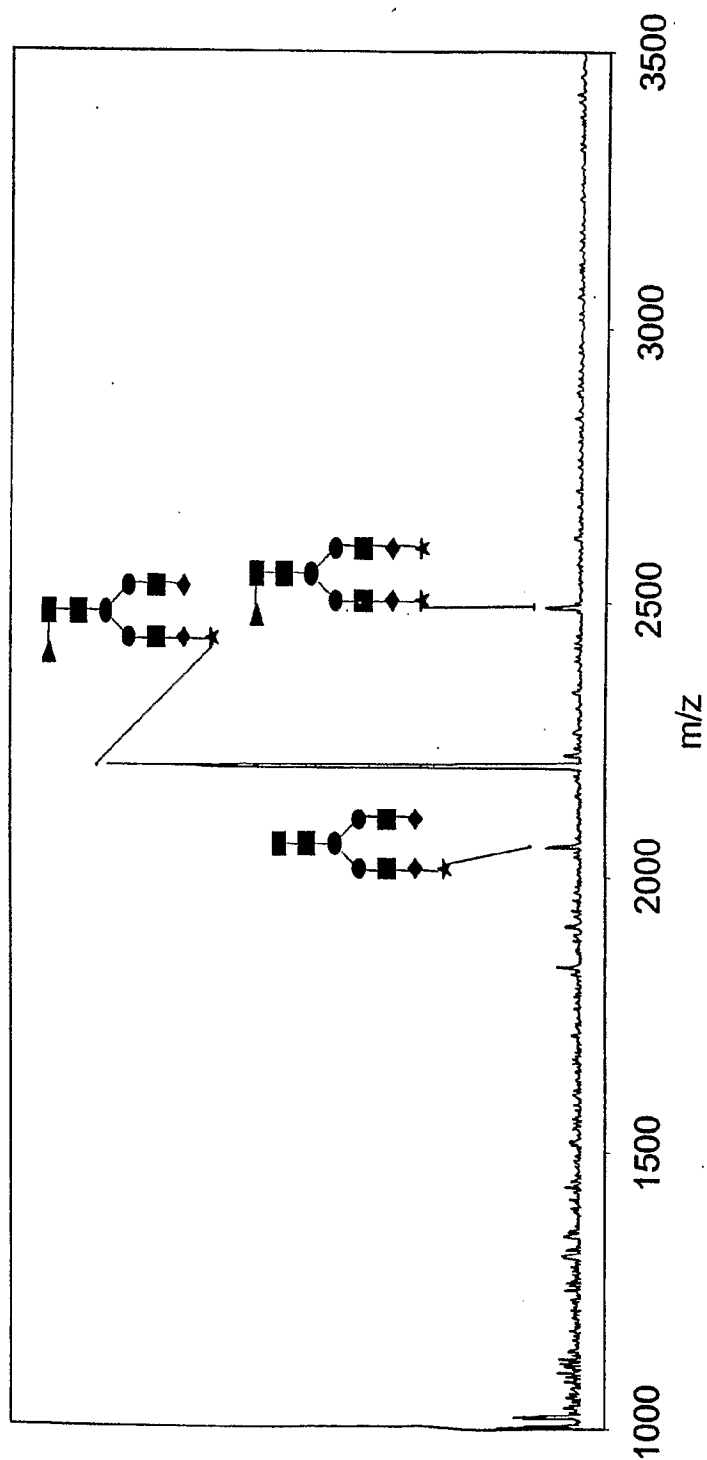


FIG. 117C



413/498

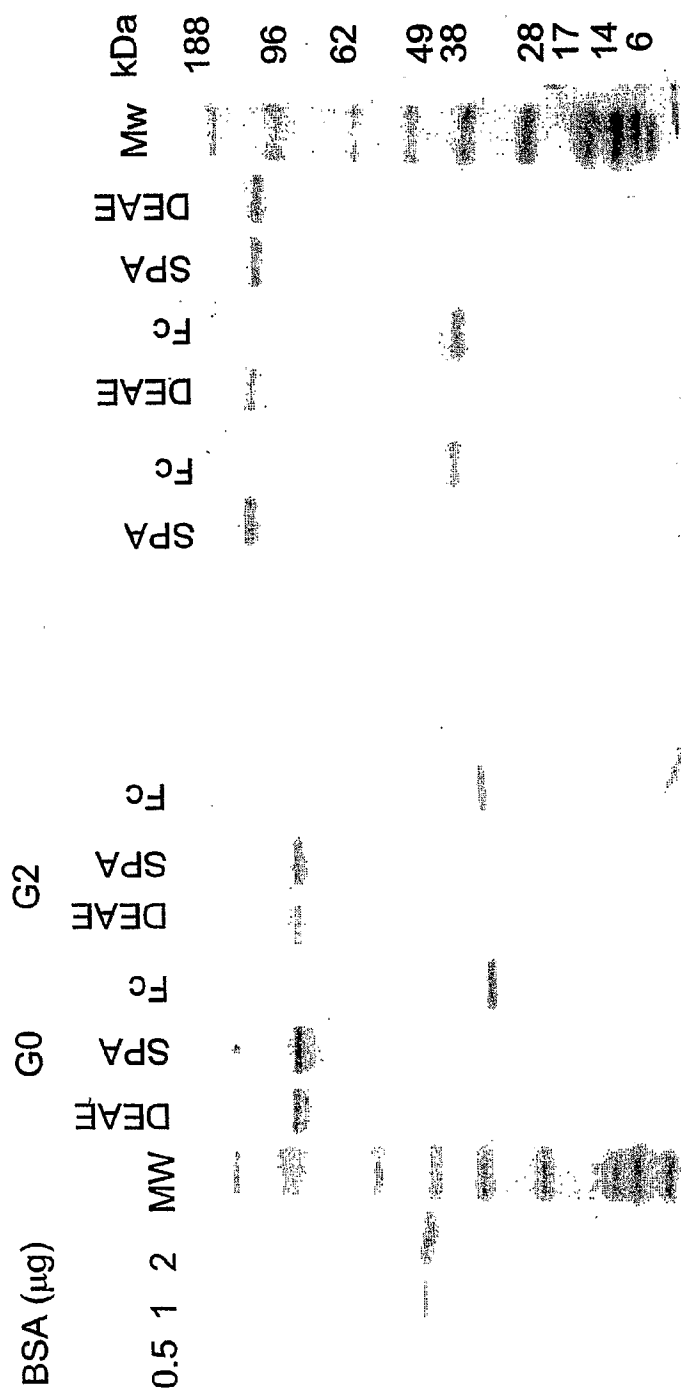


FIG. 118B

FIG. 118A

414/498

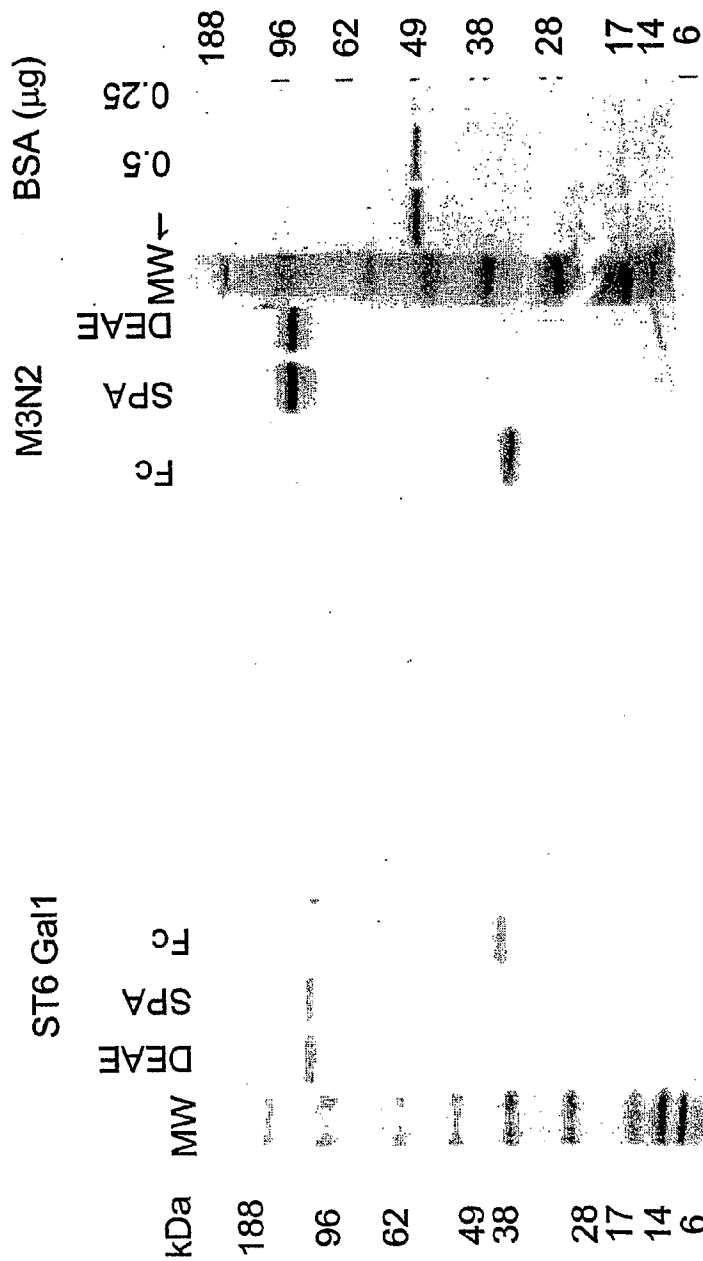


FIG. 118D

FIG. 118C

415/498

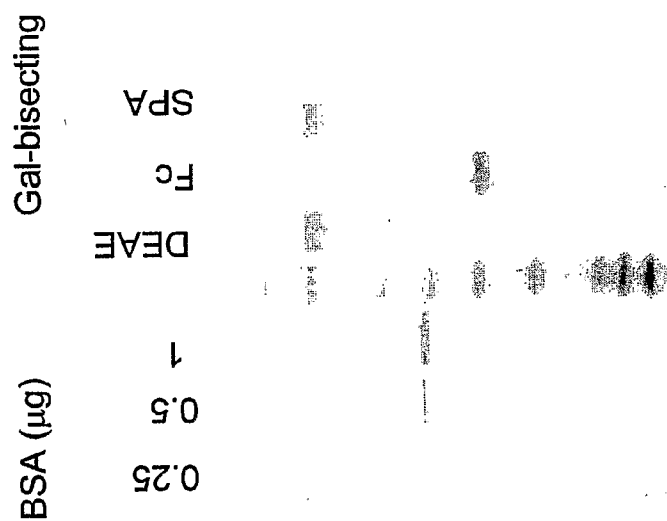


FIG. 118E

416/498

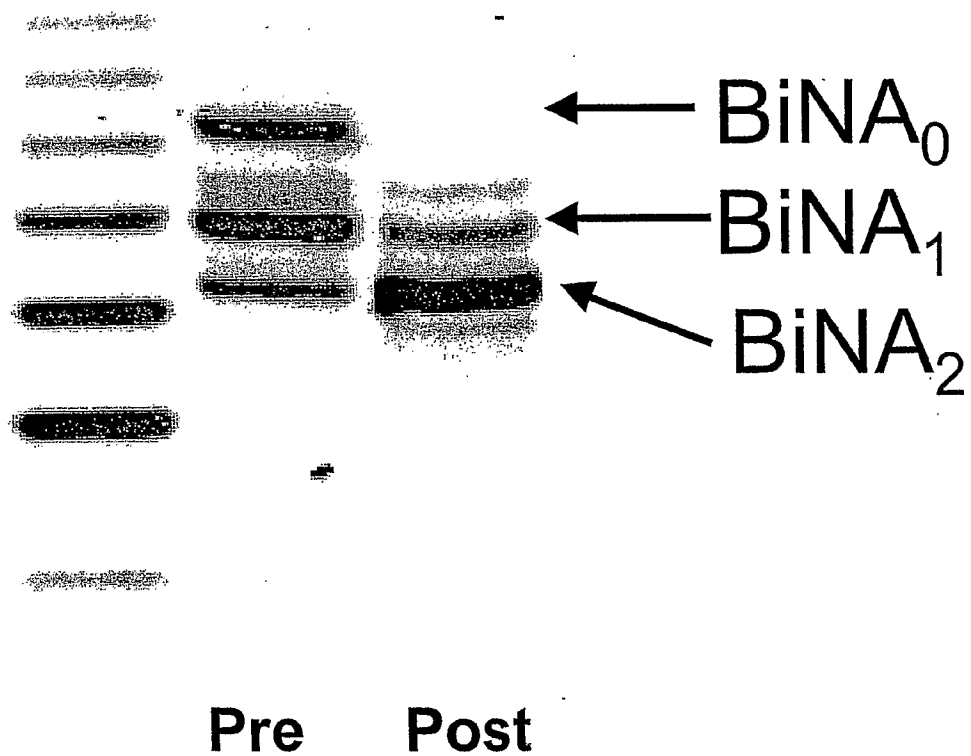


FIG. 119

417/498

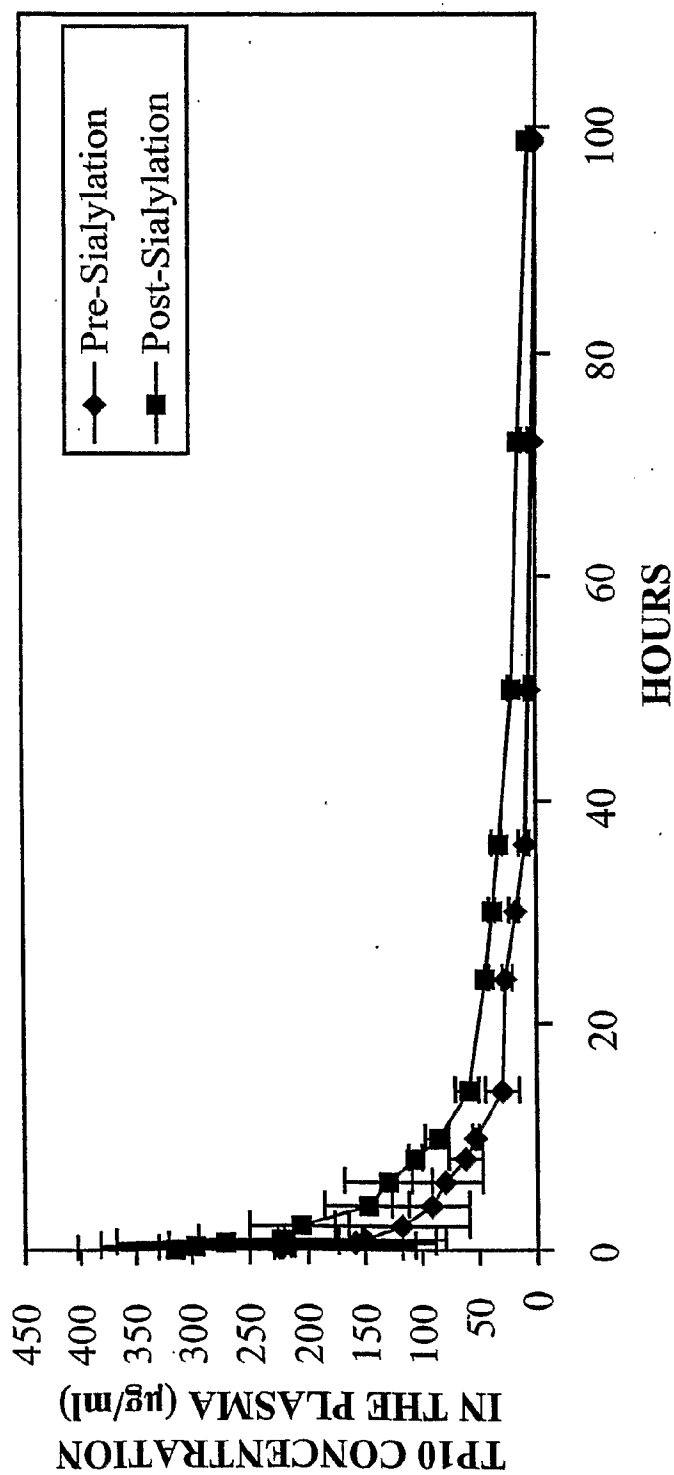


FIG. 120

418/498

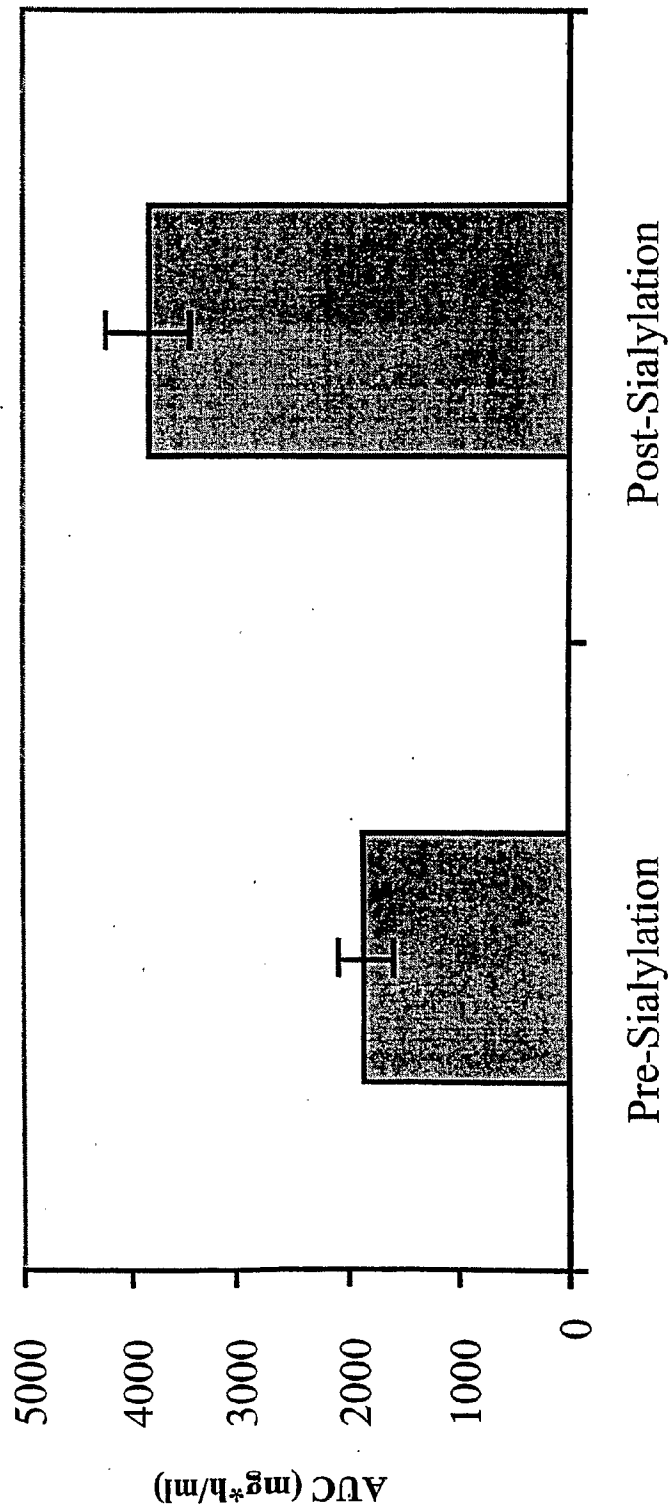


FIG. 121

419/498

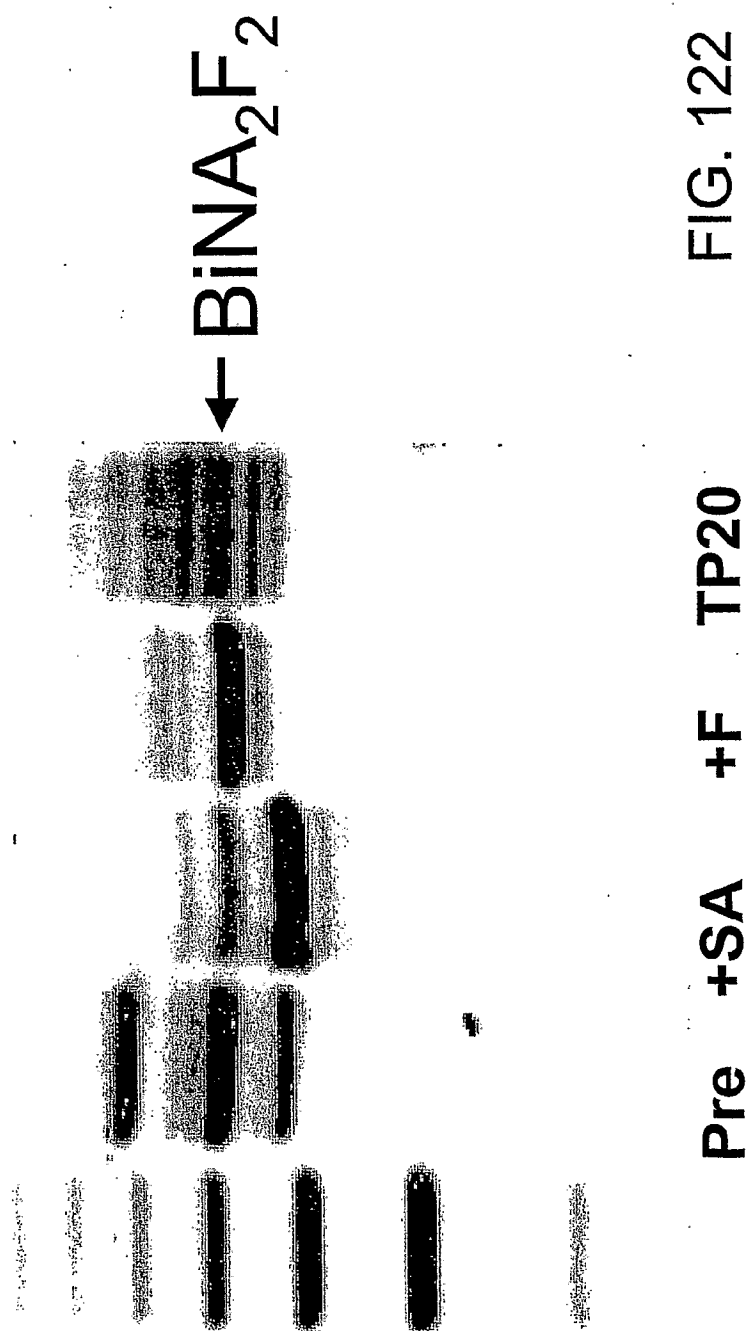


FIG. 122

420/498

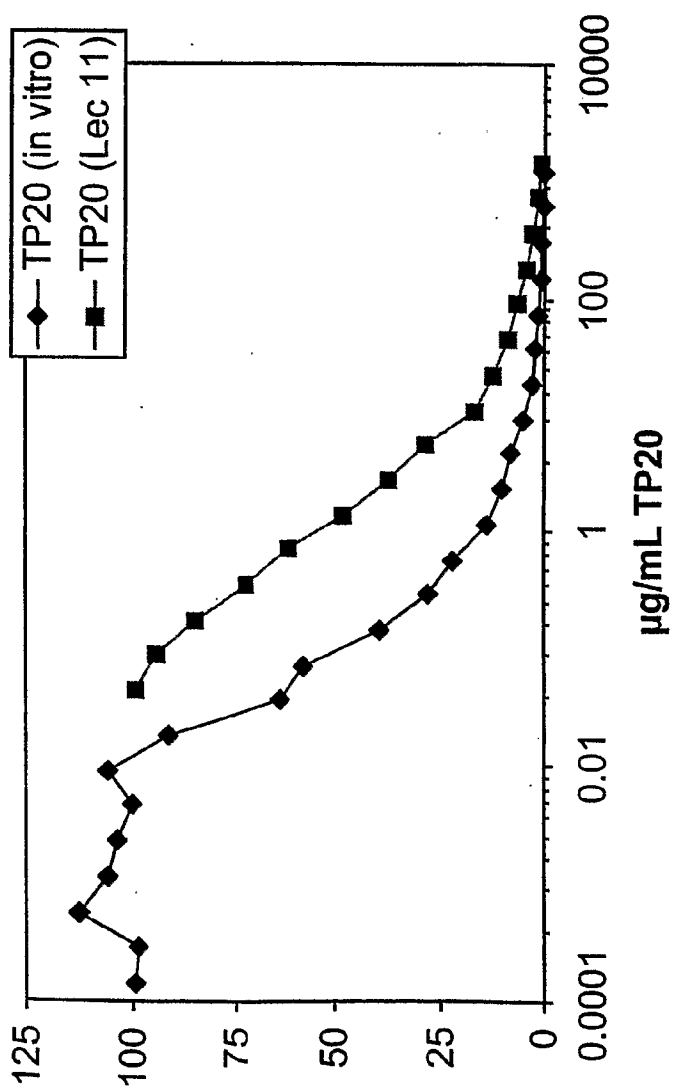


FIG. 123



421/498

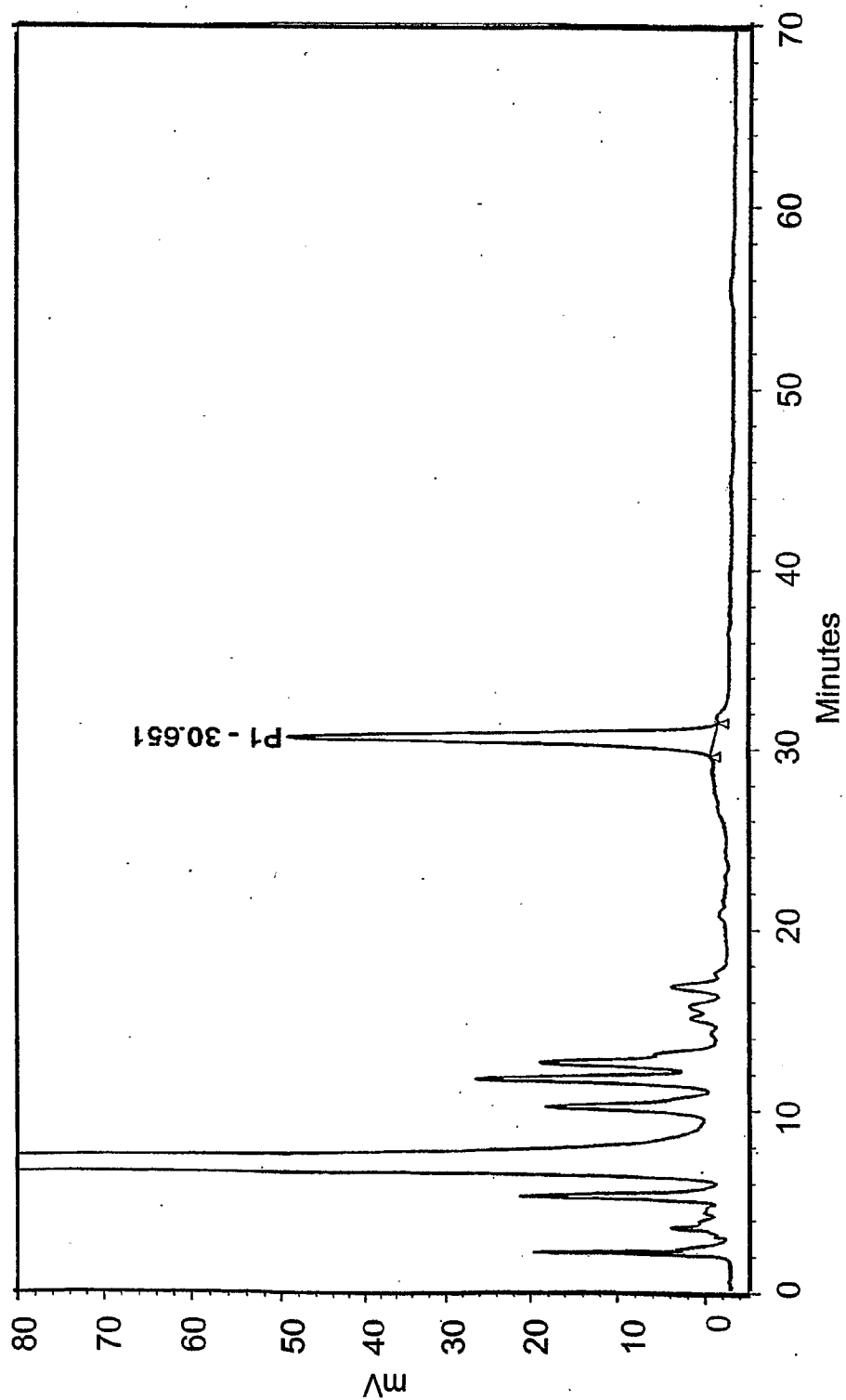


FIG. 124

422/498

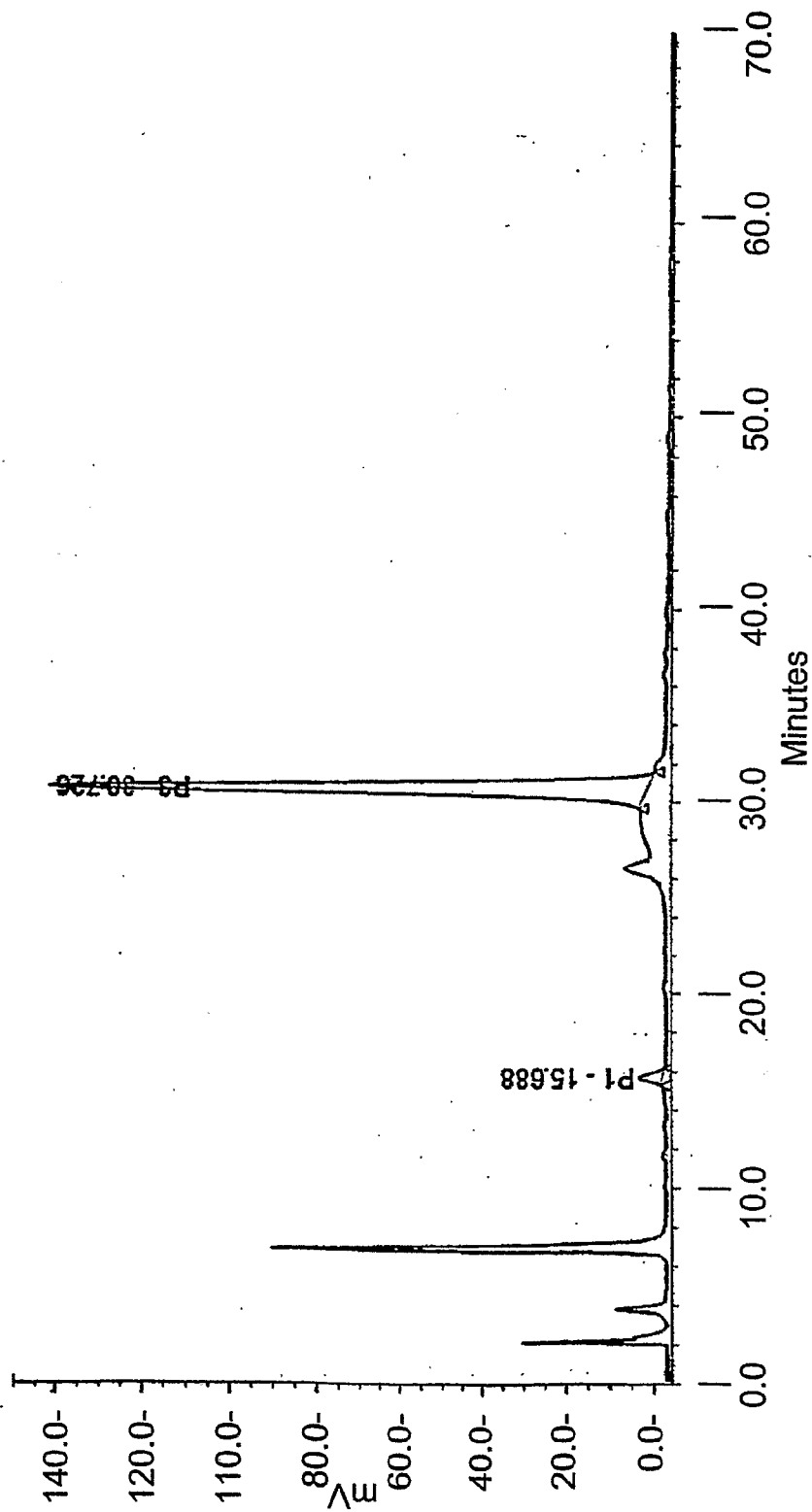


FIG. 125A

423/498

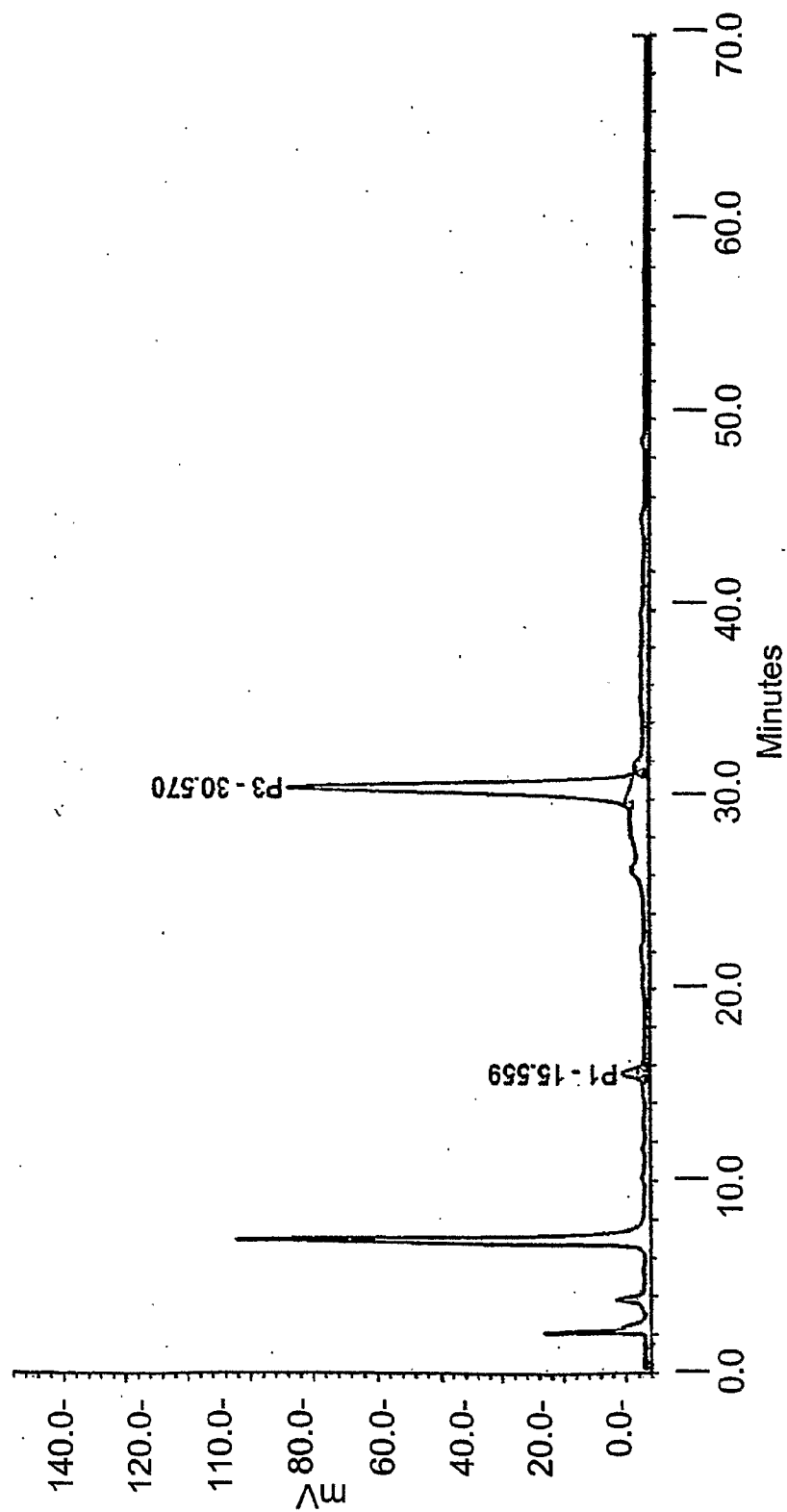


FIG. 125B

424/498

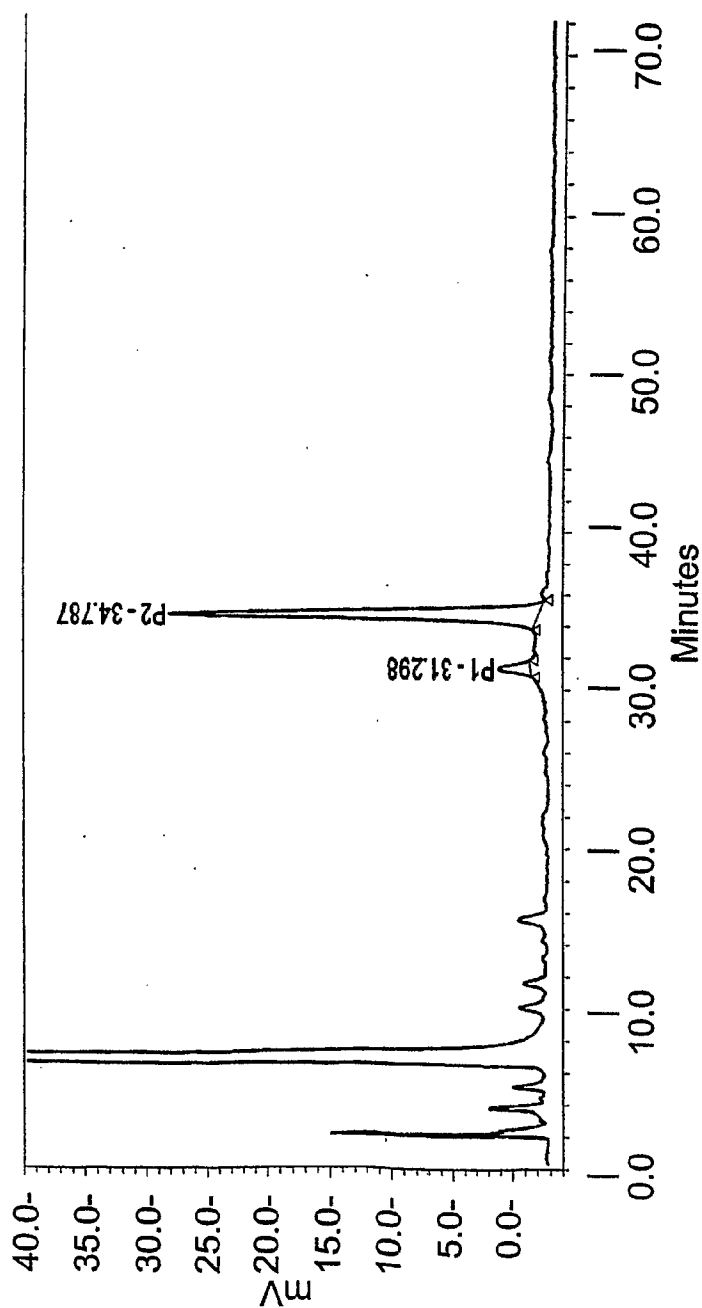


FIG. 126

425/498

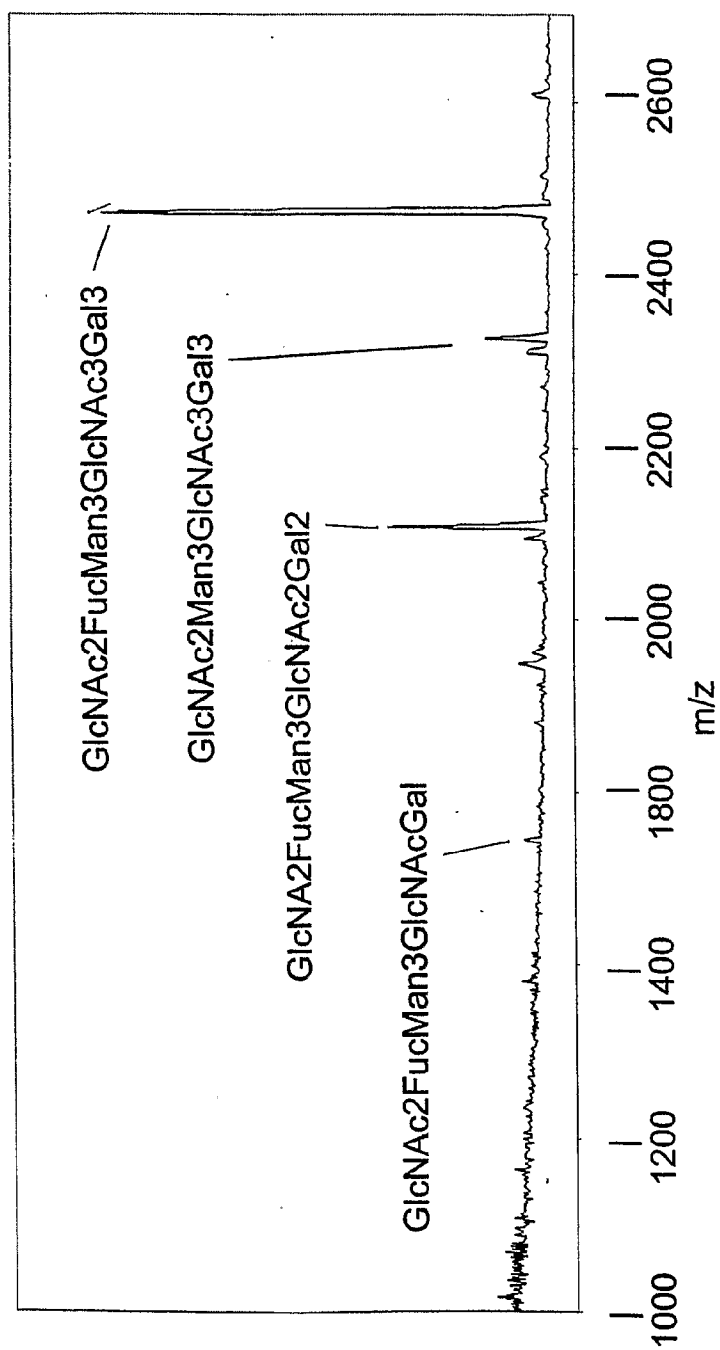


FIG. 127

426/498

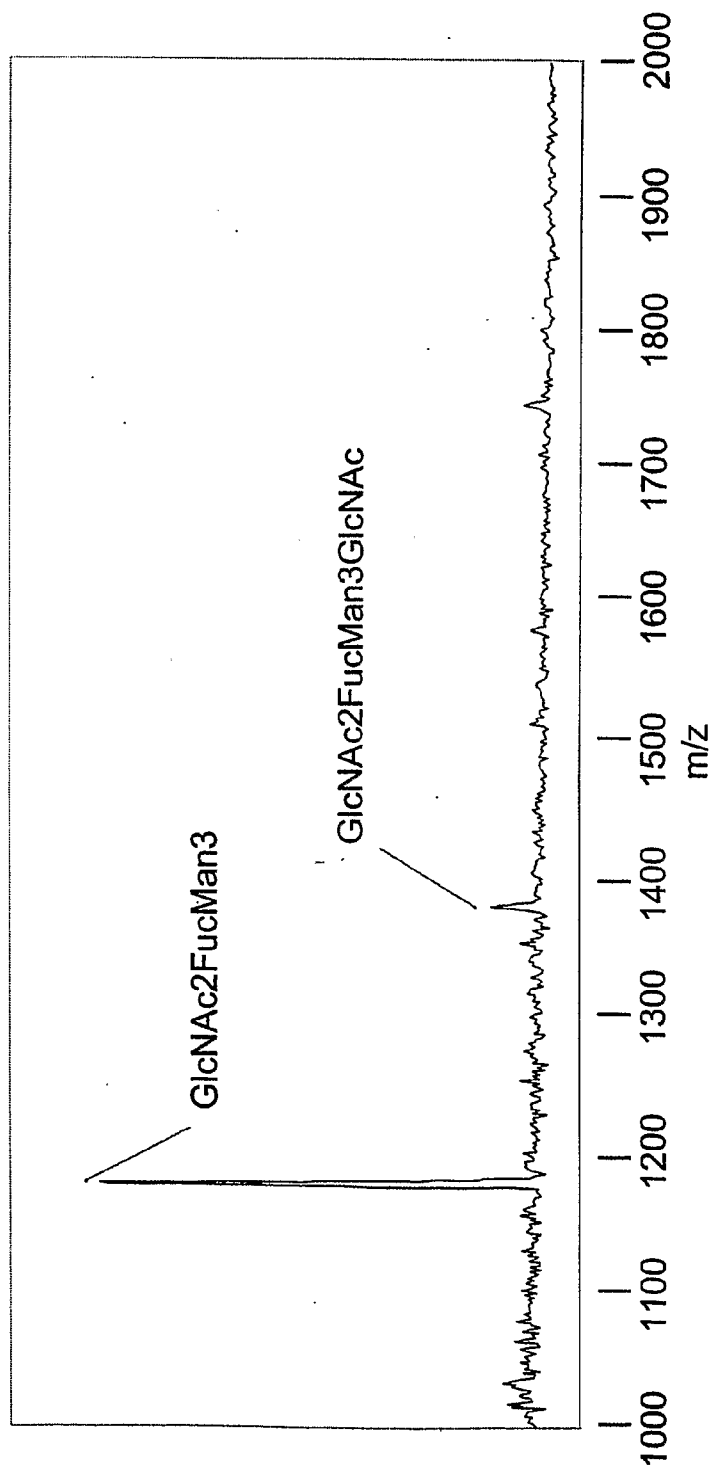


FIG. 128

427/498

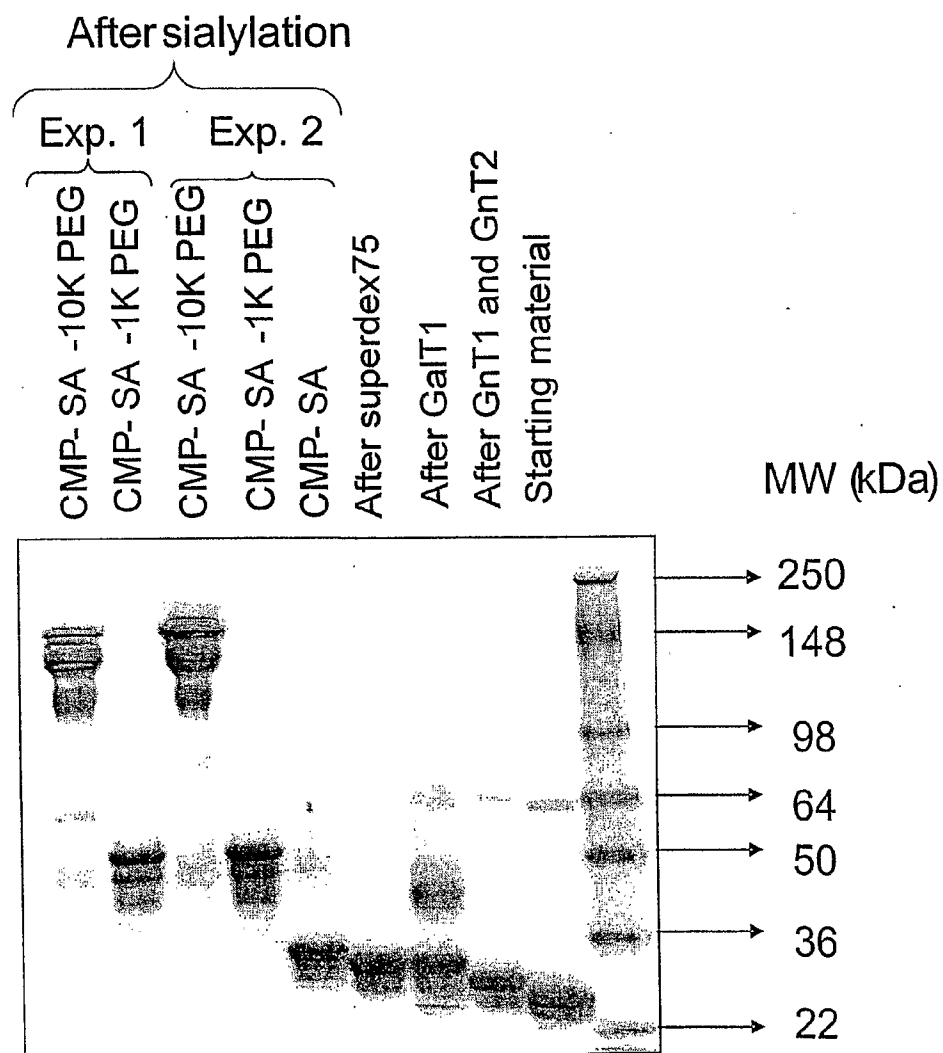


FIG. 129

428/498

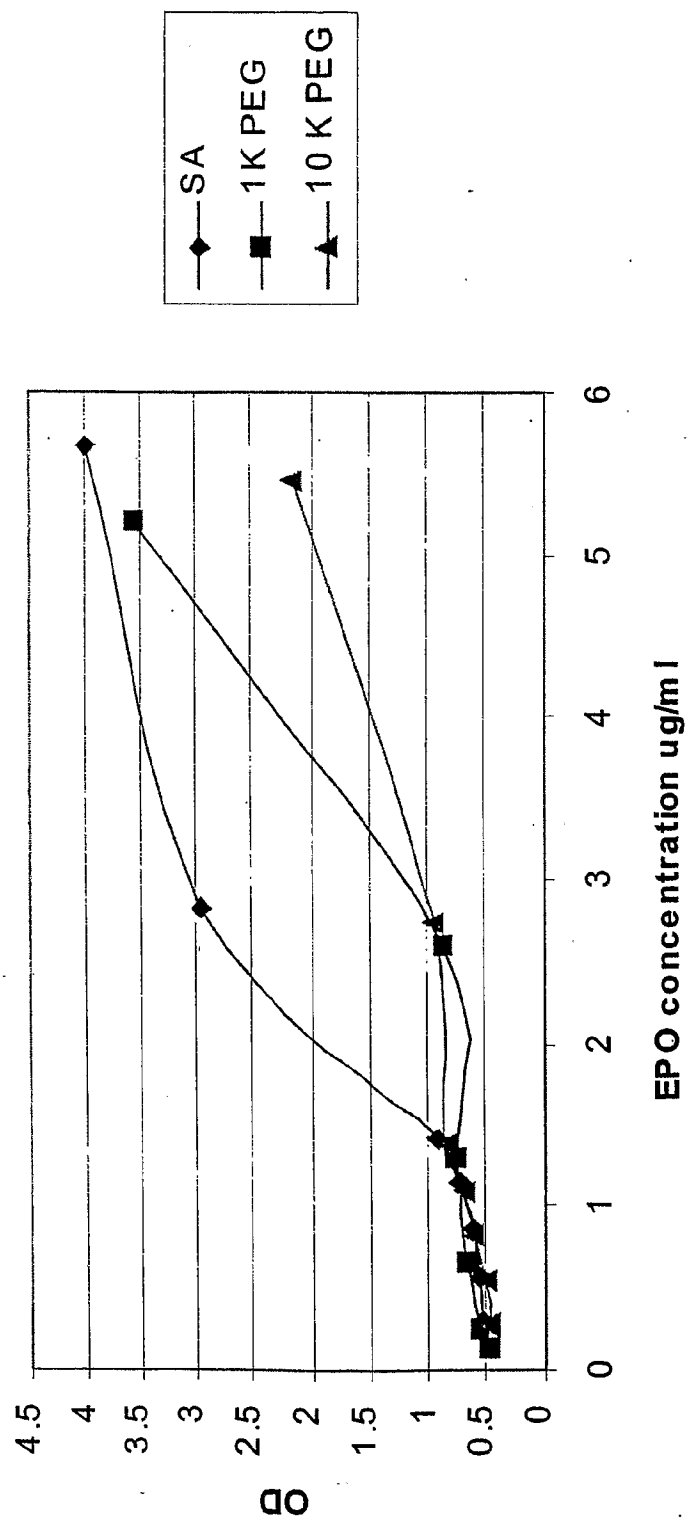
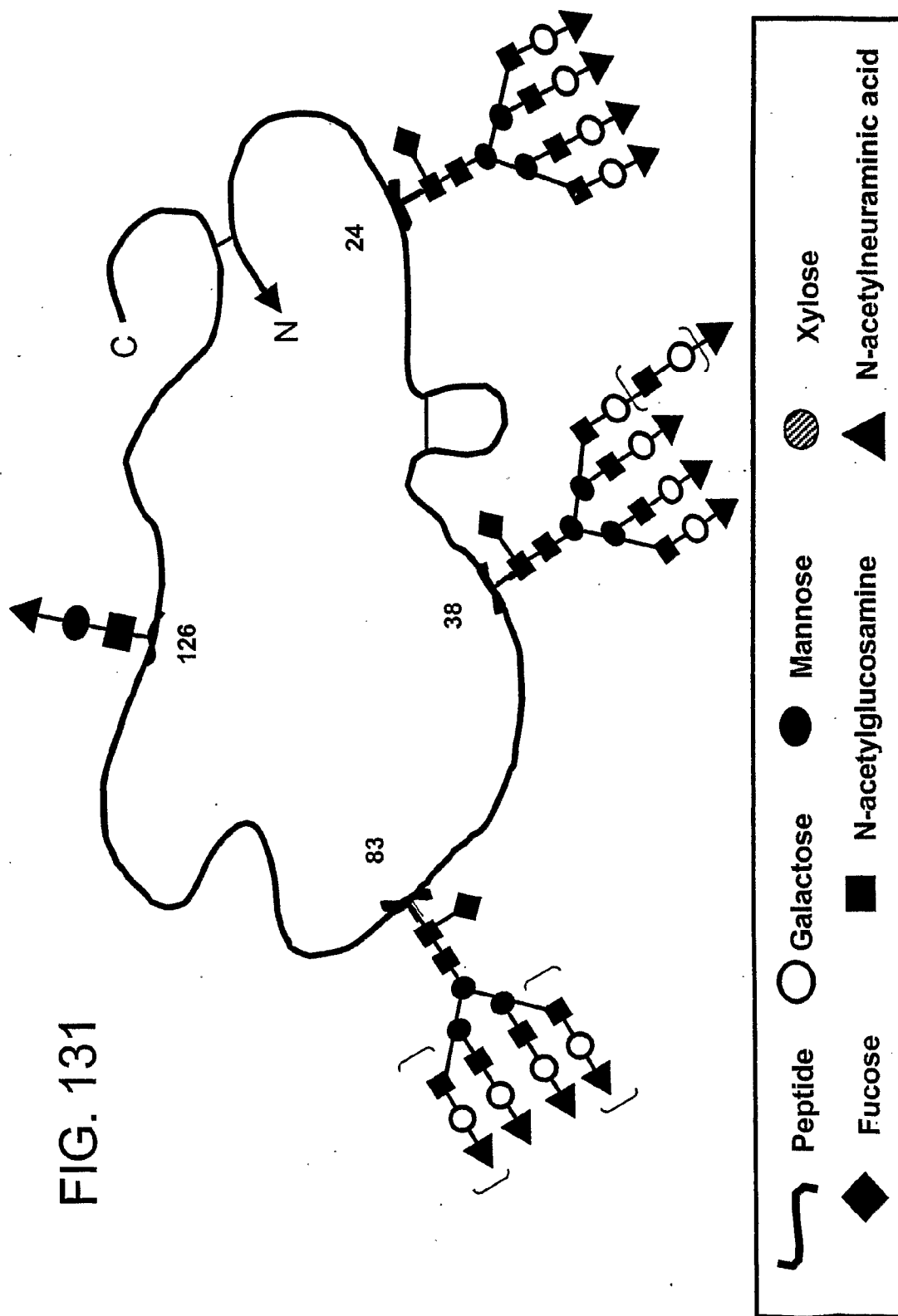


FIG. 130

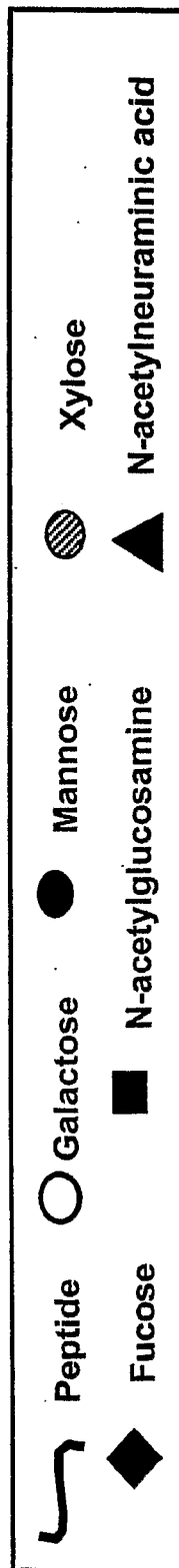
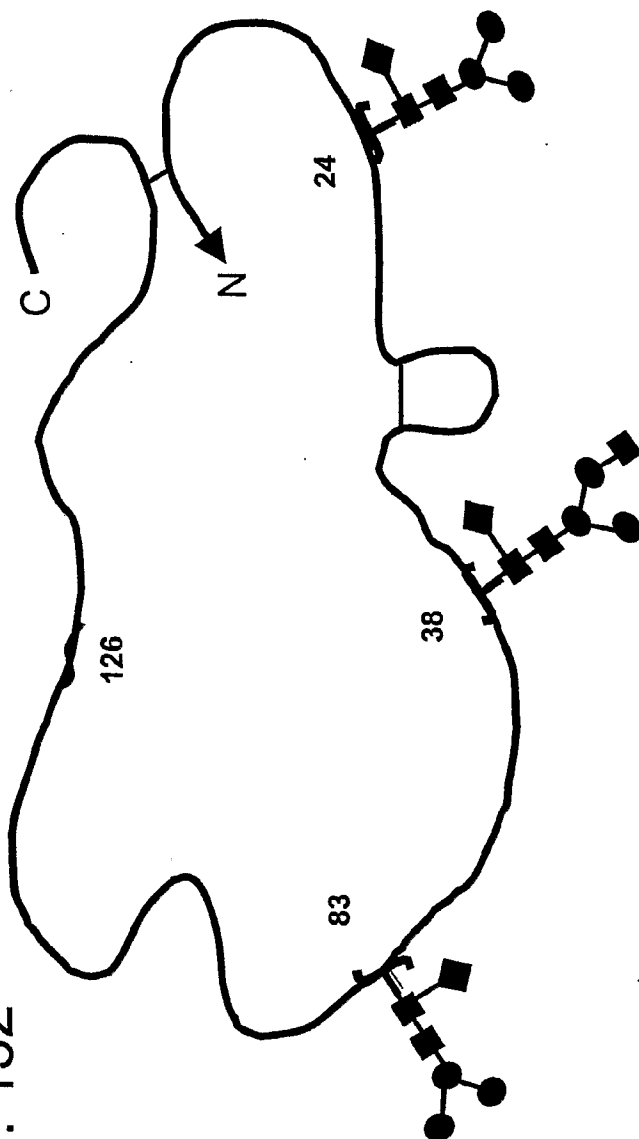


429/498



430/498

FIG. 132



431/498

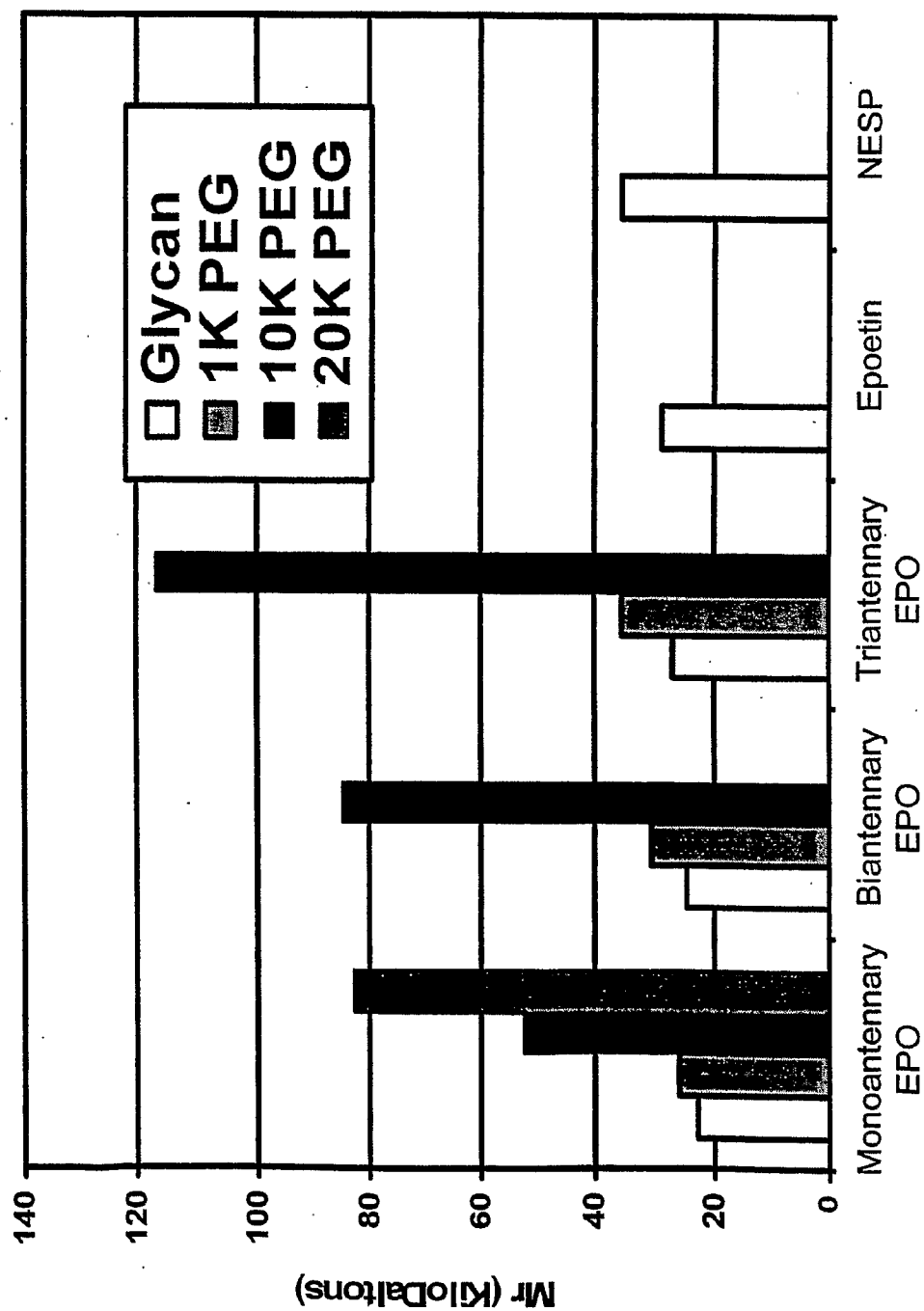
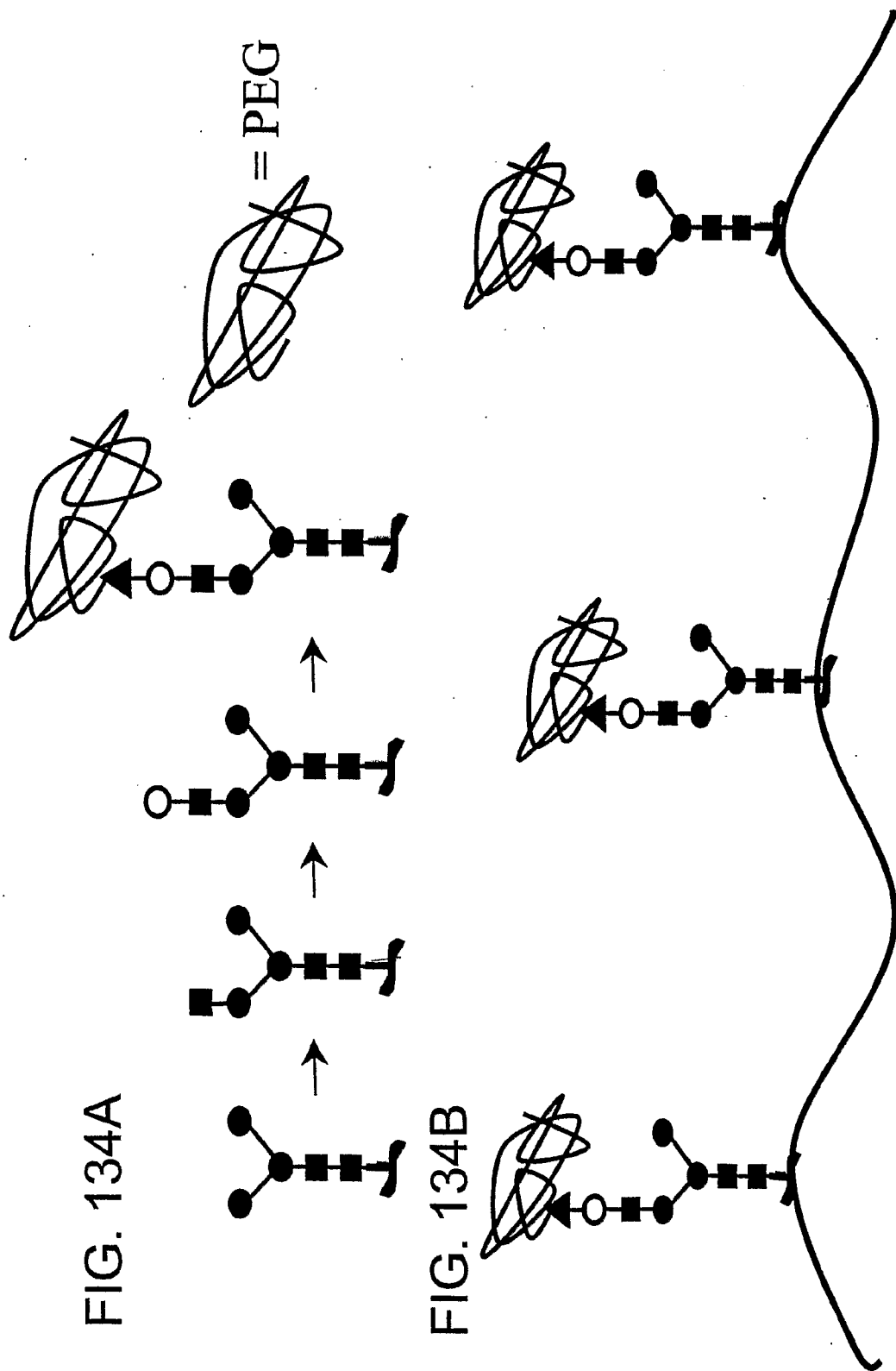


FIG. 133

432/498



433/498

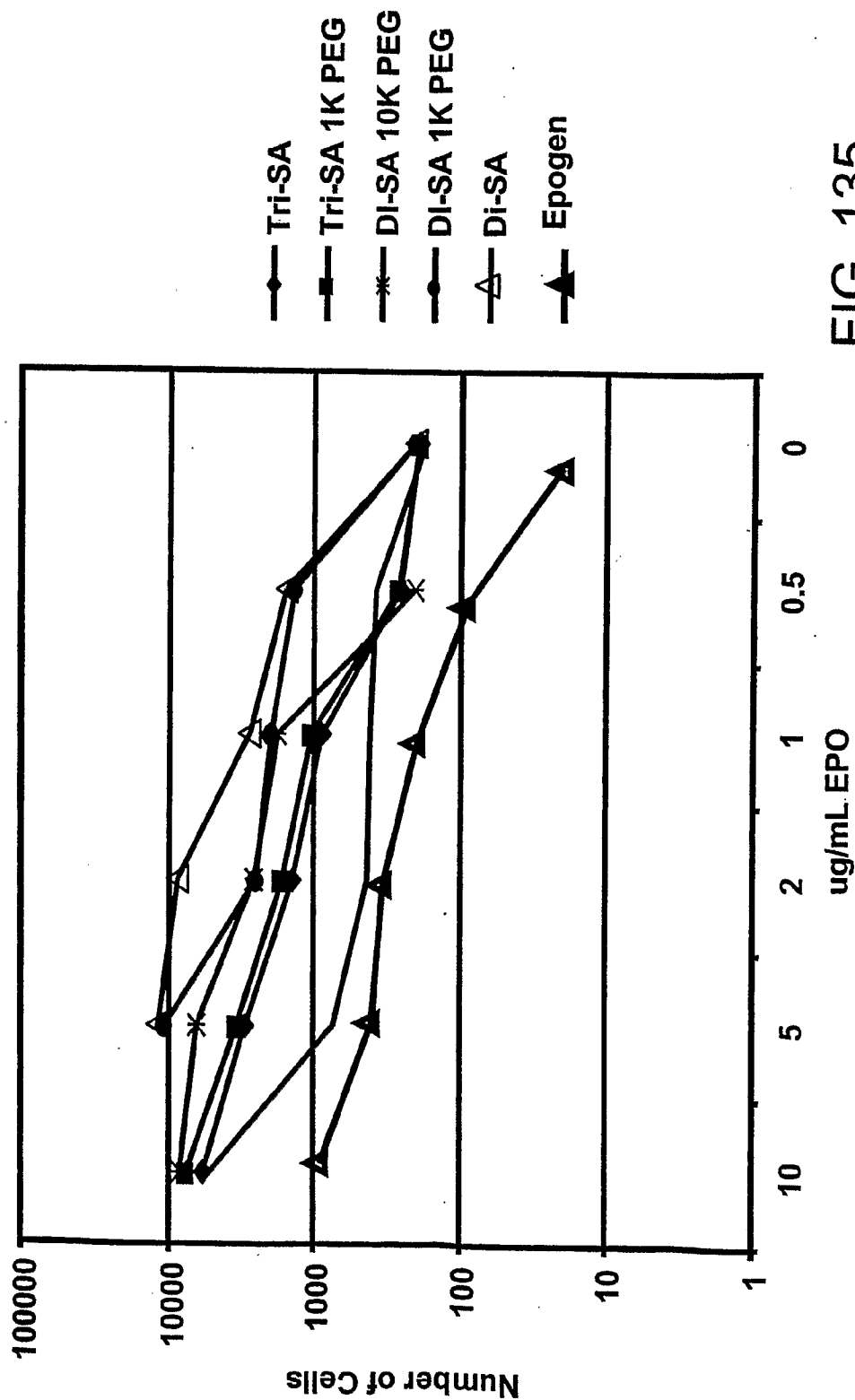


FIG. 135

434/498

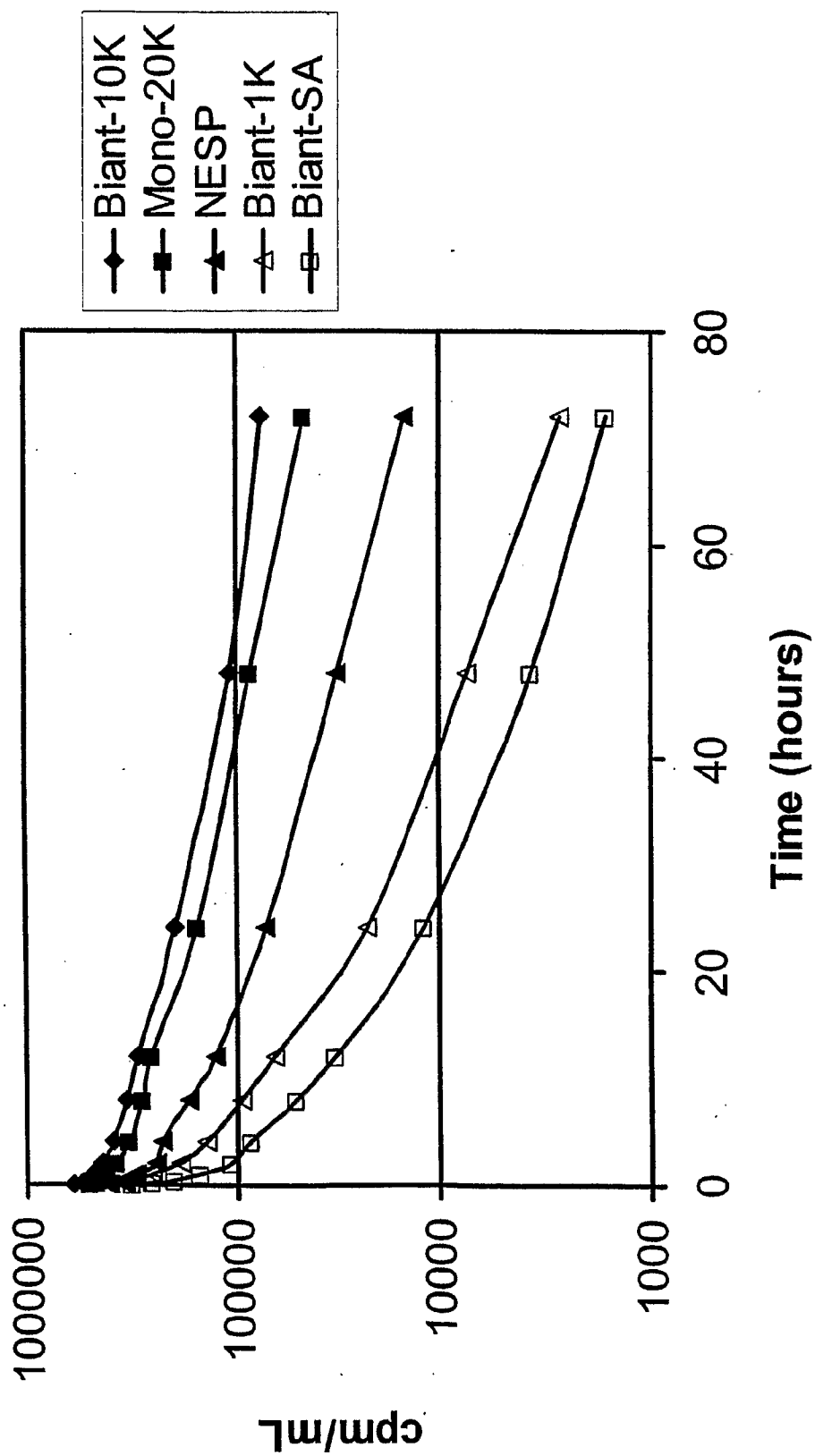


FIG. 136

435/498

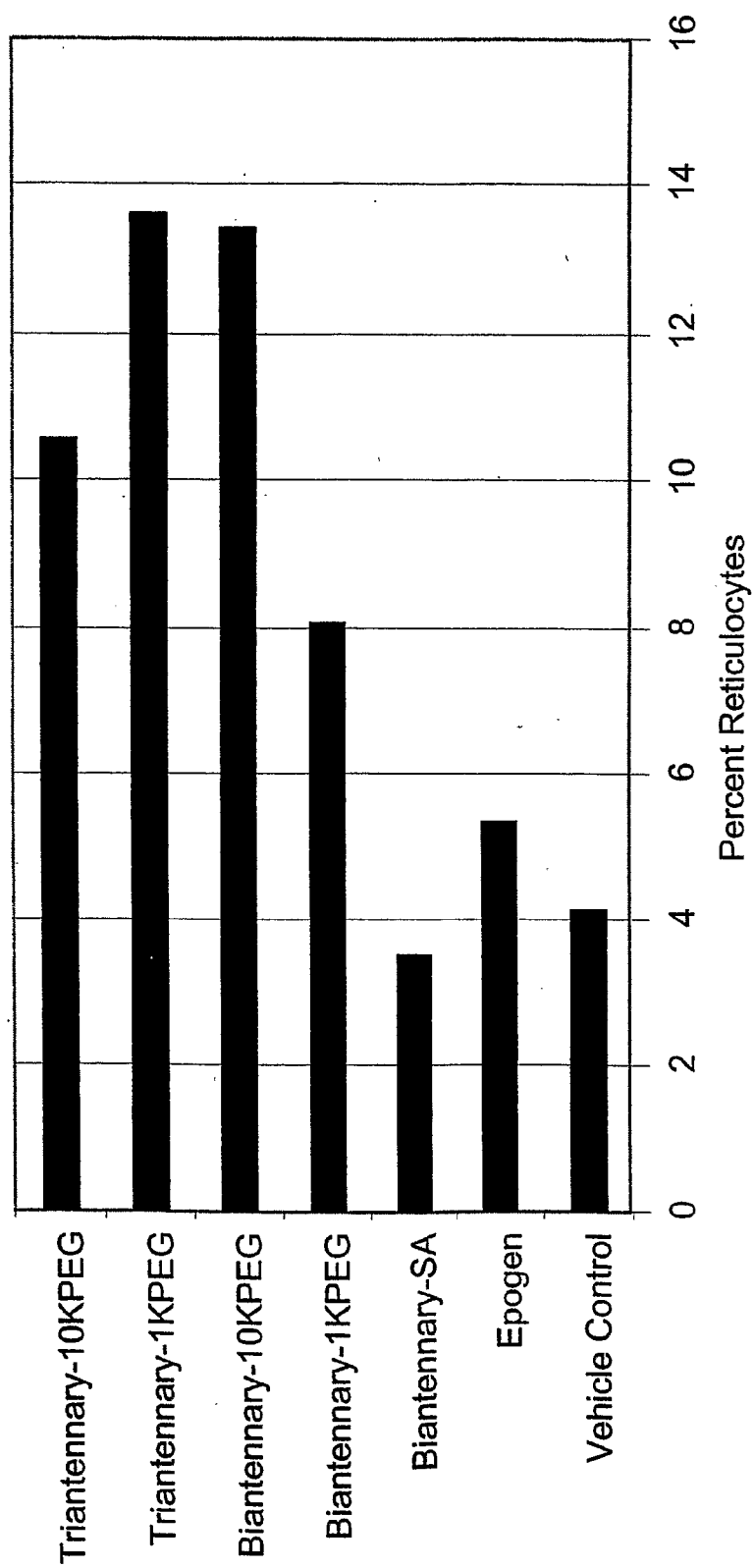


FIG. 137

436/498

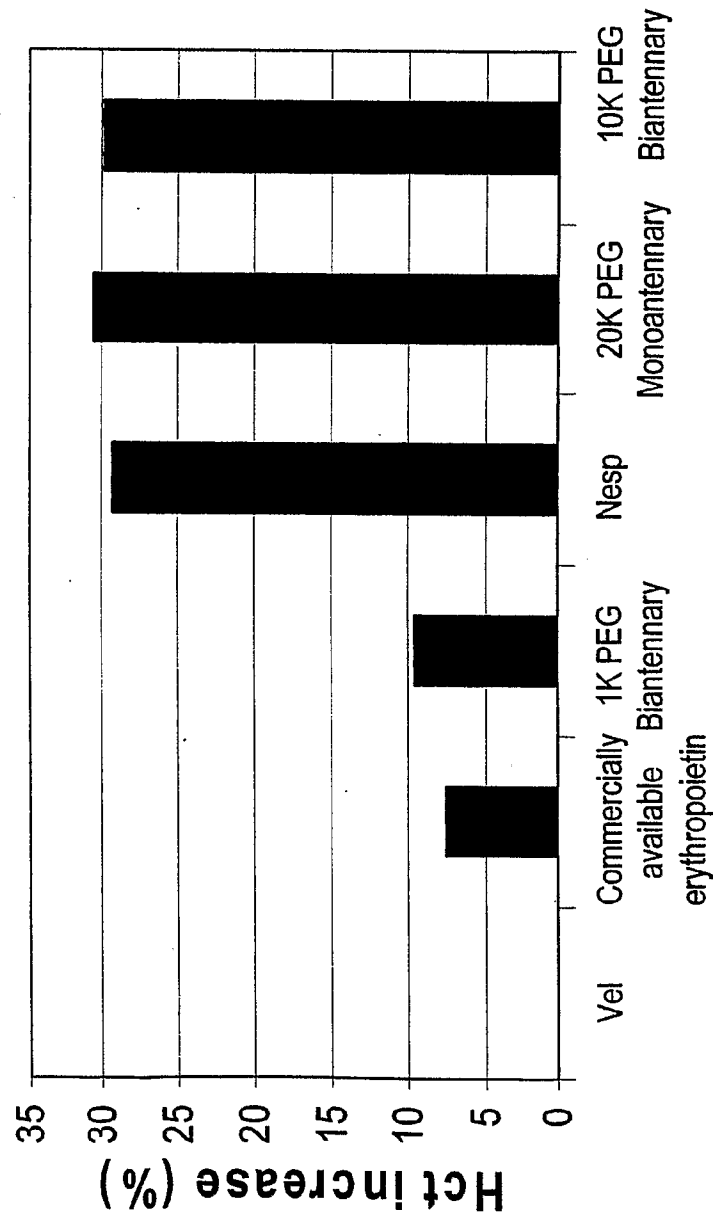


FIG. 138



437/498

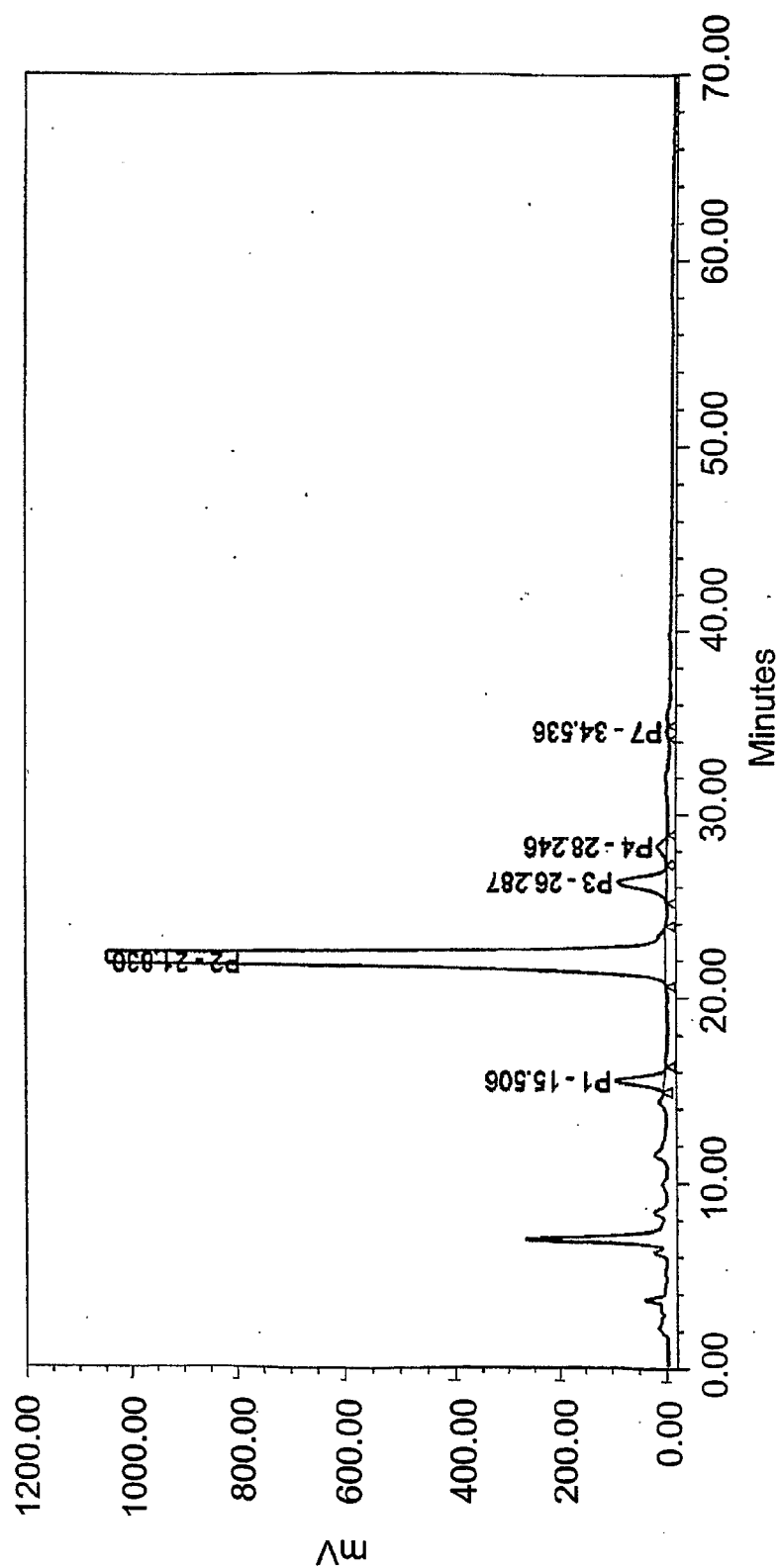


FIG. 139A

438/498

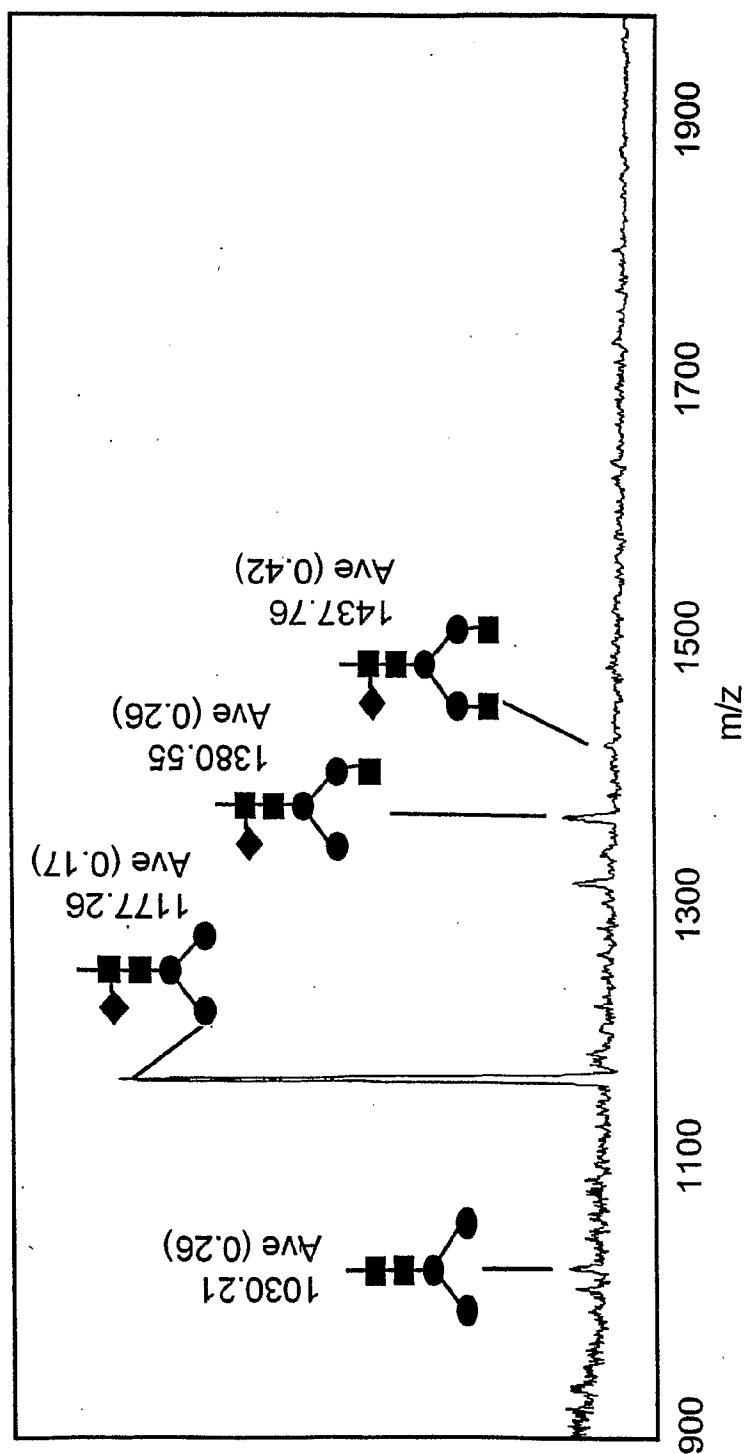


FIG. 139B

439/498

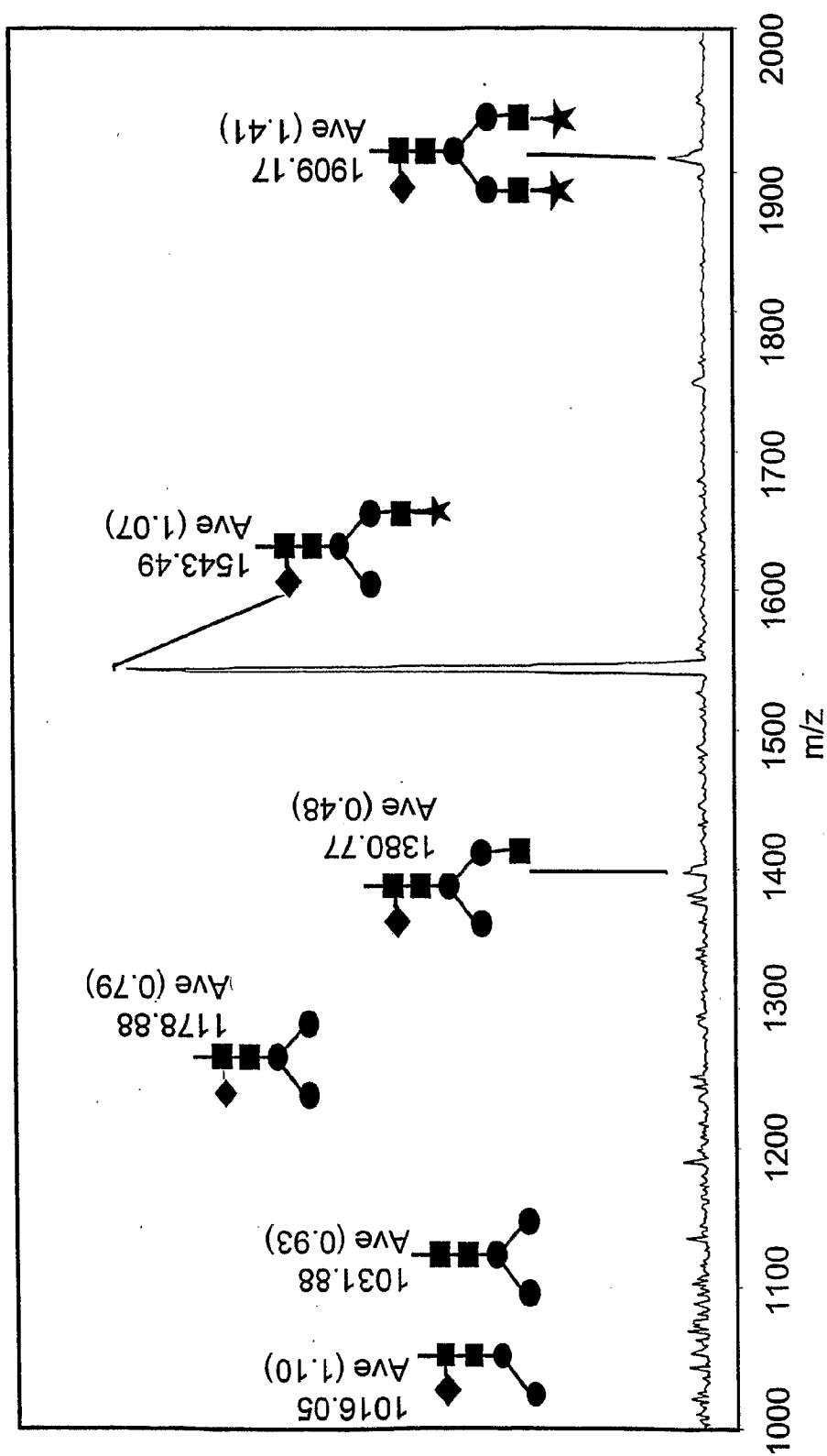


FIG. 140

440/498

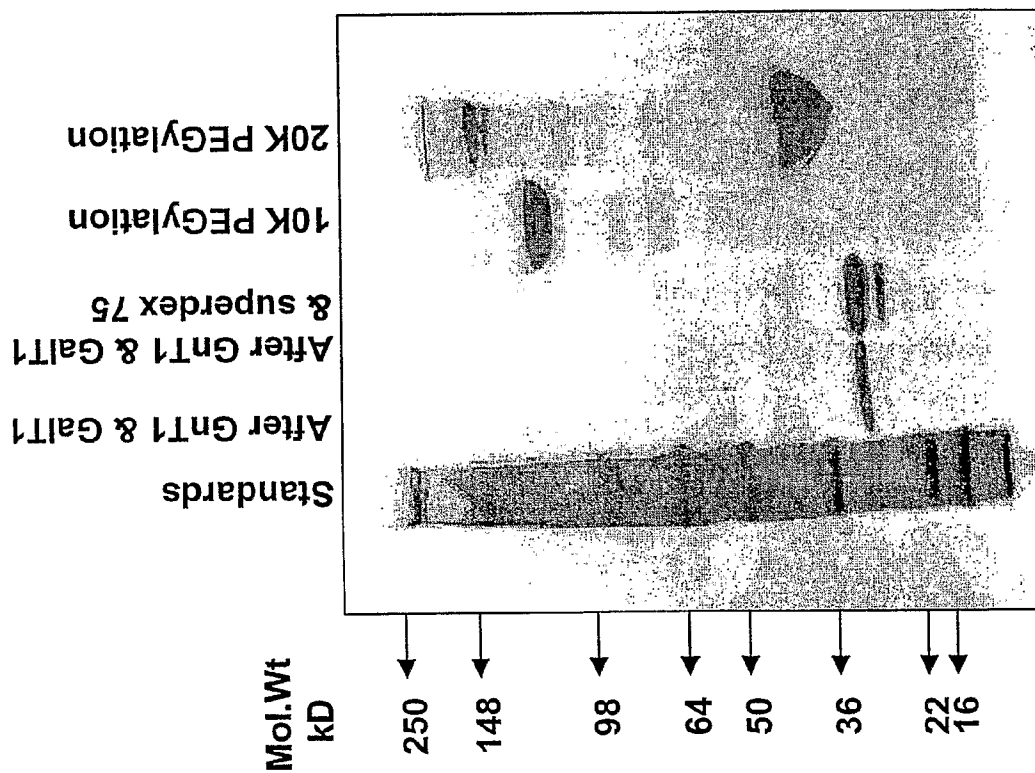


FIG. 141

441/498

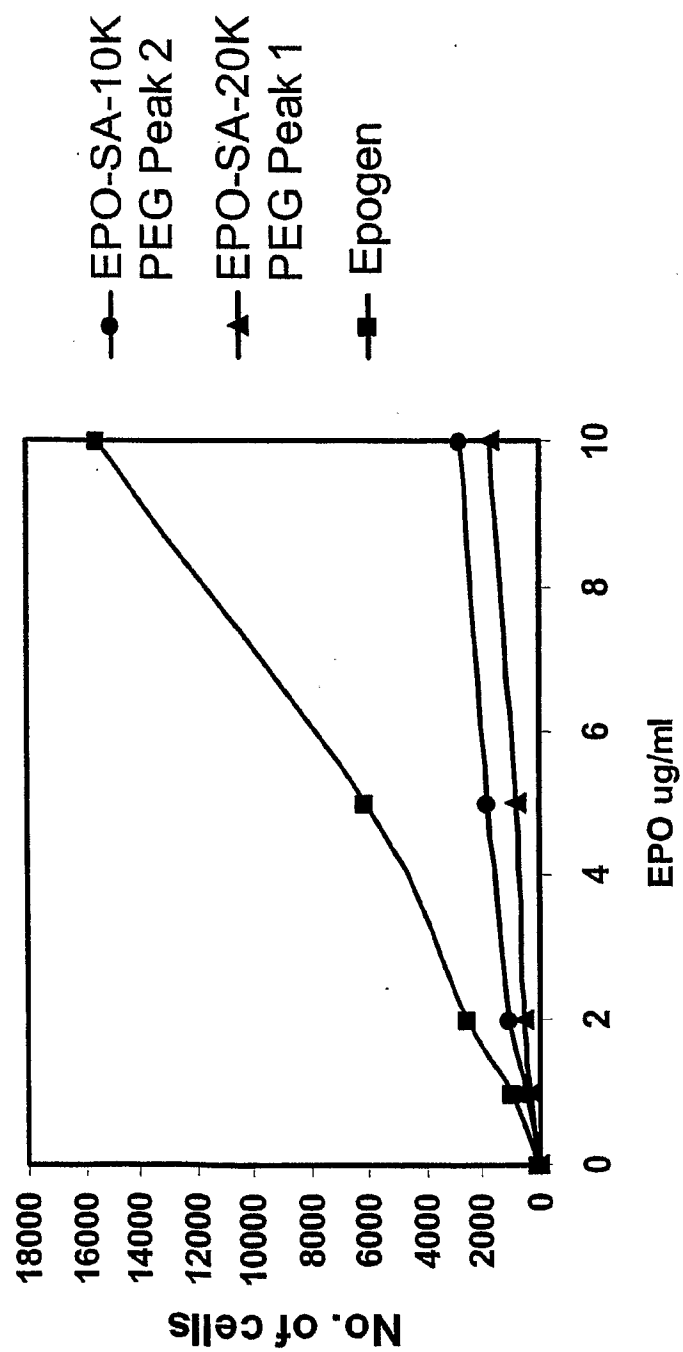


FIG. 142

442/498

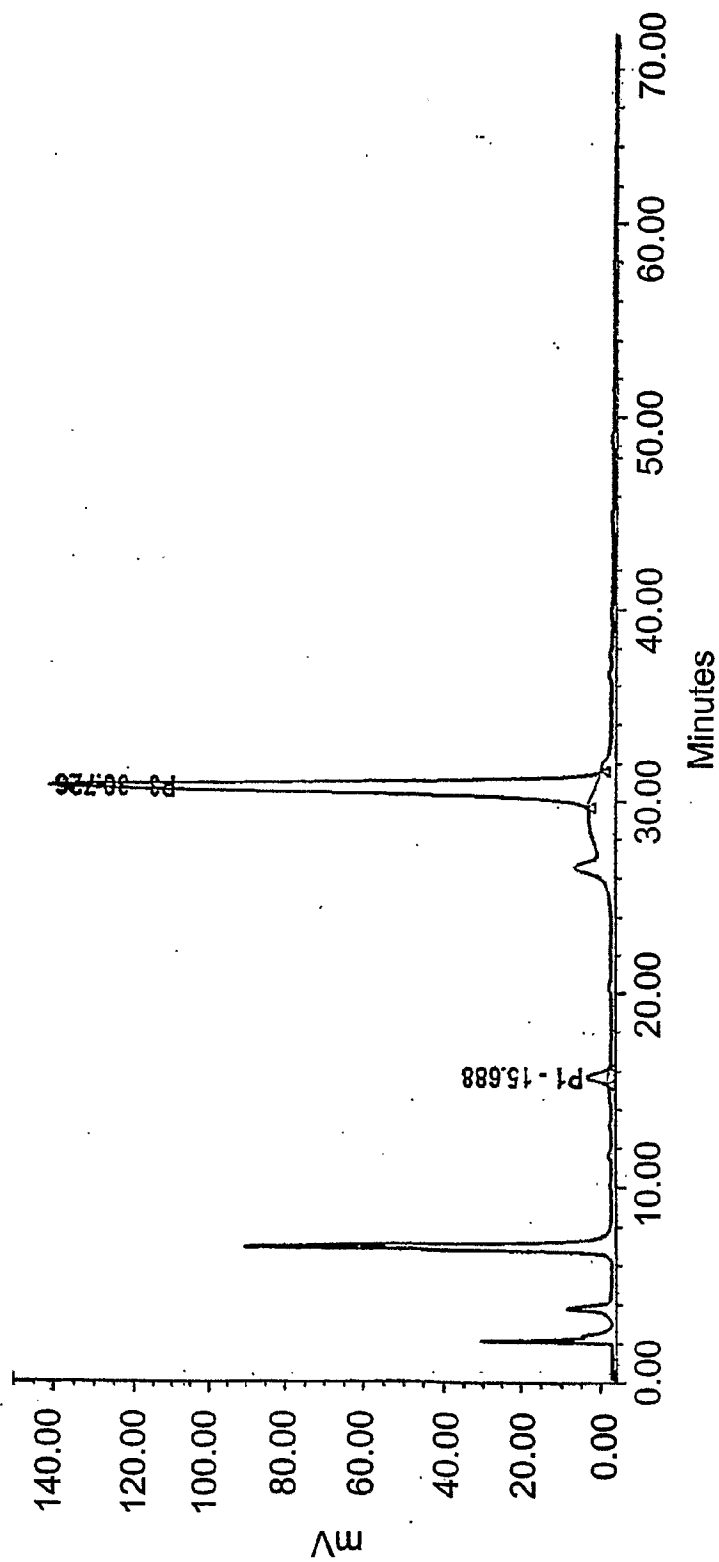


FIG. 143A

443/498

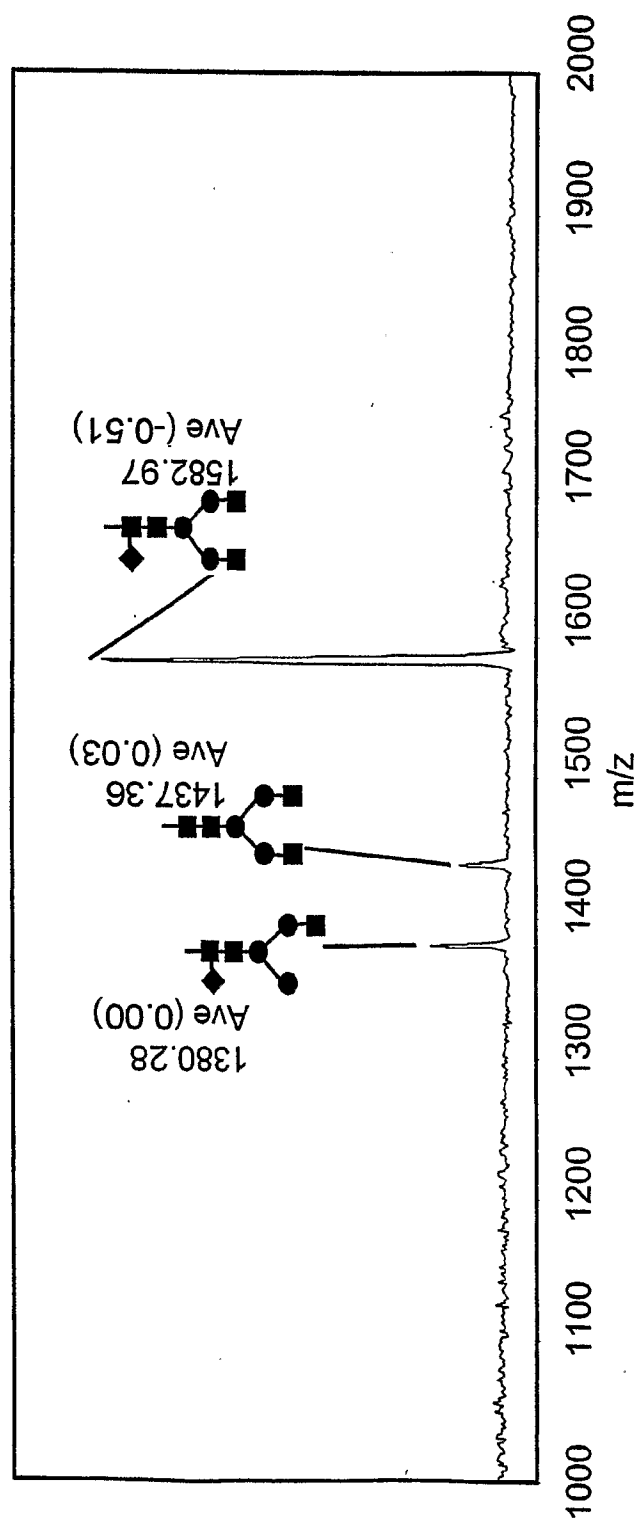


FIG. 143B

444/498

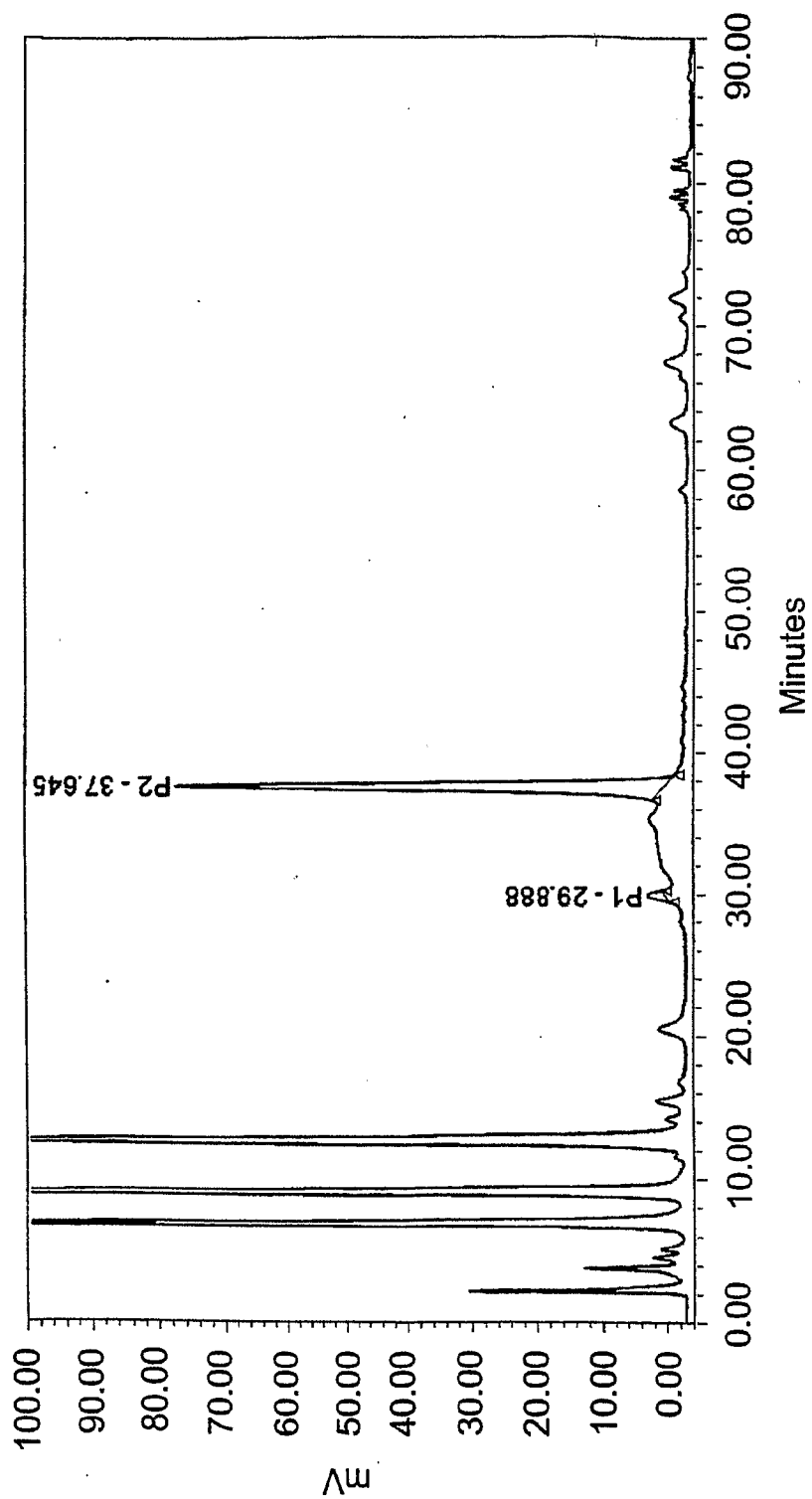


FIG. 144A



445/498

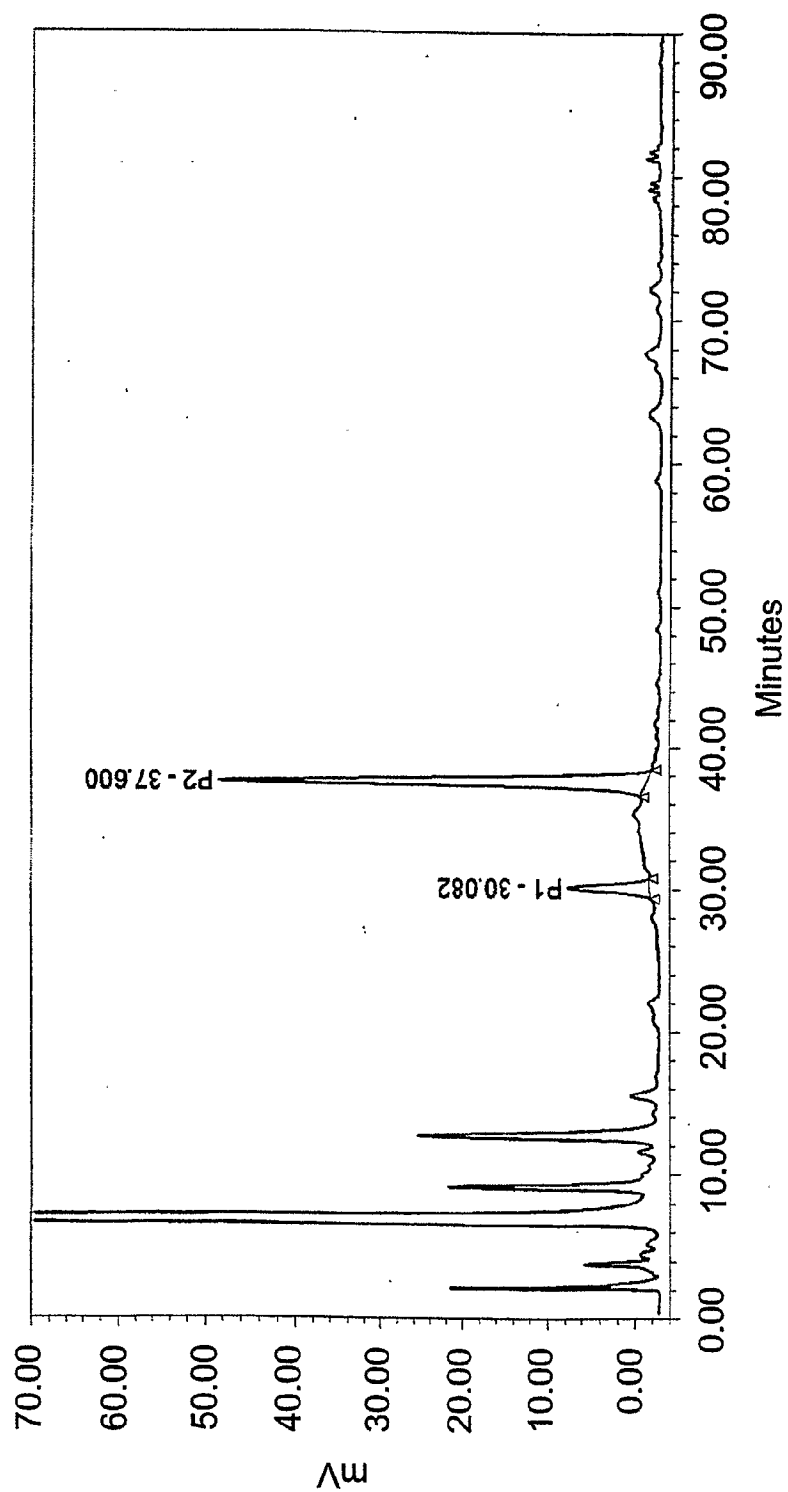


FIG. 144B

446/498

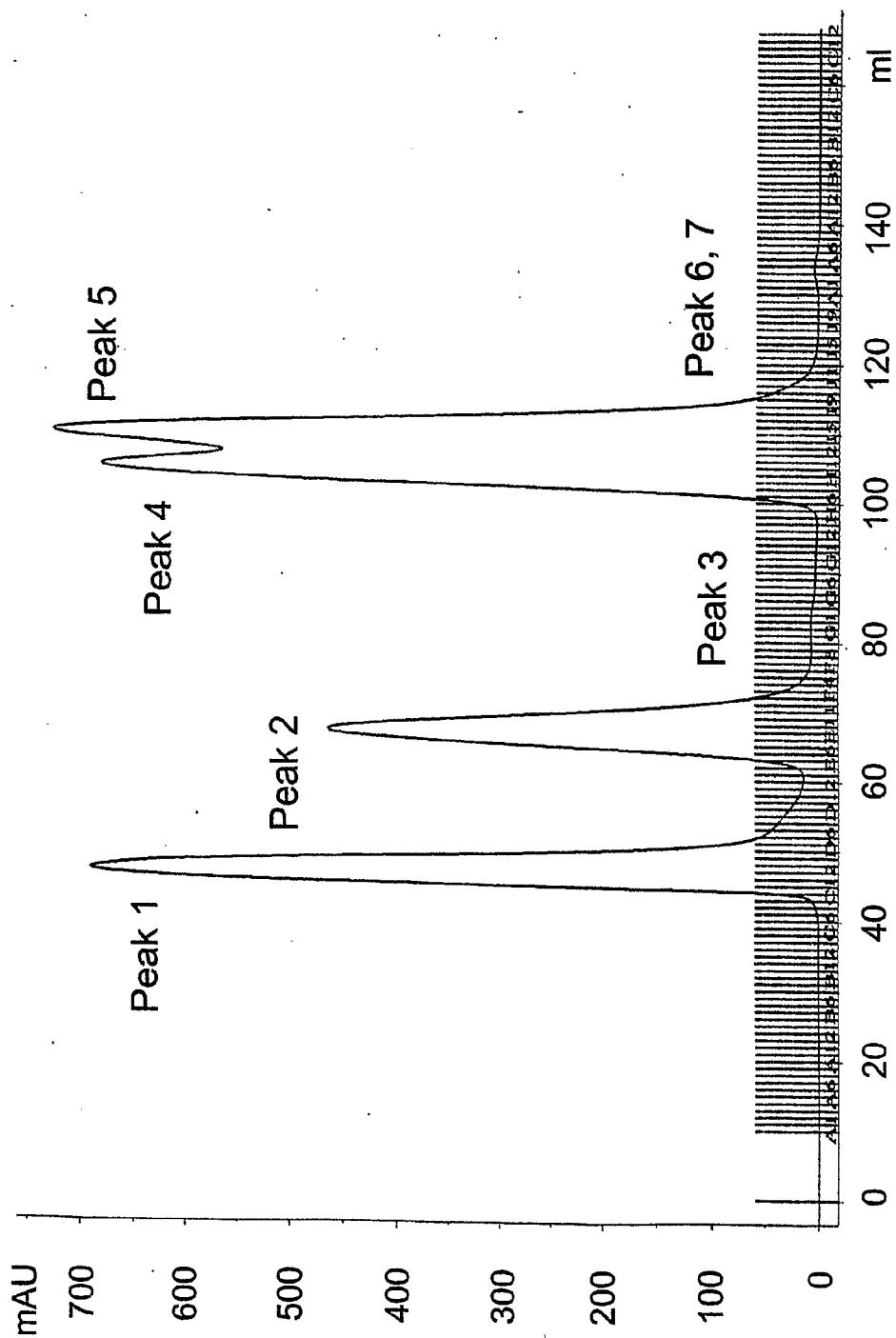


FIG. 145

447/498

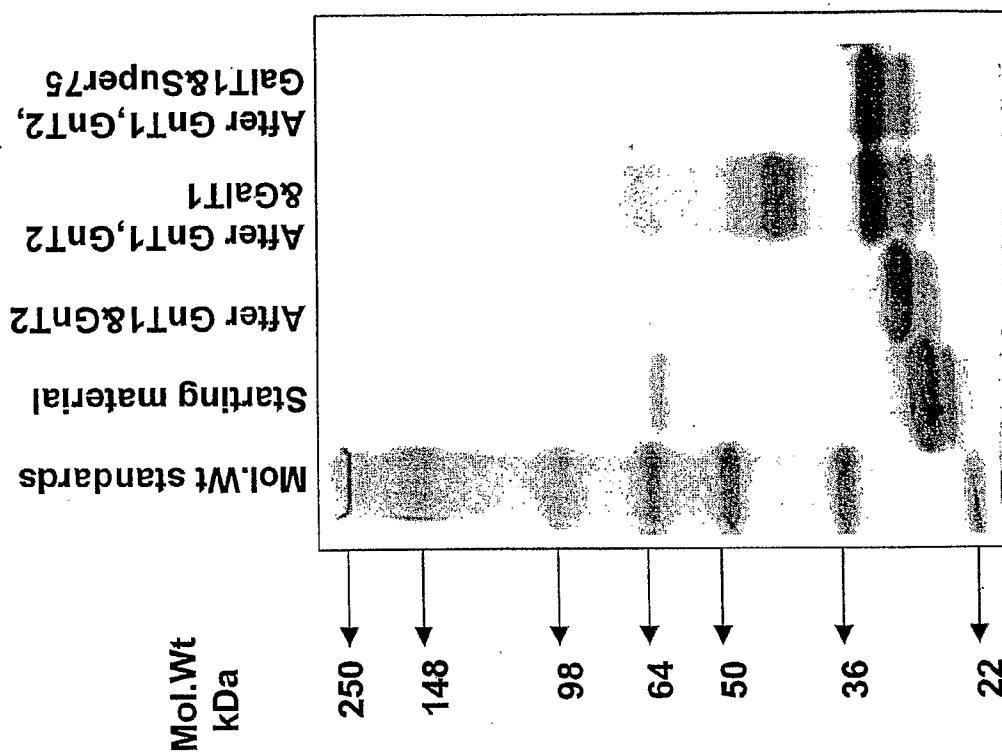


FIG. 146

448/498

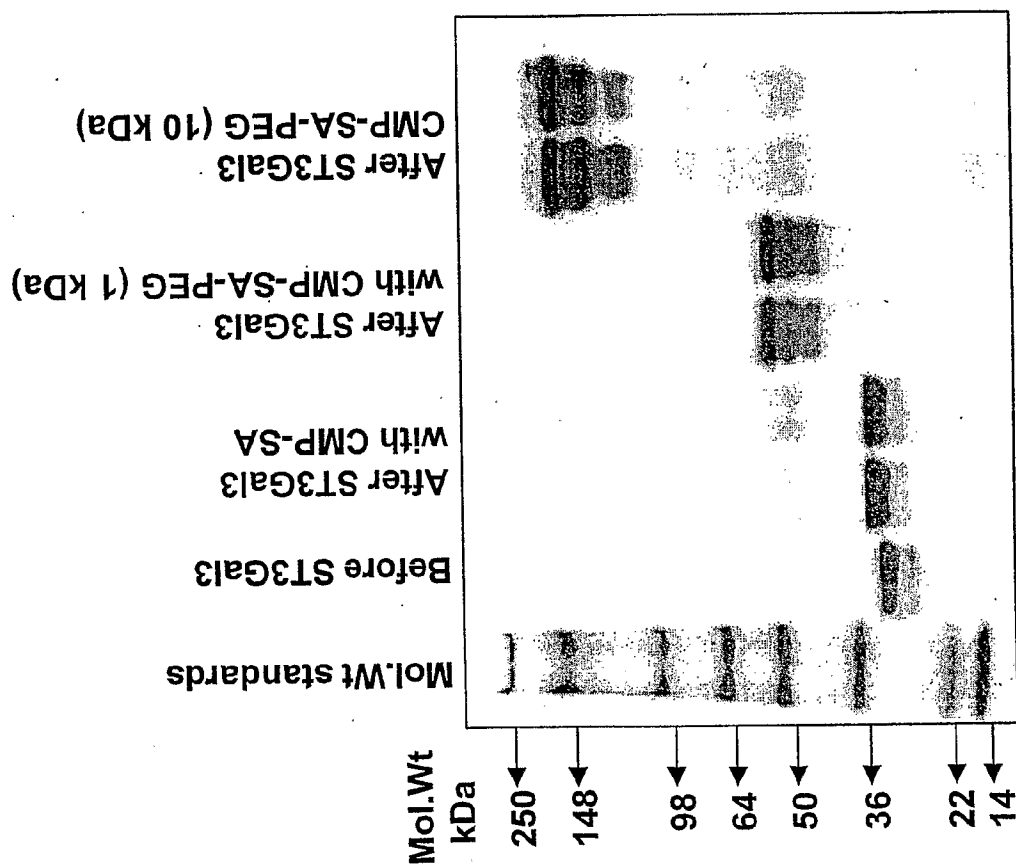


FIG. 147

449/498

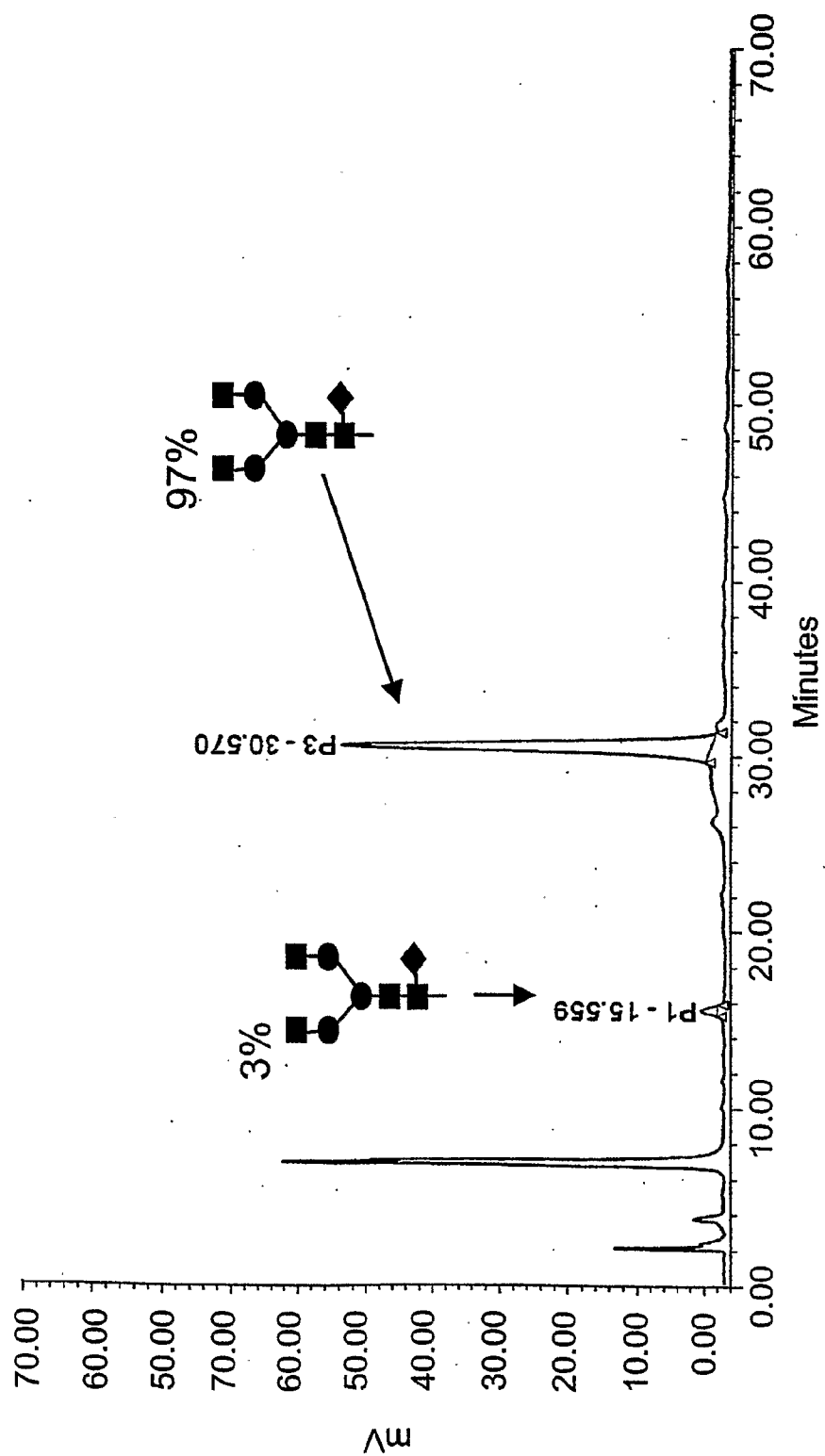


FIG. 148

450/498

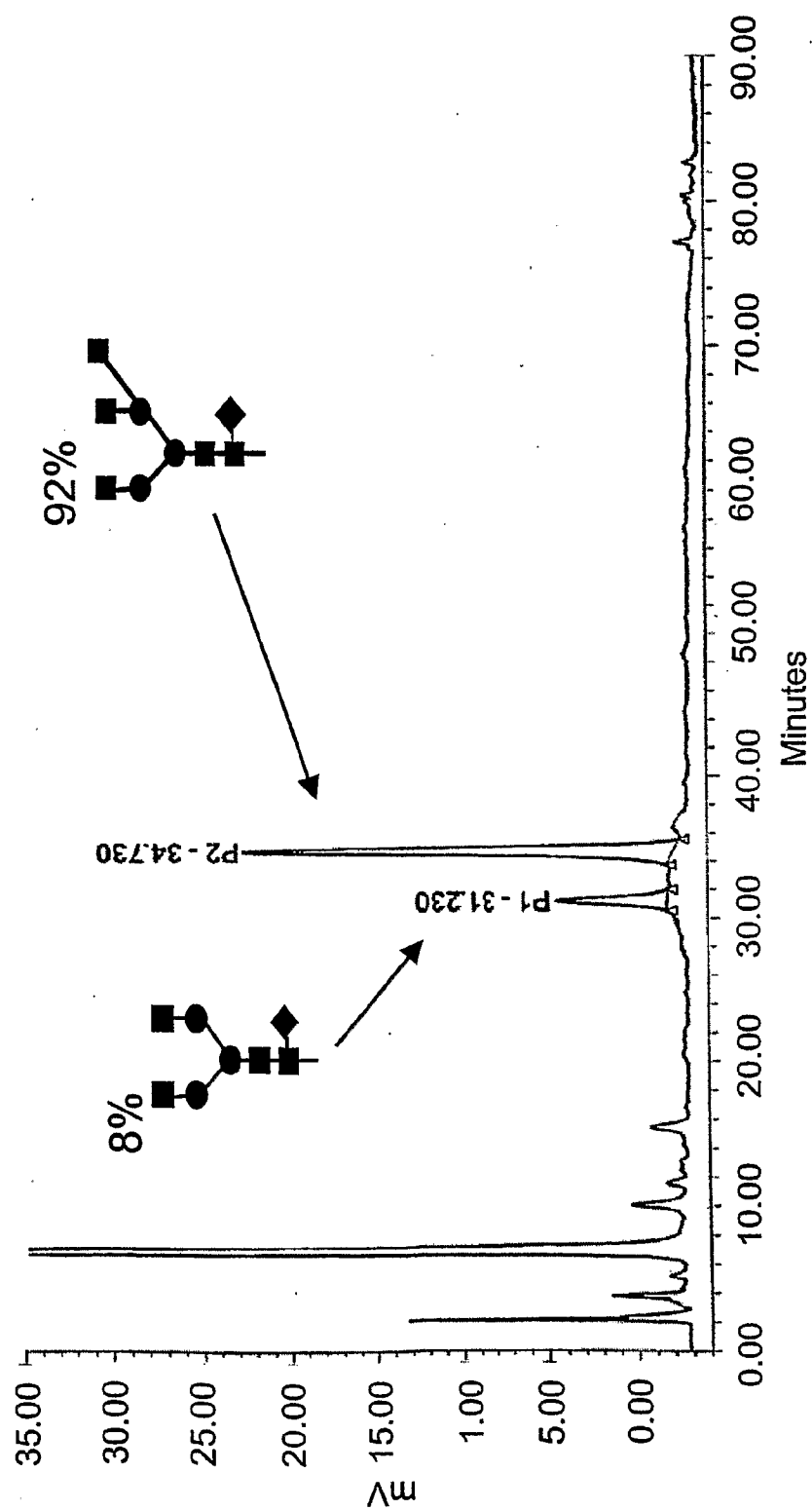


FIG. 149

451/498

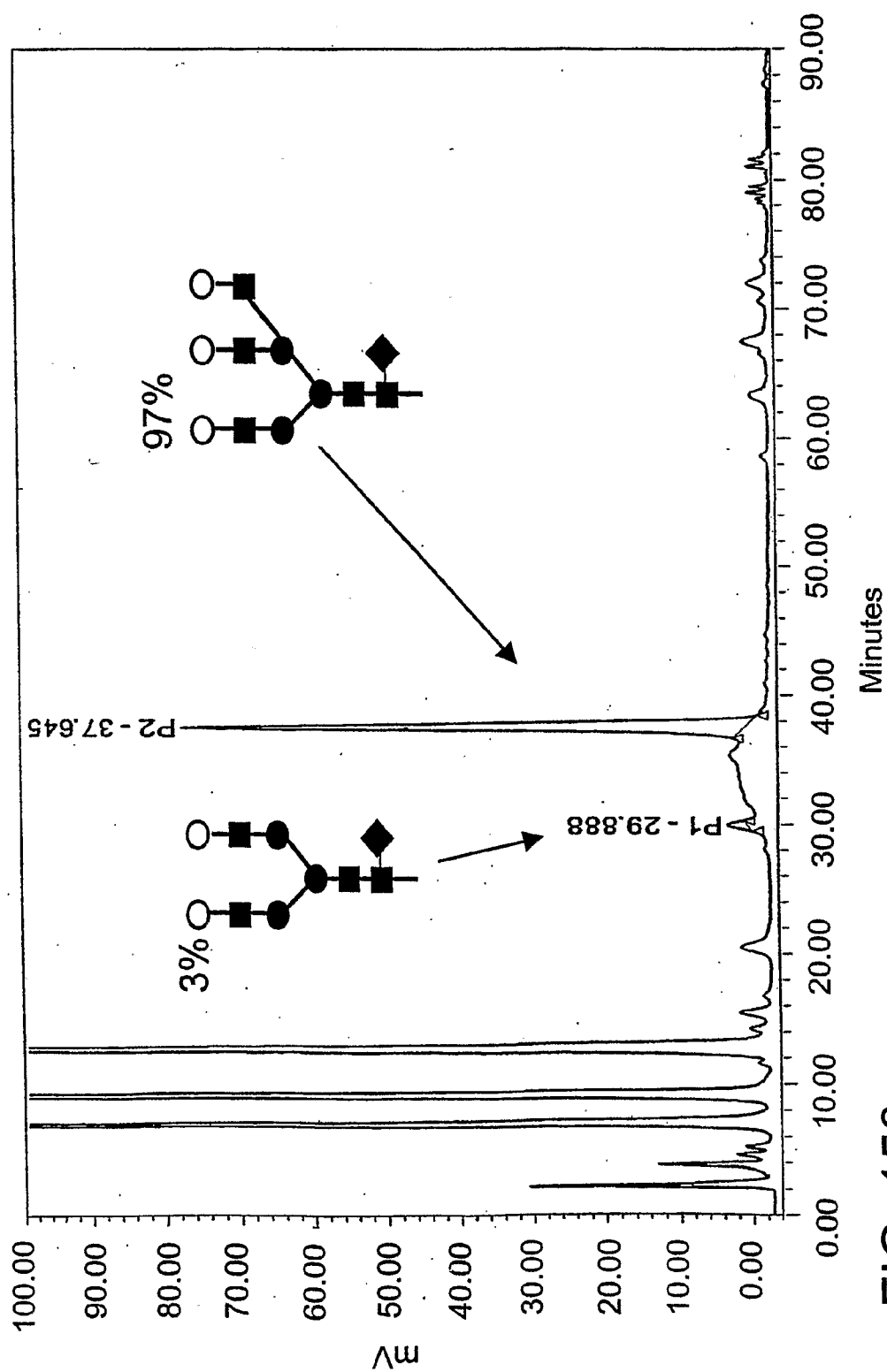


FIG. 150

452/498

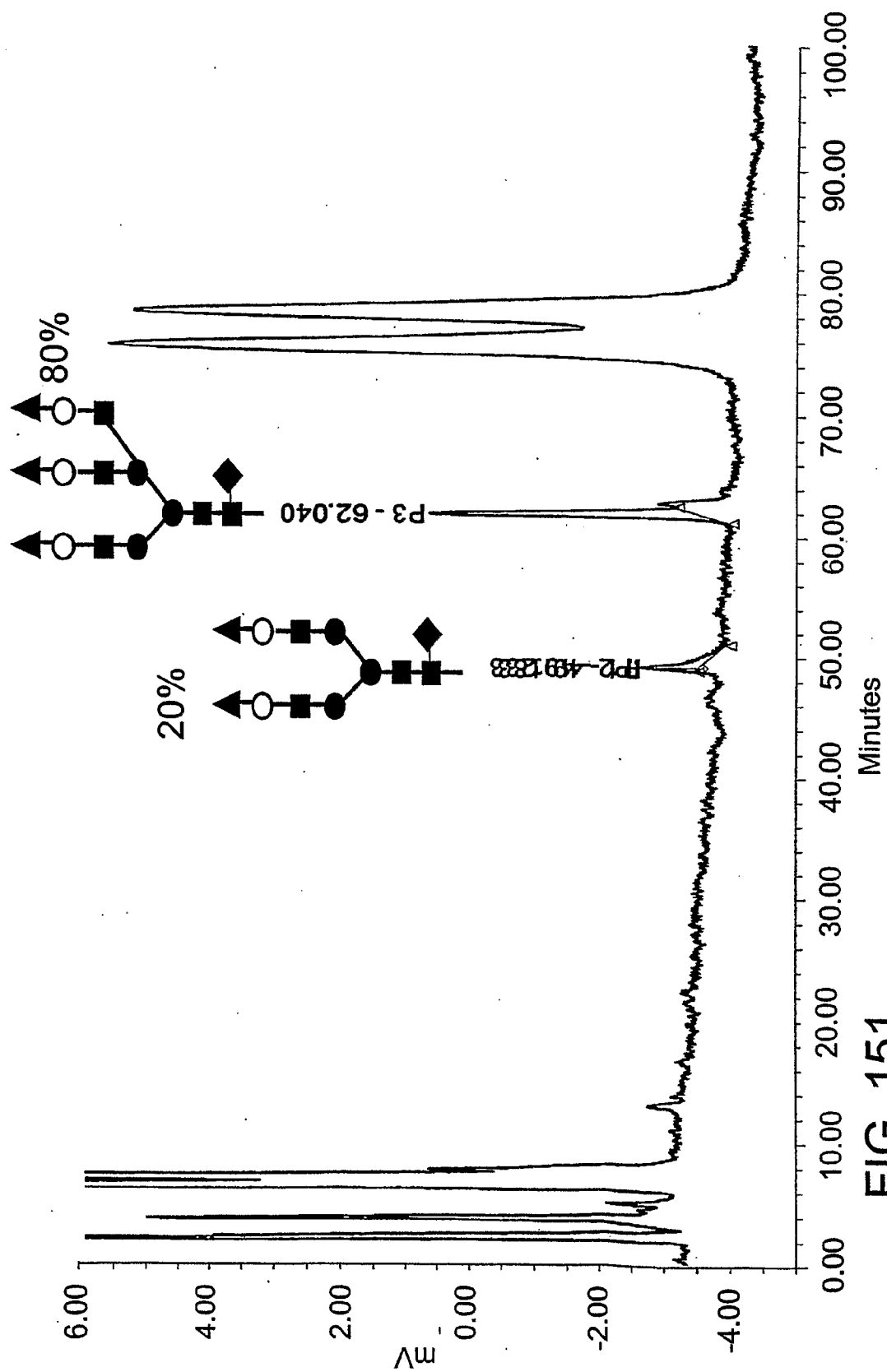


FIG. 151



453/498

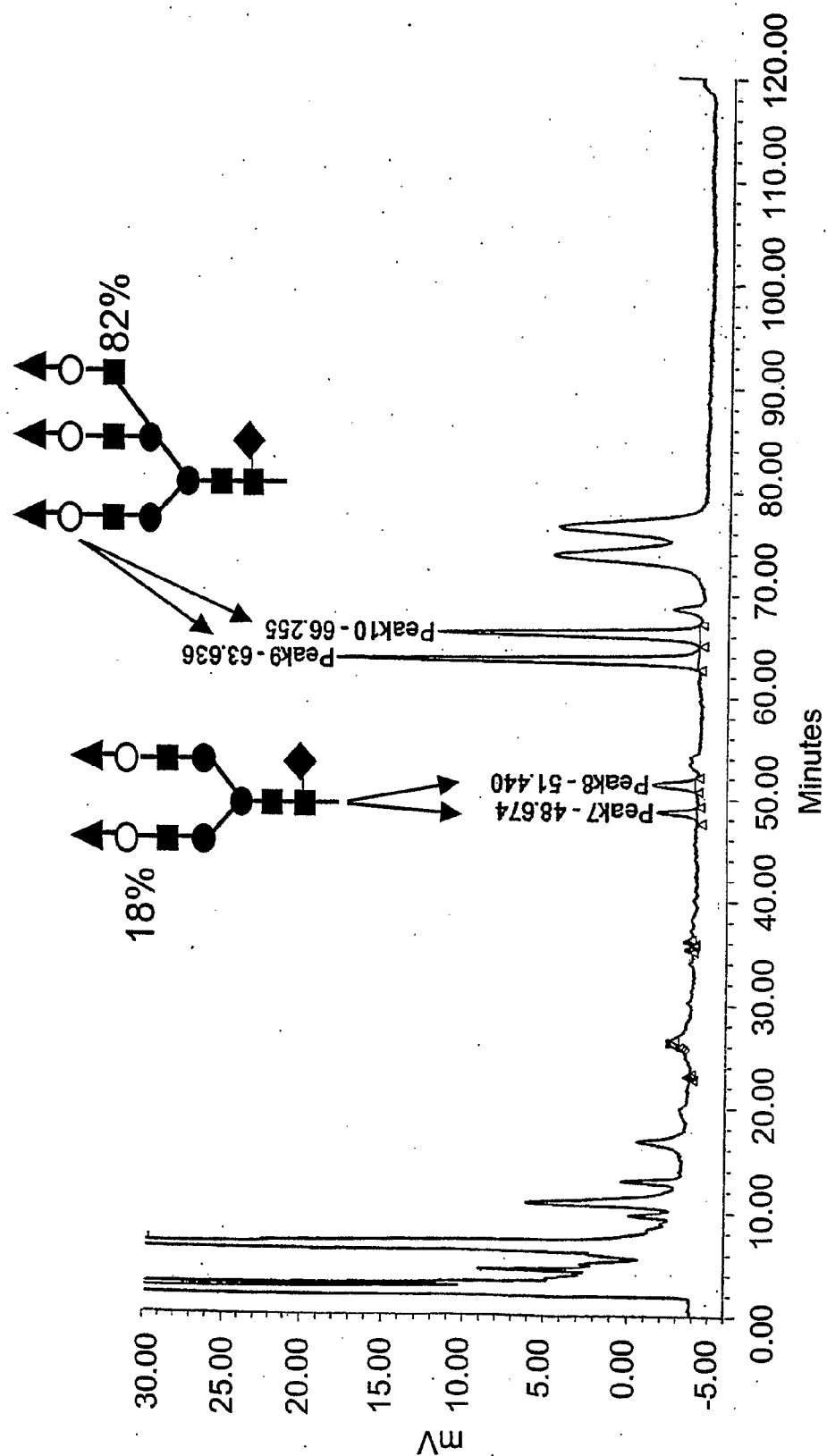


FIG. 152

454/498

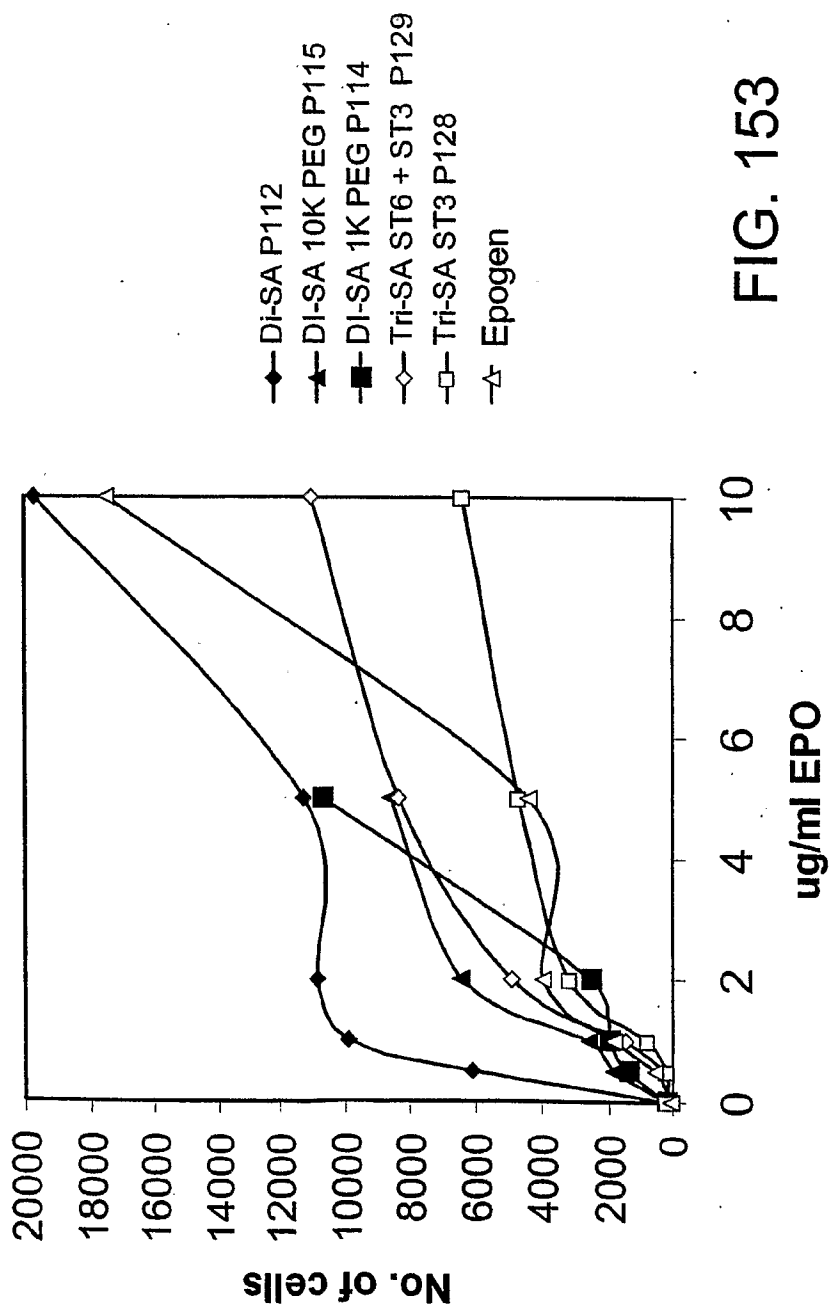


FIG. 153

455/498

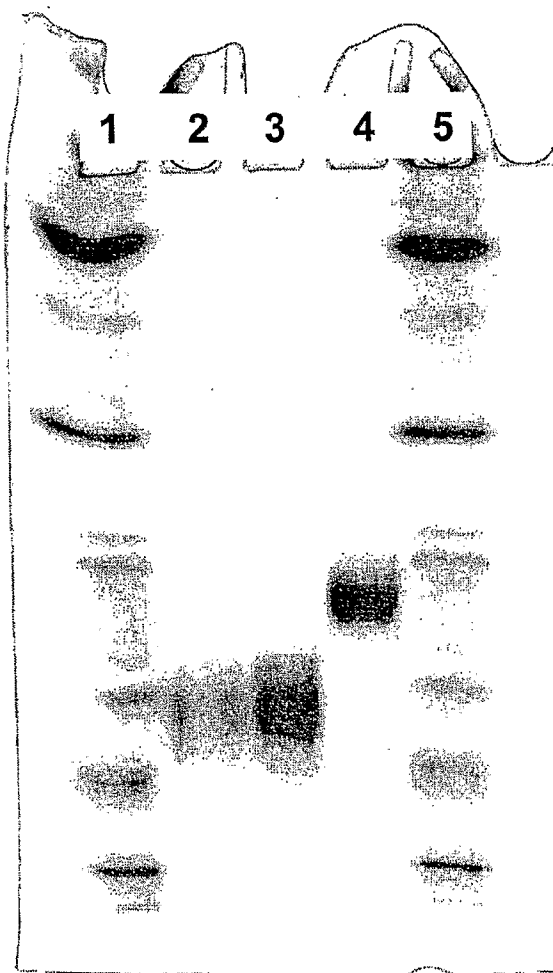


FIG. 154

456/498

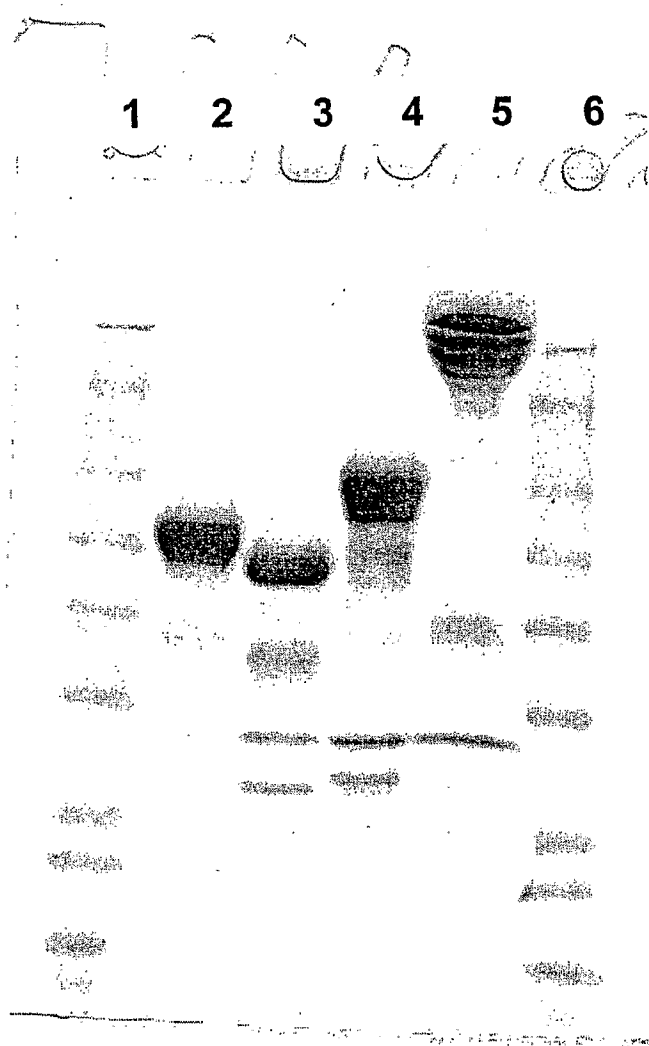


FIG. 155

457/498

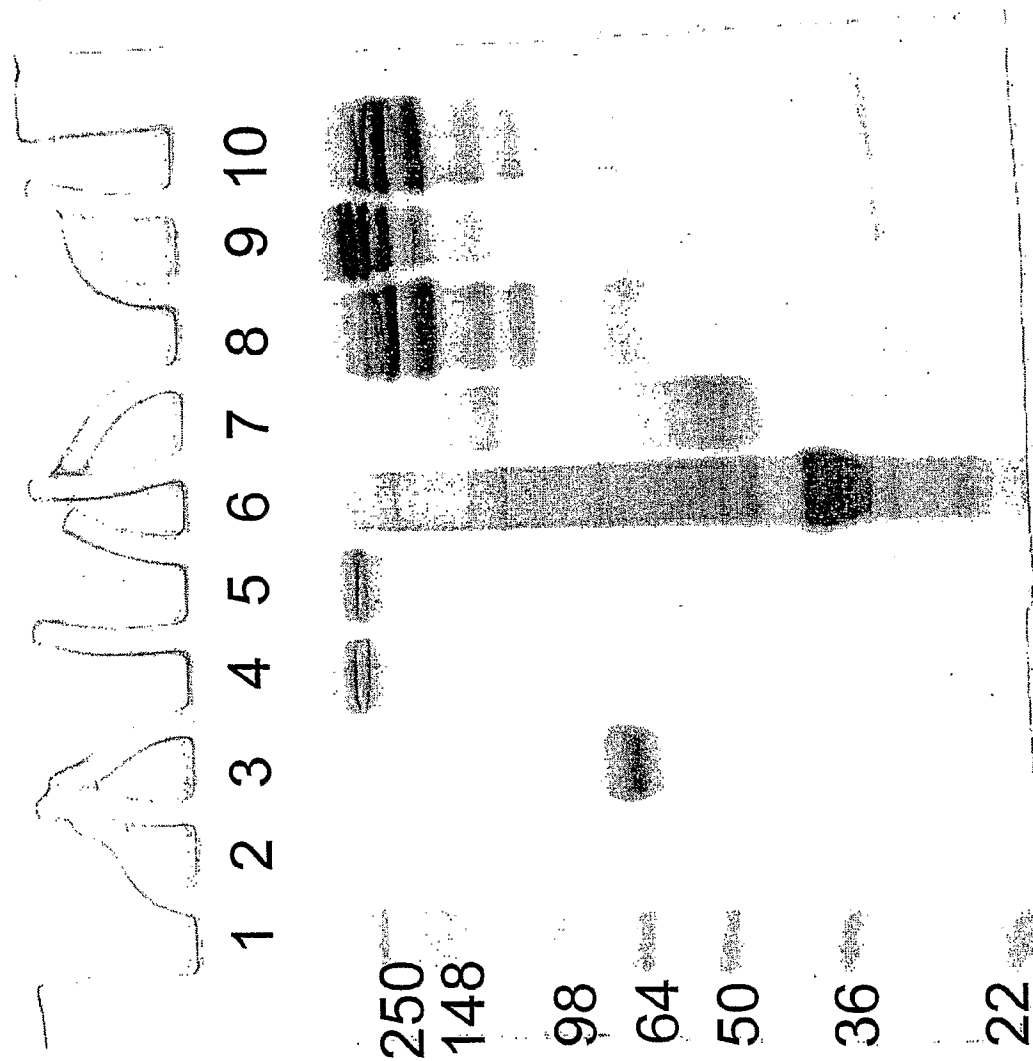


FIG. 156

458/498

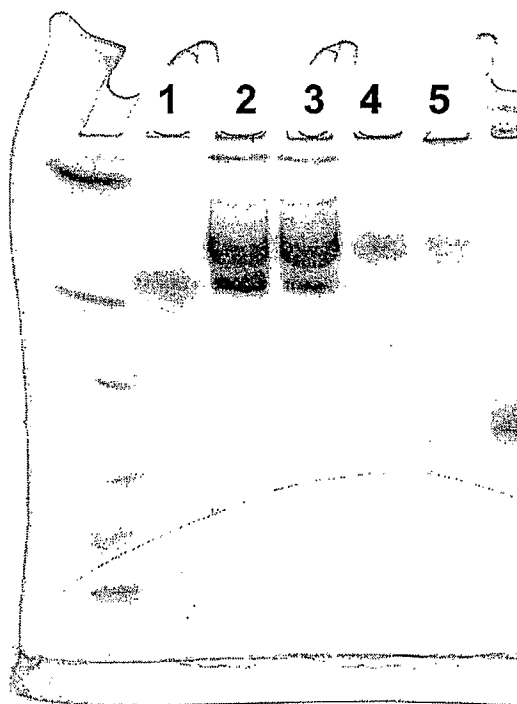


FIG. 157

459/498

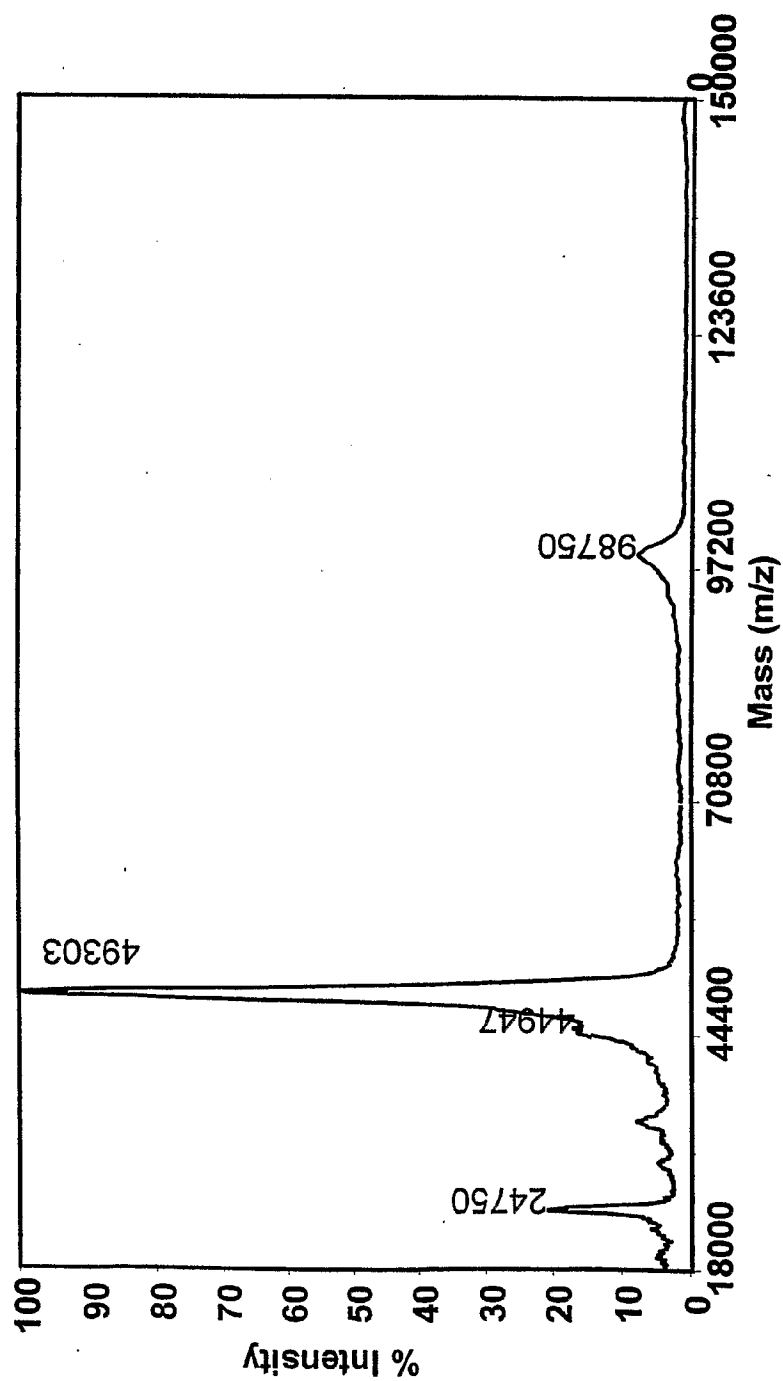


FIG. 158

460/498

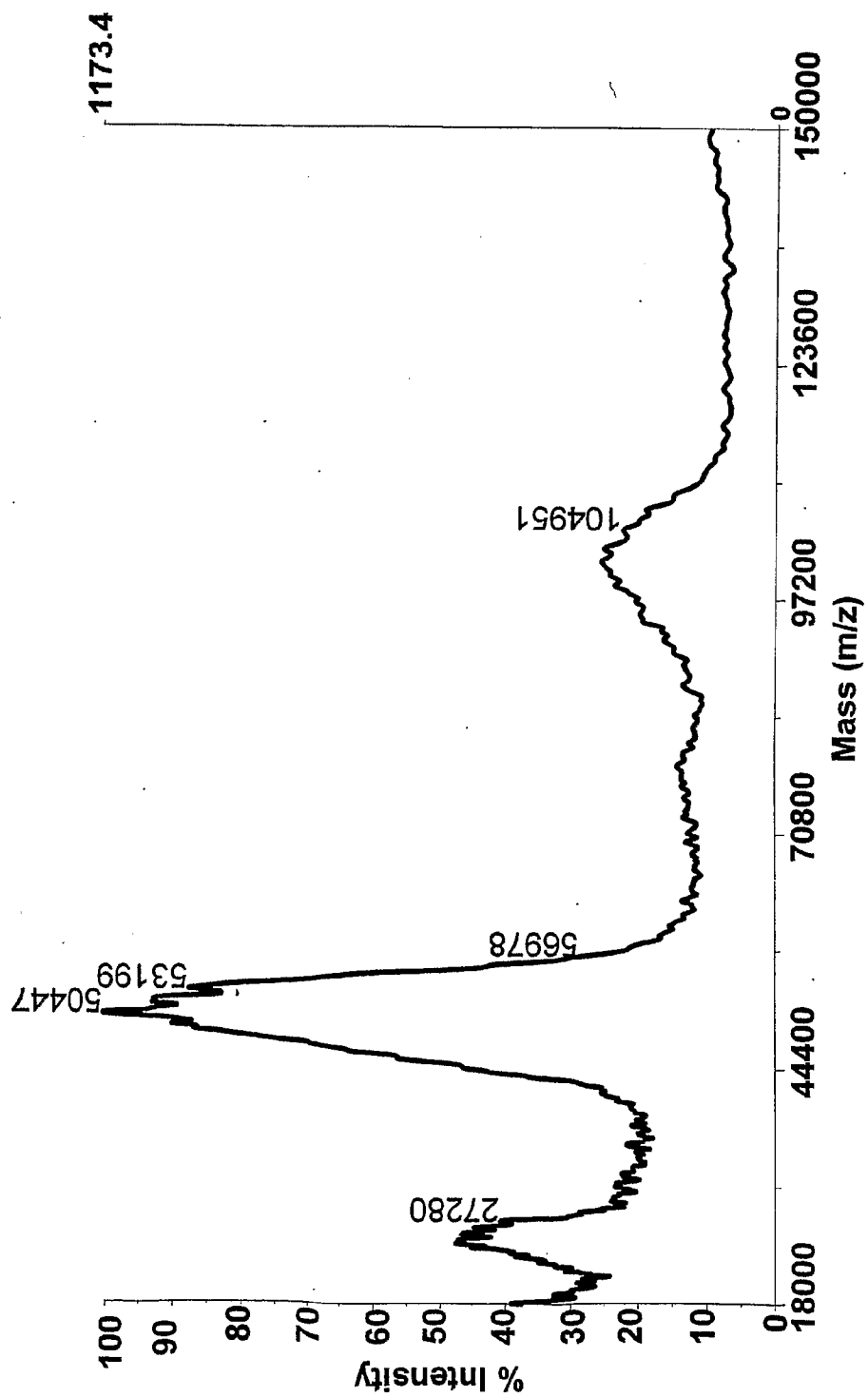


FIG. 159



461/498

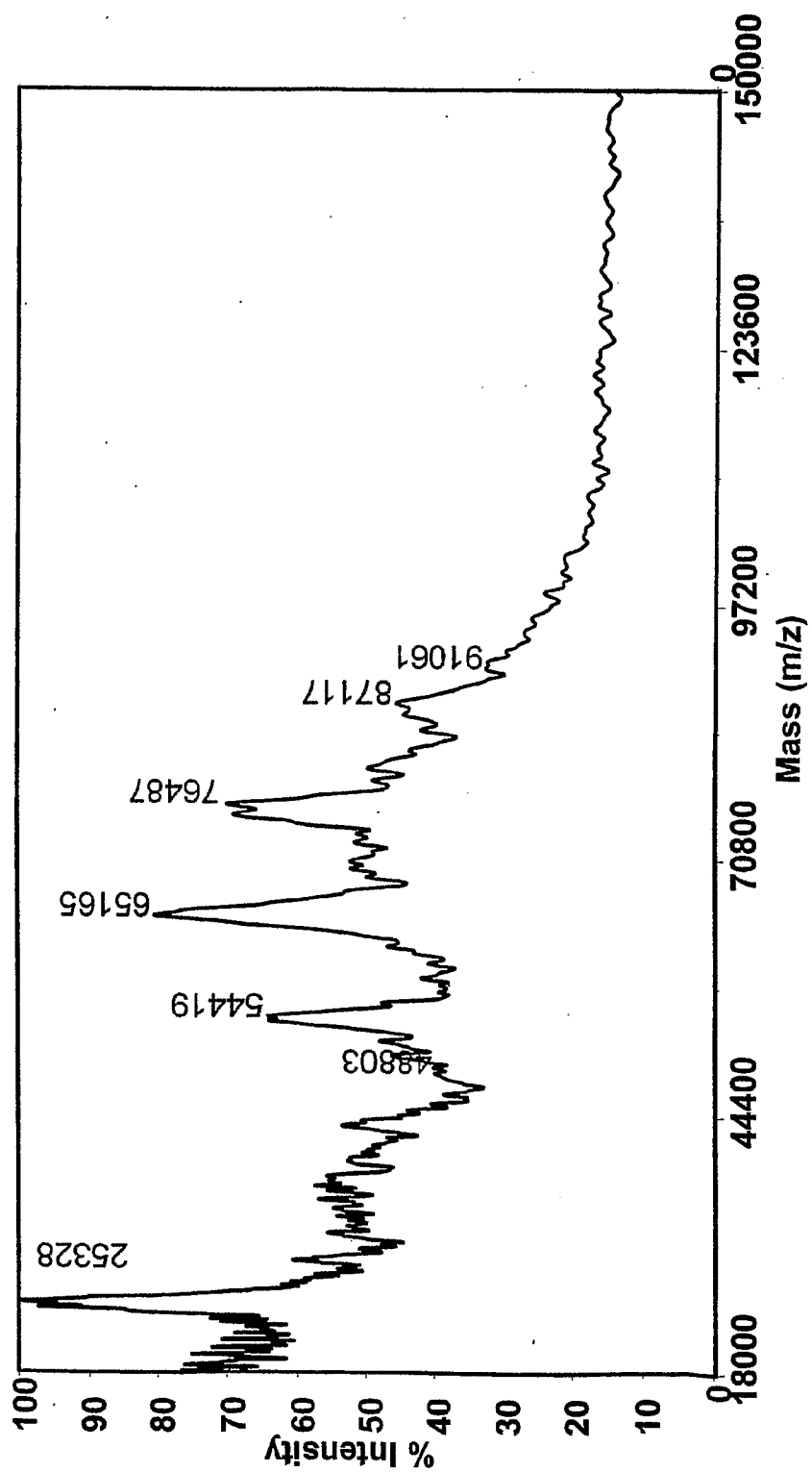


FIG. 160

462/498



FIG. 161

463/498

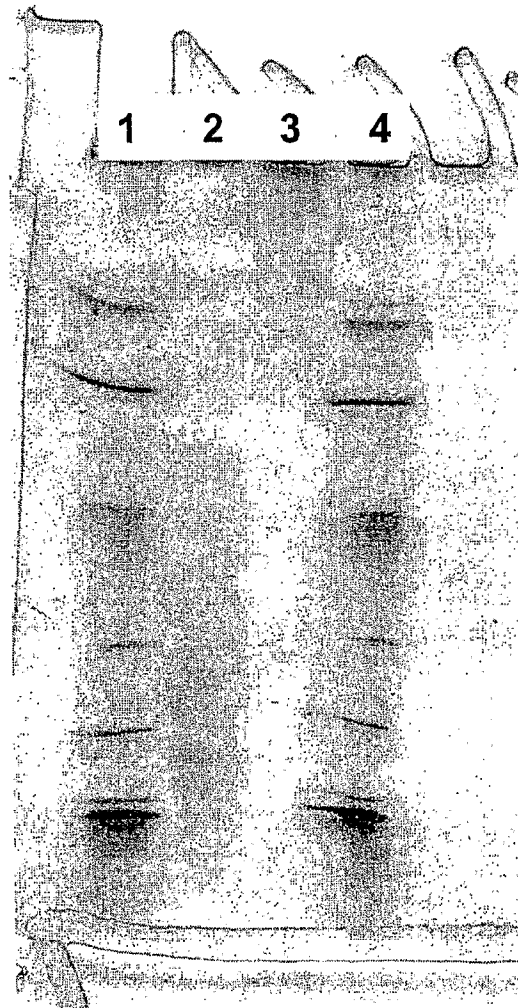


FIG. 162

464/498

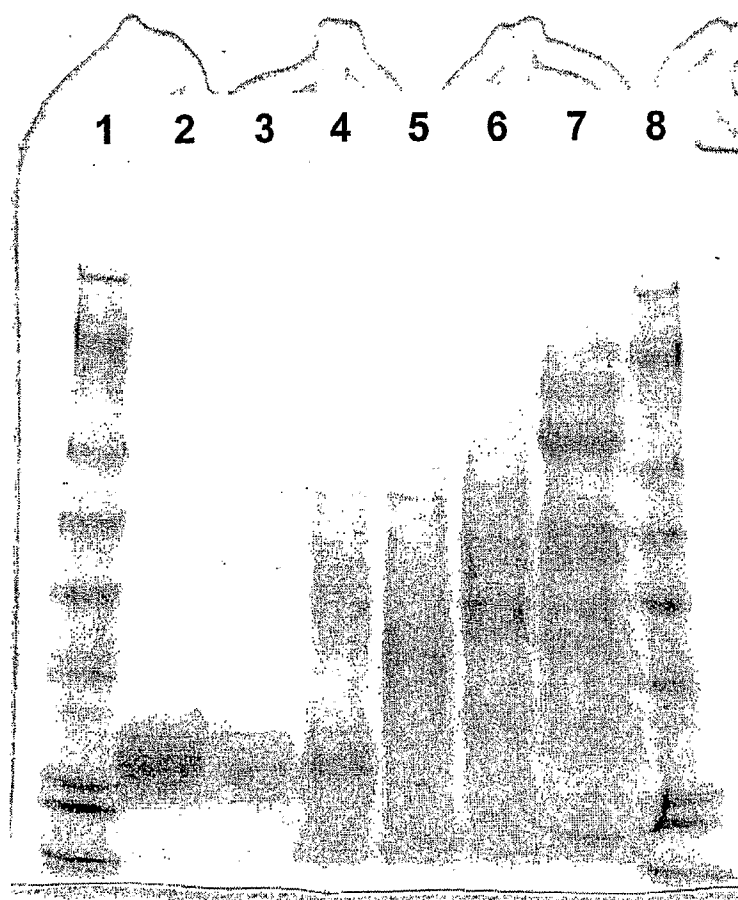


FIG. 163

465/498



FIG. 164

466/498



FIG. 165

467/498

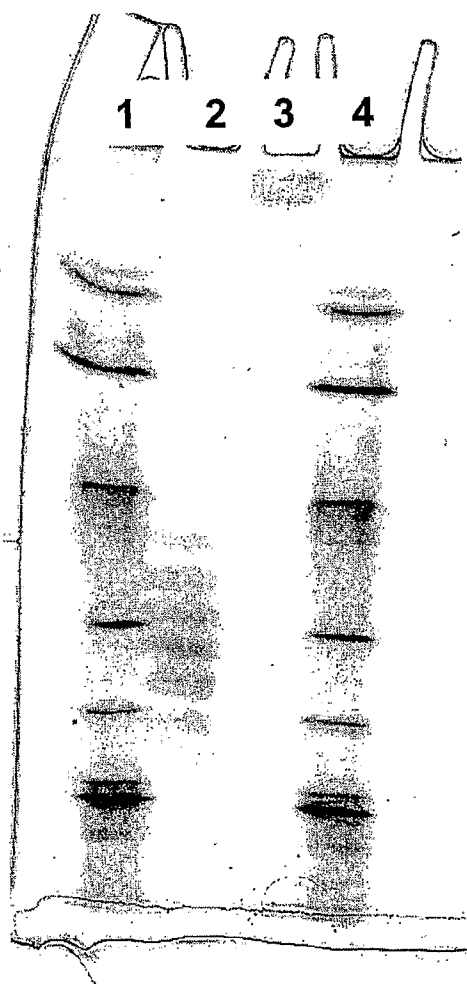


FIG. 166

468/498

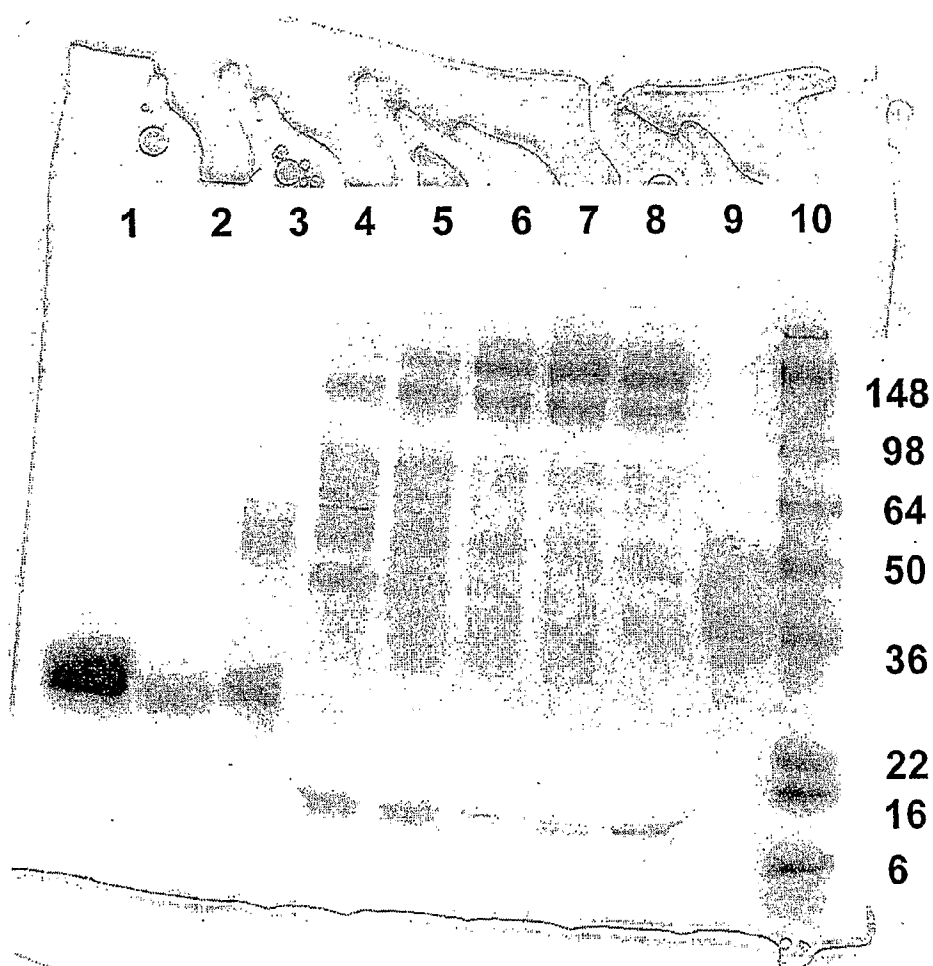


FIG. 167



469/498

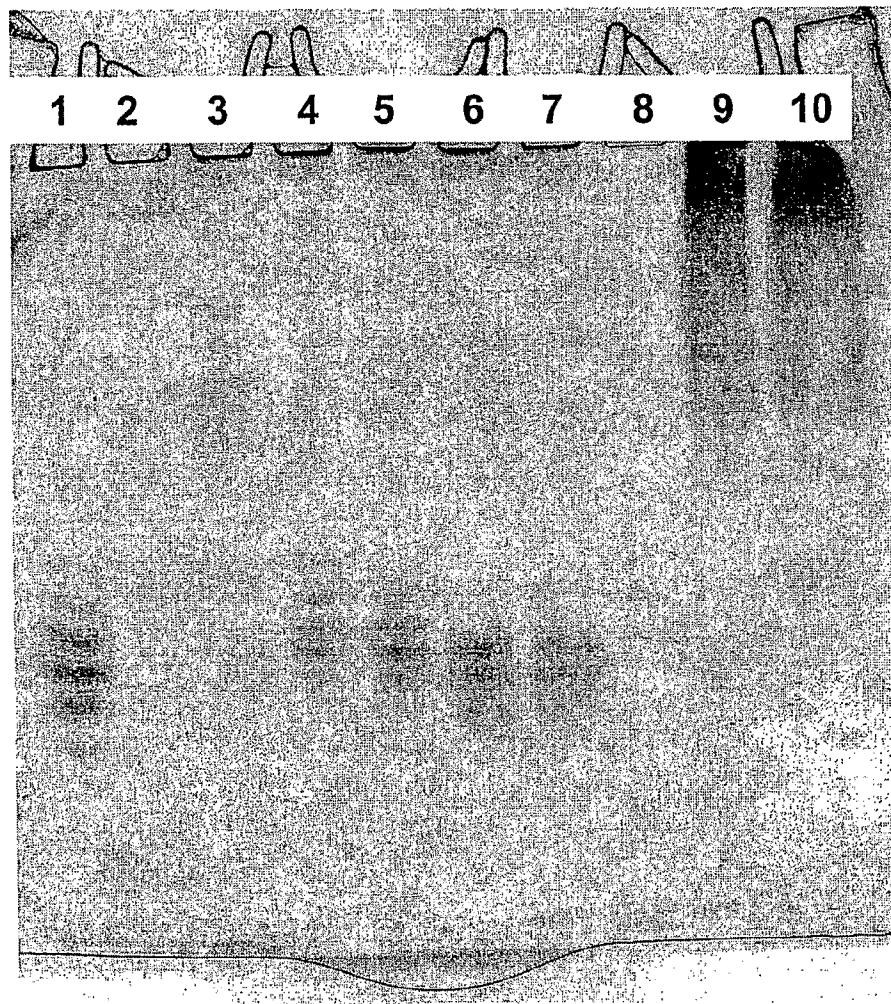


FIG. 168

470/498

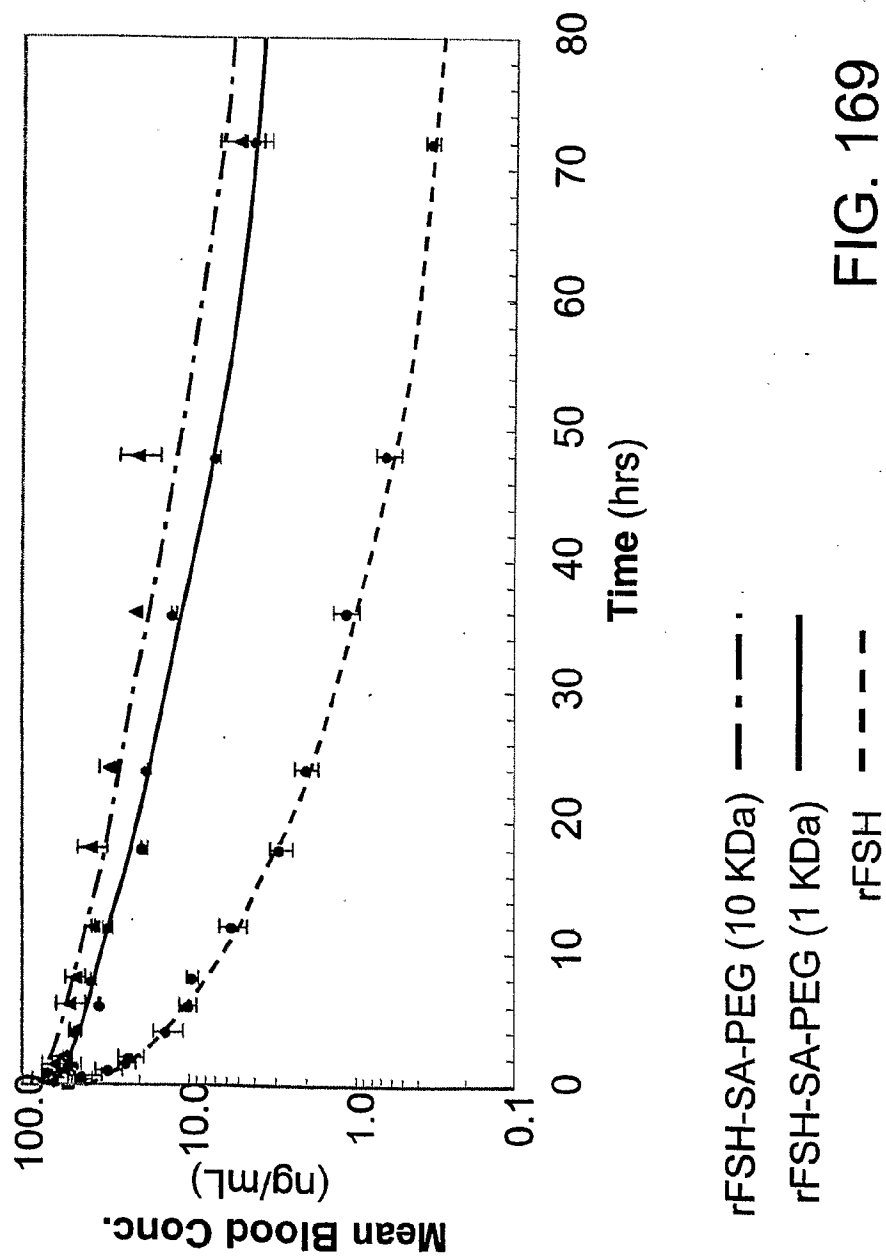


FIG. 169

471/498

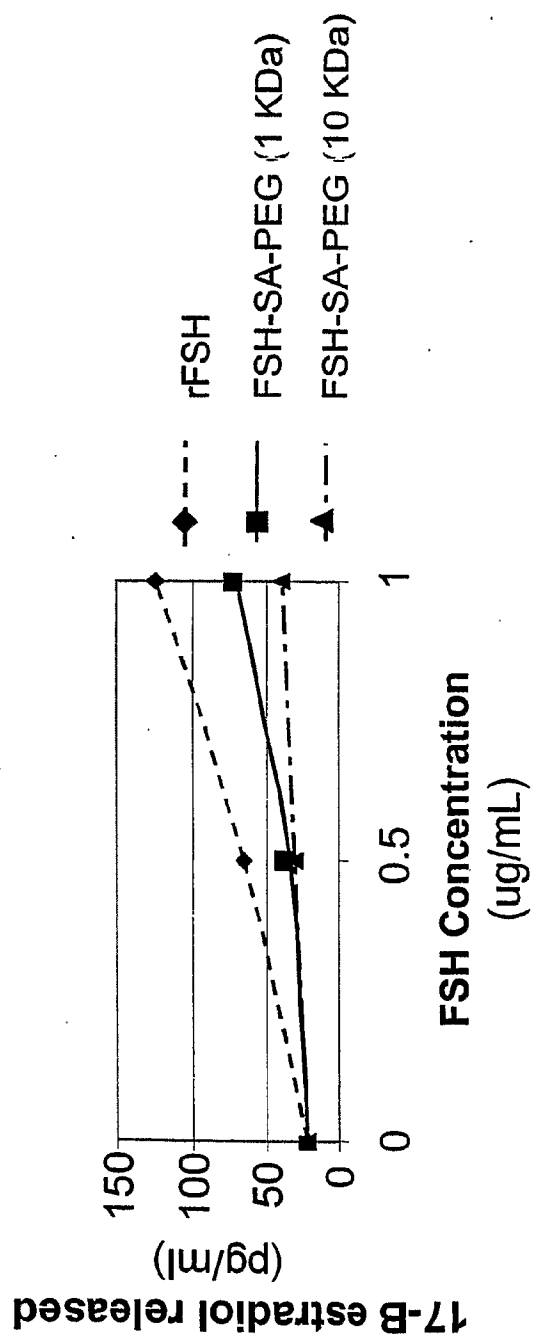


FIG. 170

472/498

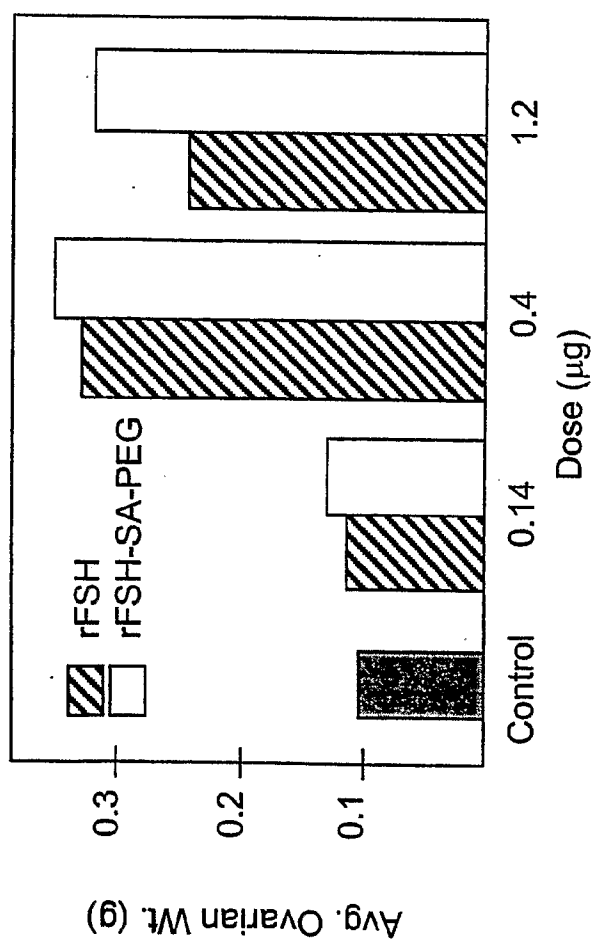


FIG. 171

473/498

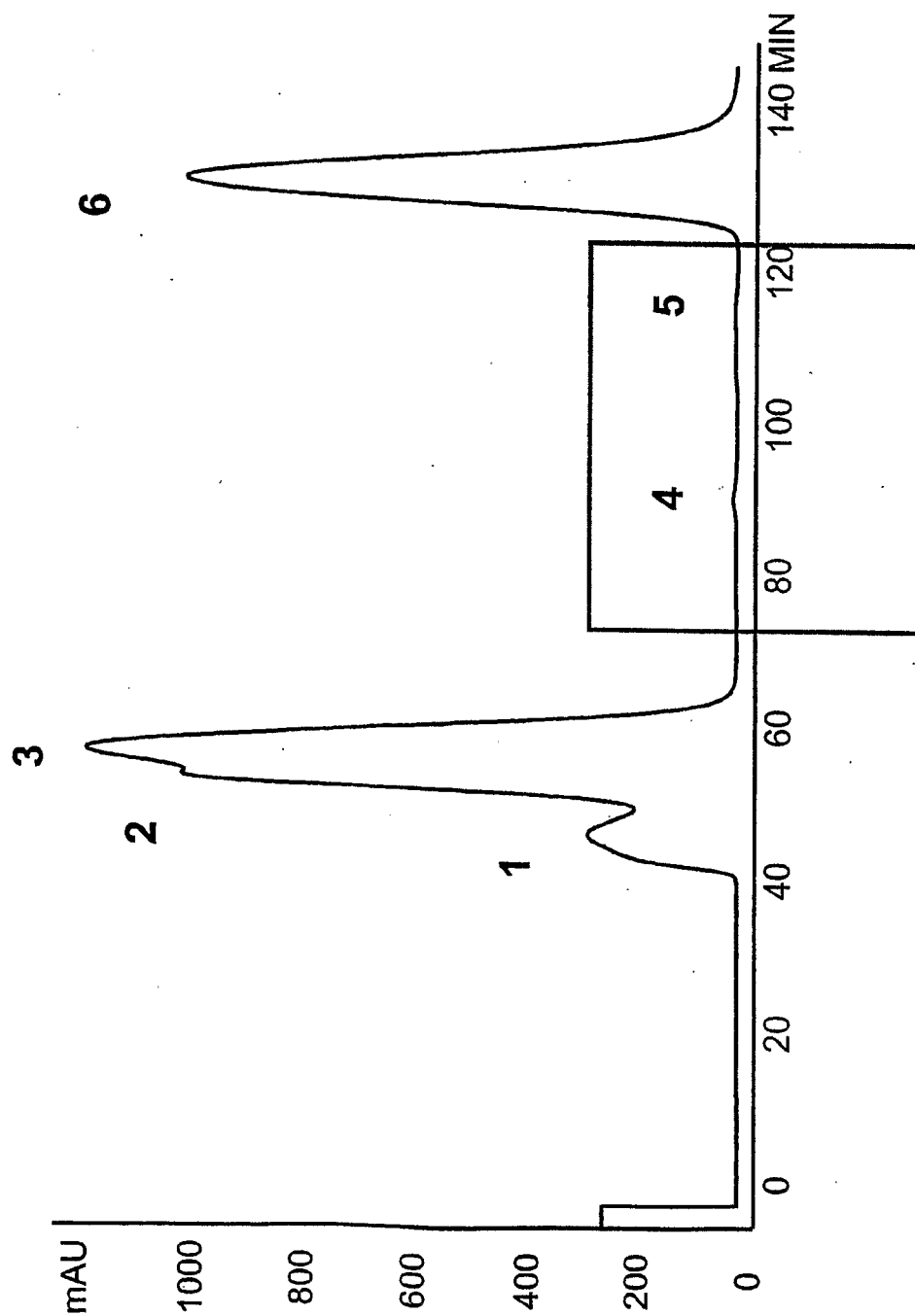


FIG. 172A

474/498

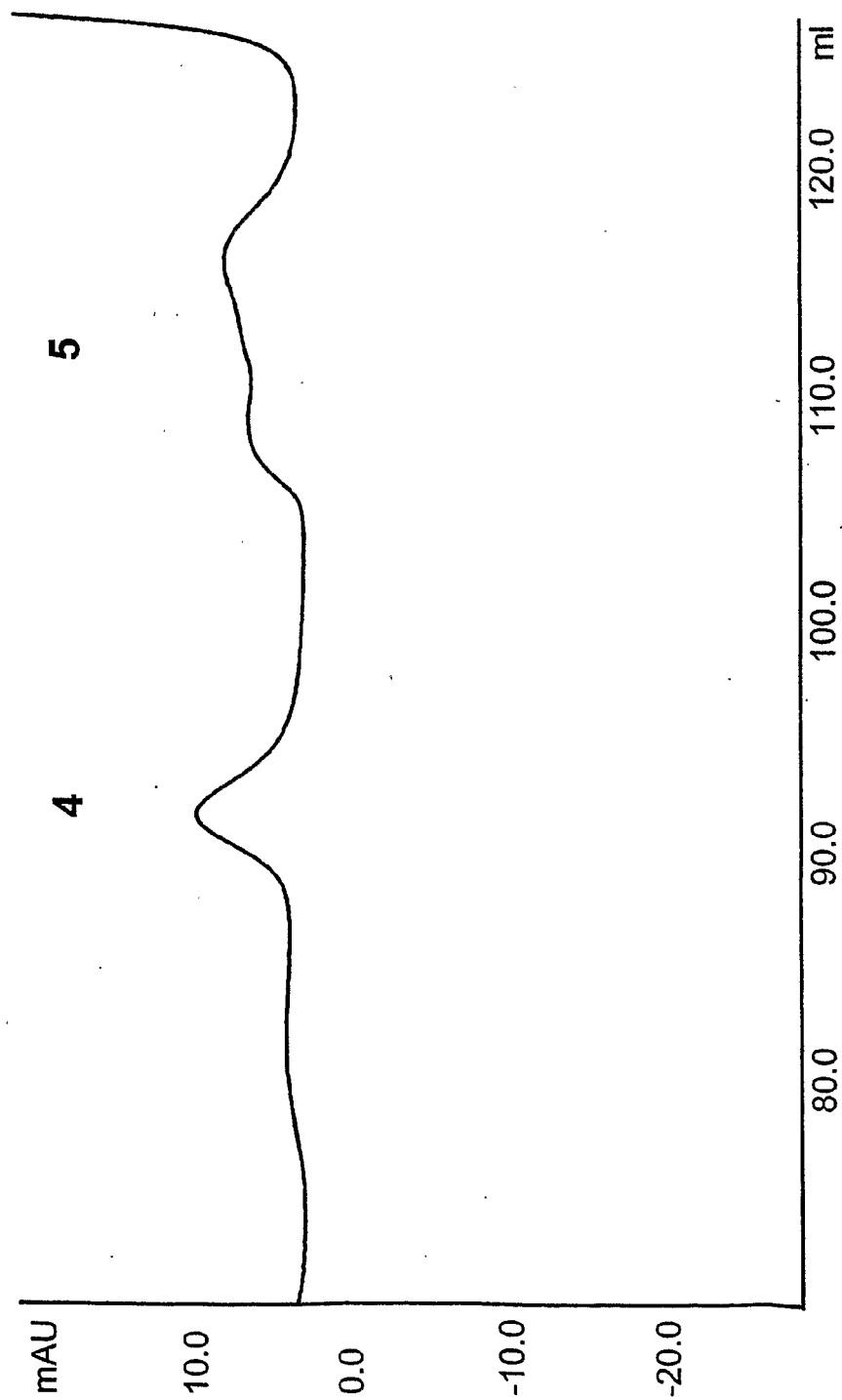


FIG. 172B

475/498

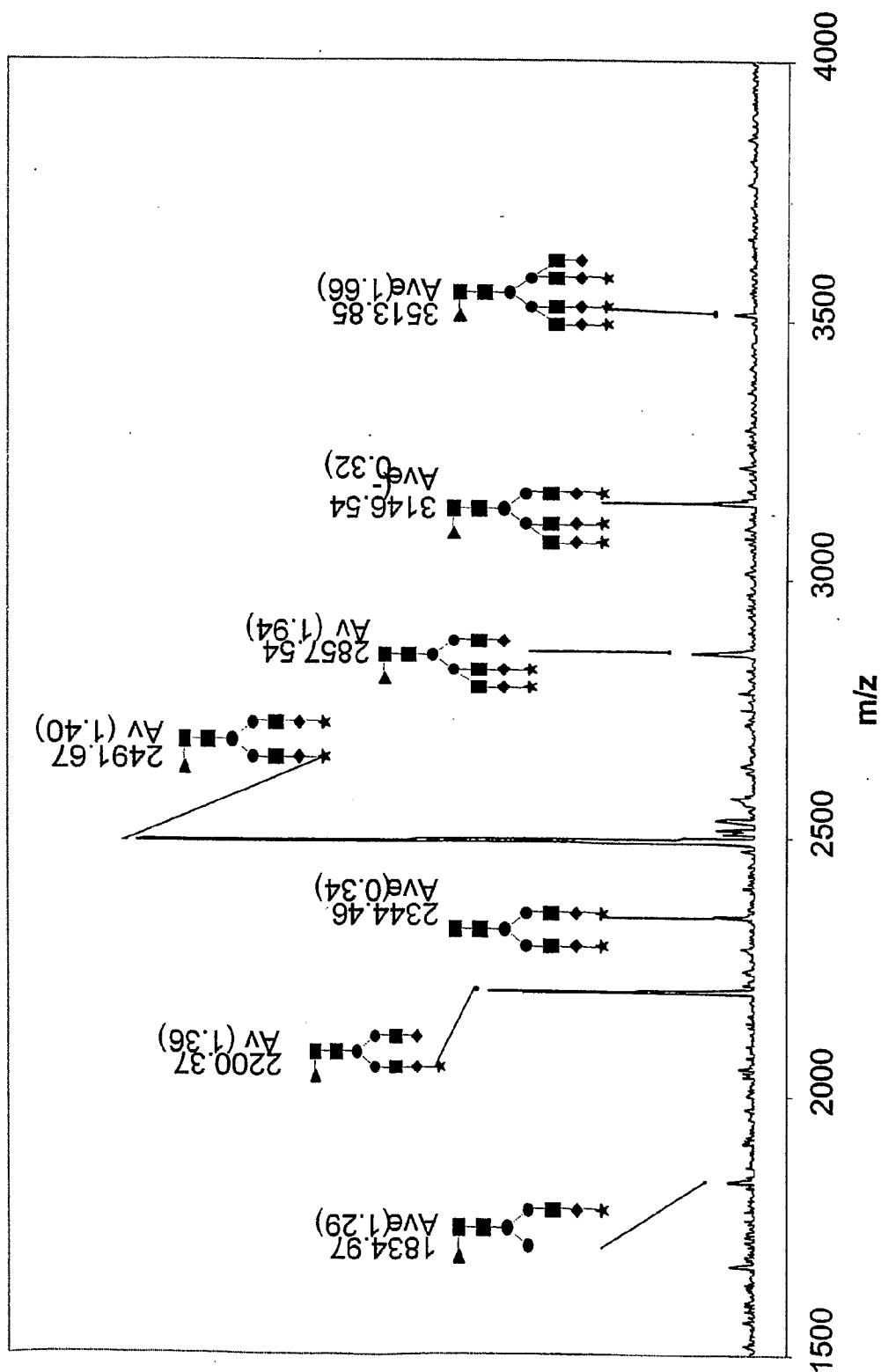


FIG. 173A

476/498

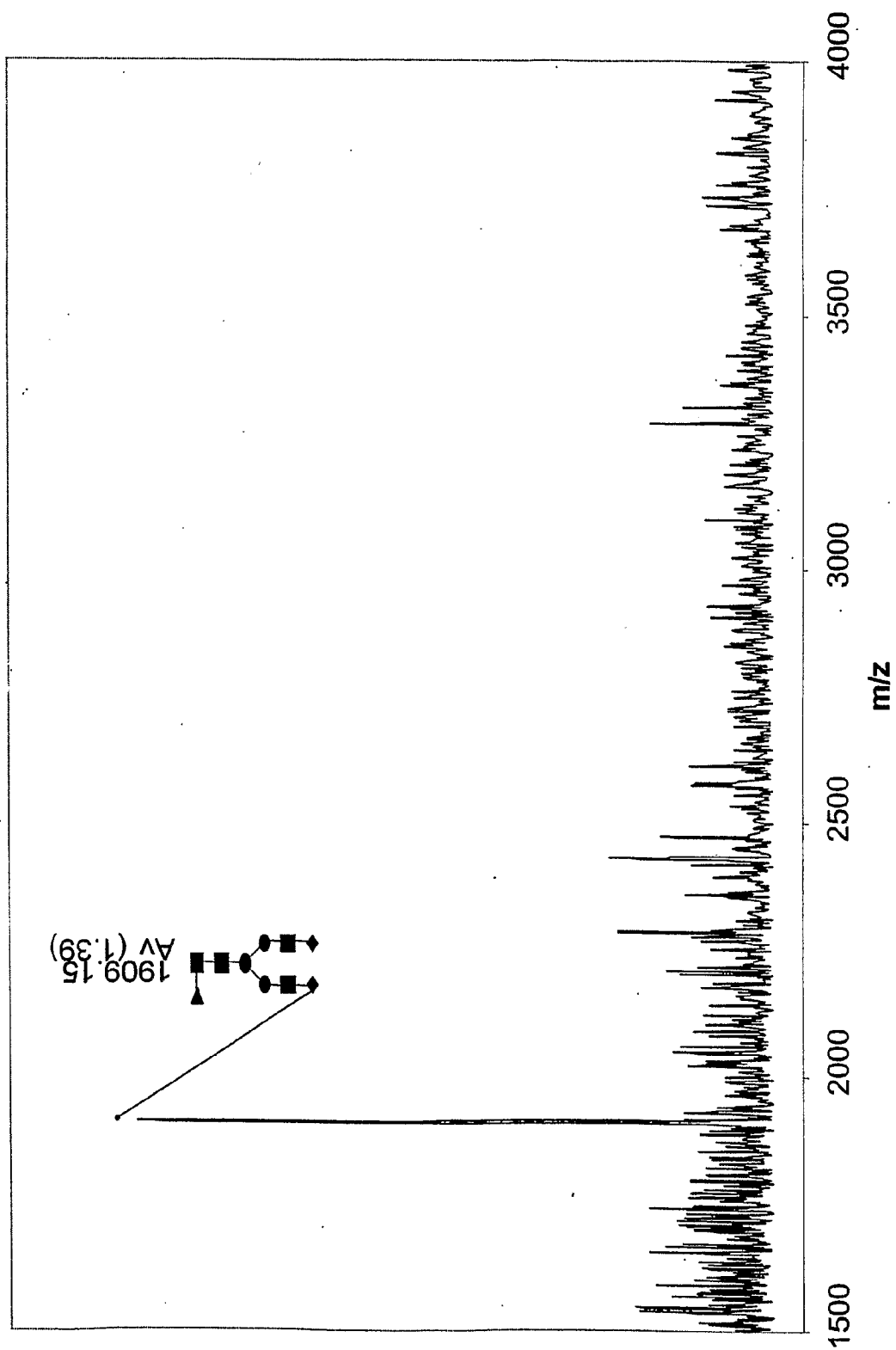


FIG. 173B



477/498

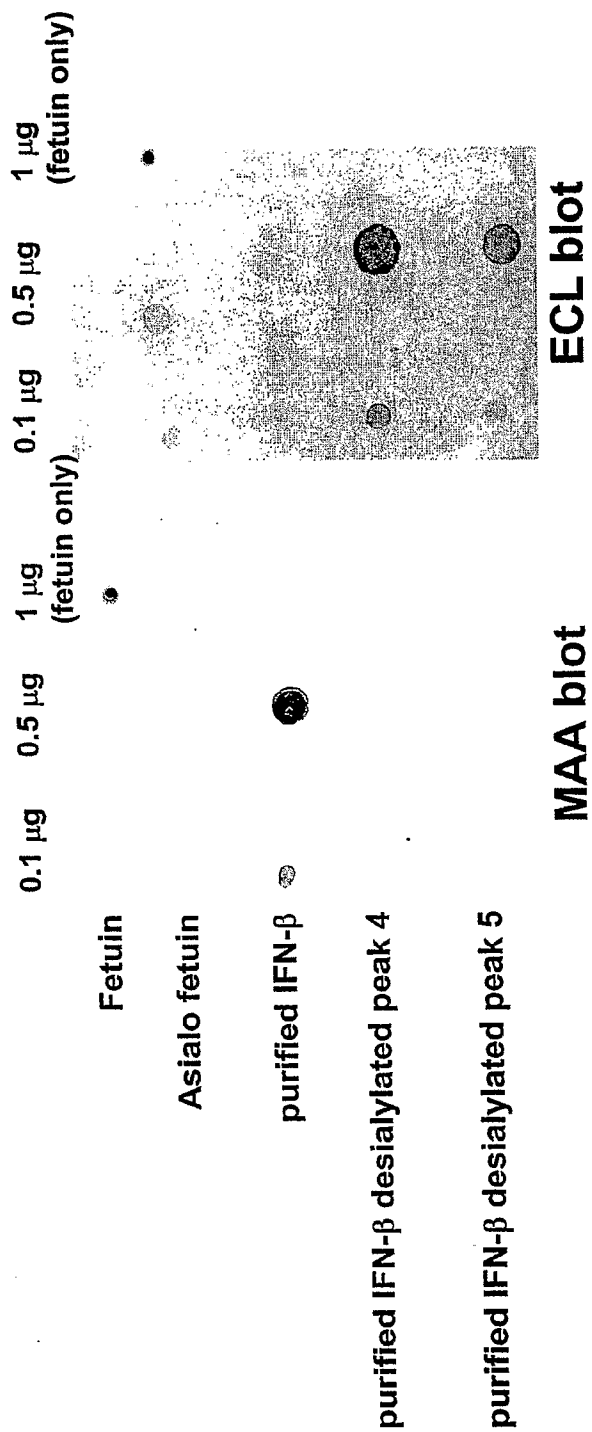


FIG. 174

478/498

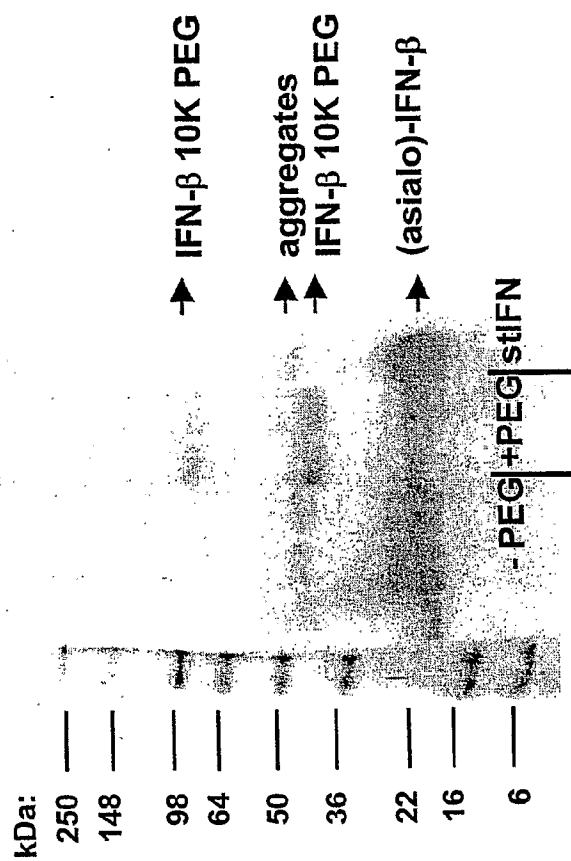


FIG. 175

479/498

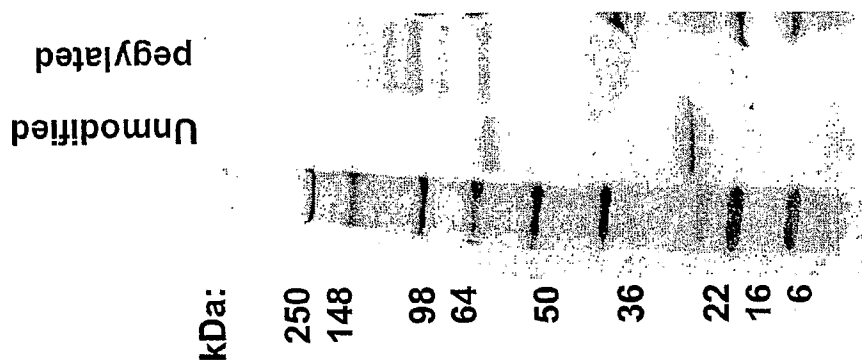


FIG. 176

480/498

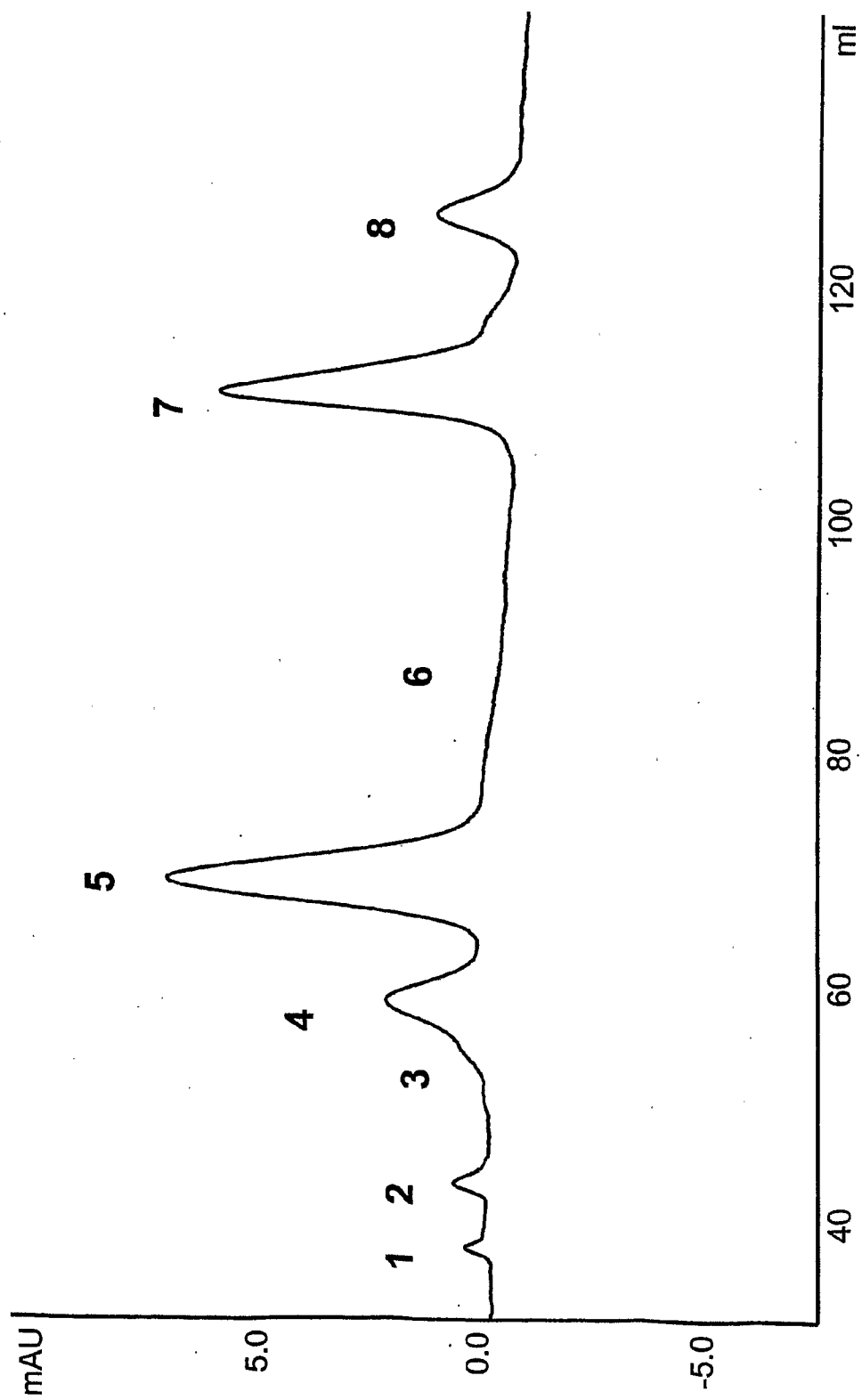


FIG. 177

481/498

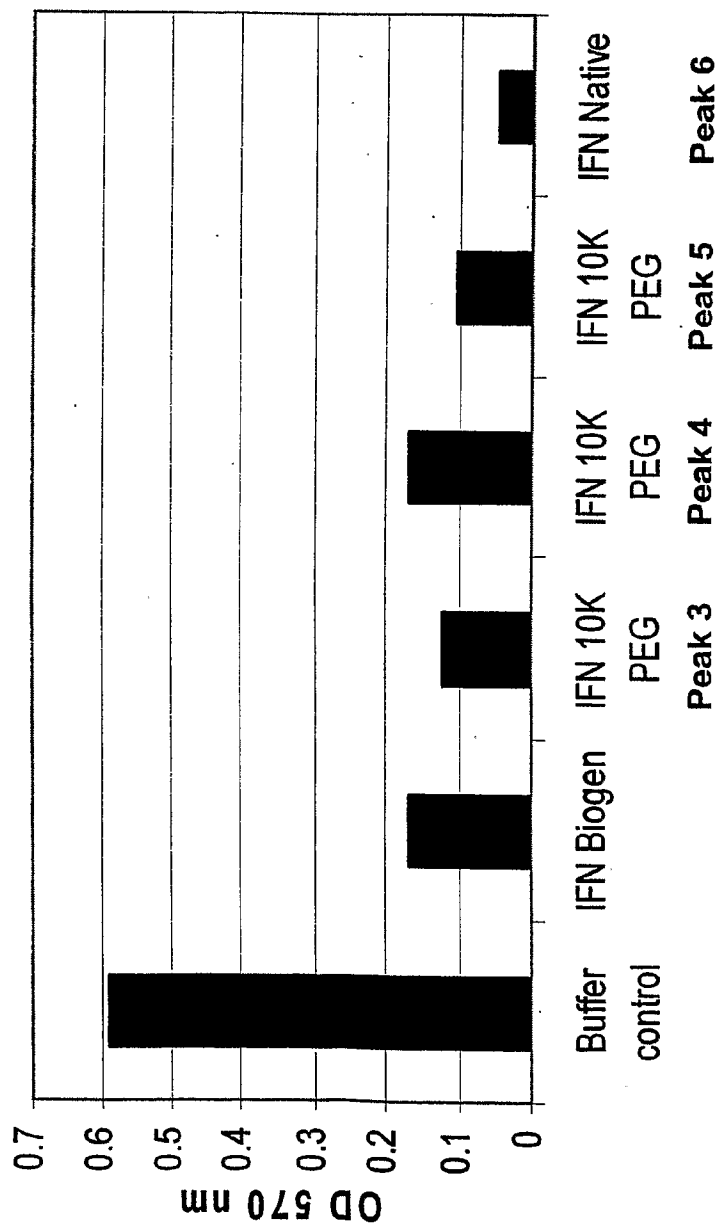


FIG. 178

482/498

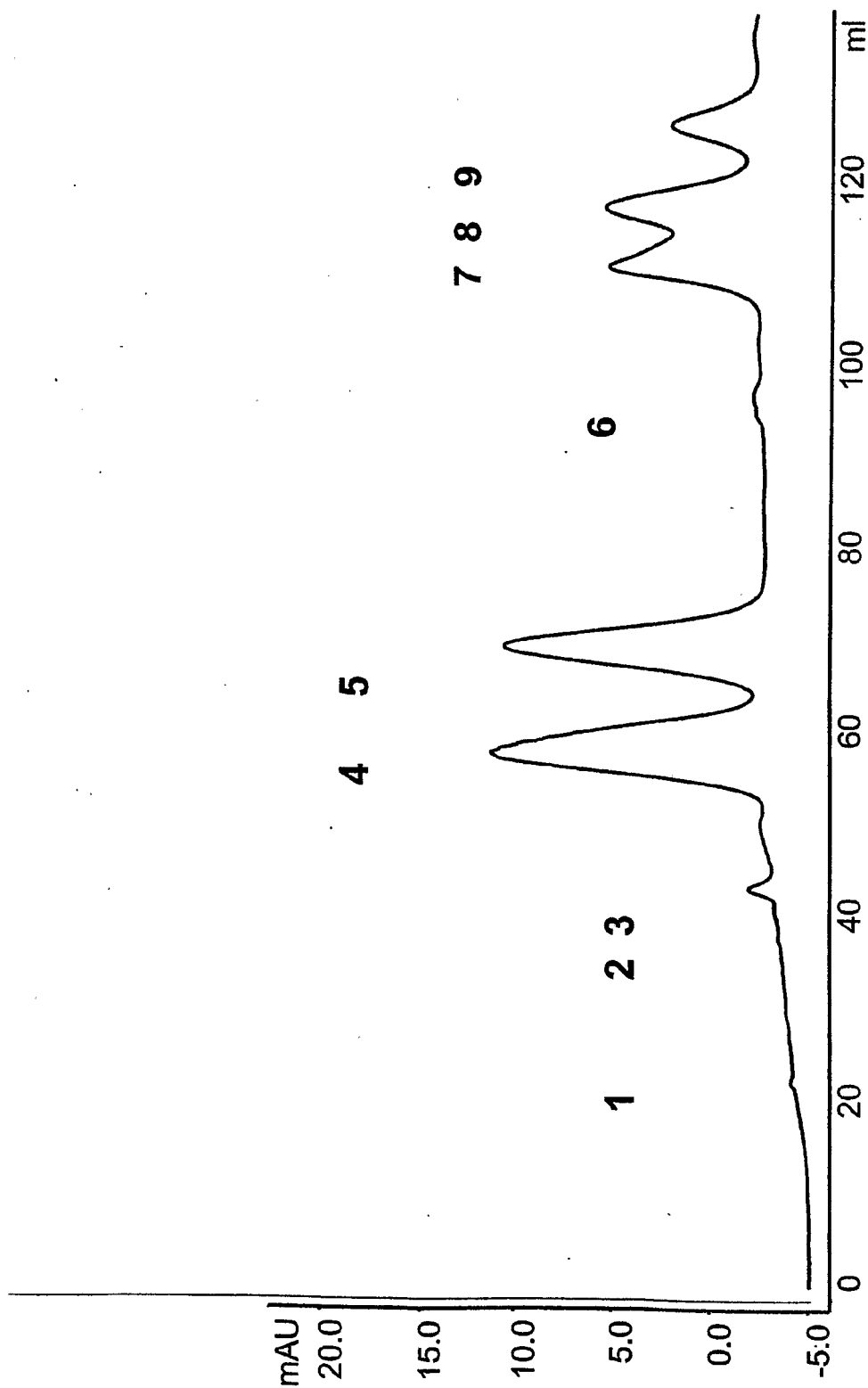


FIG. 179

483/498

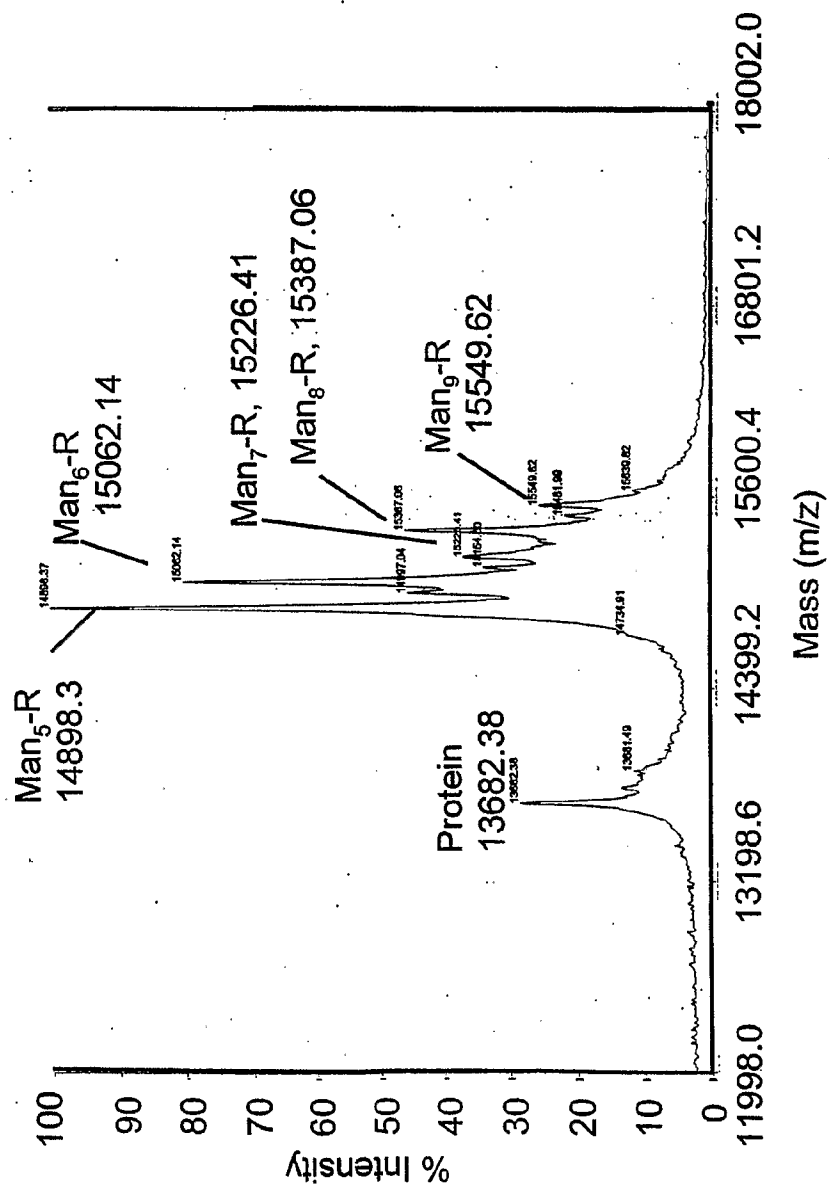


FIG. 180A

484/498

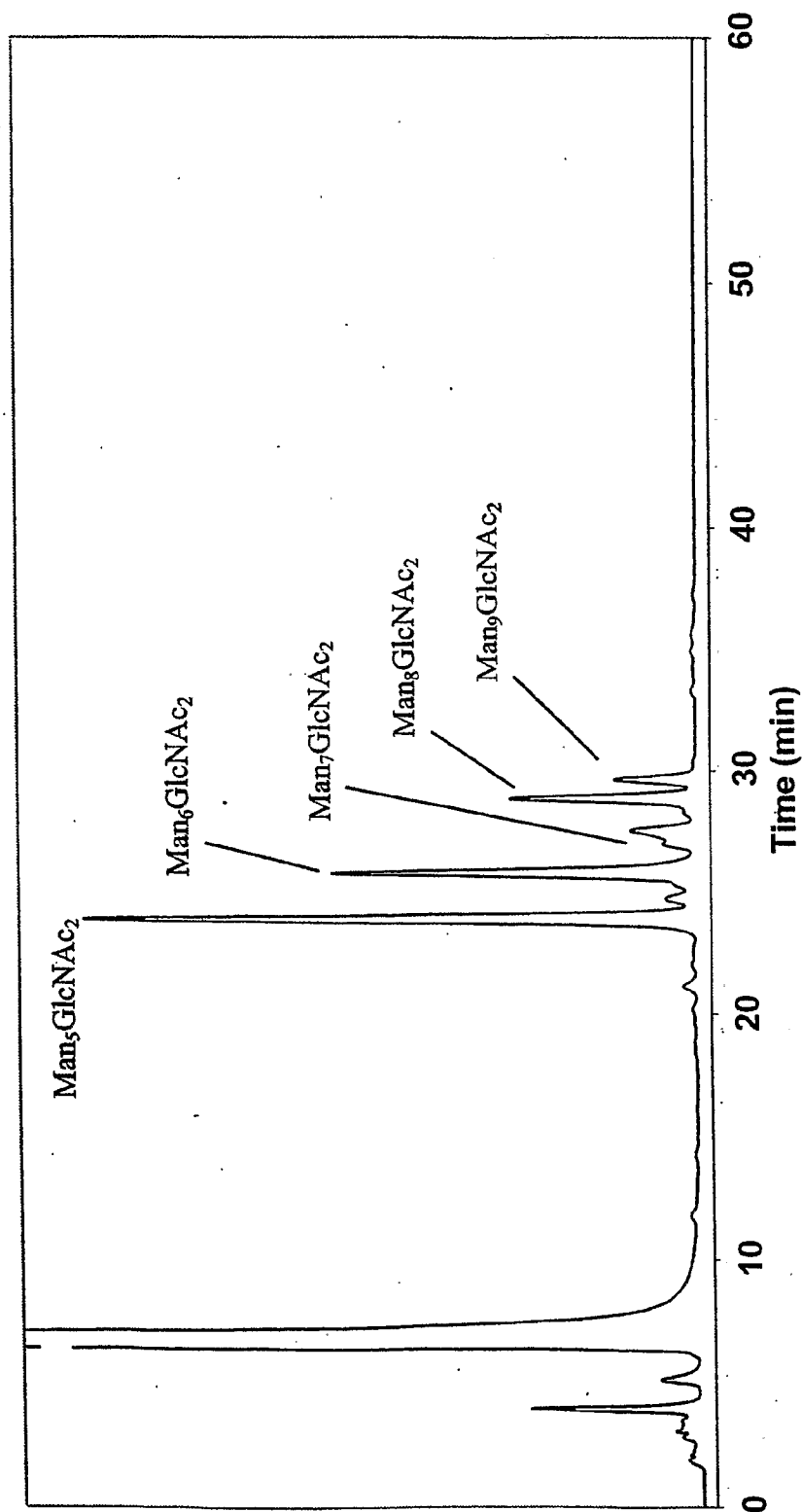


FIG. 180B



485/498

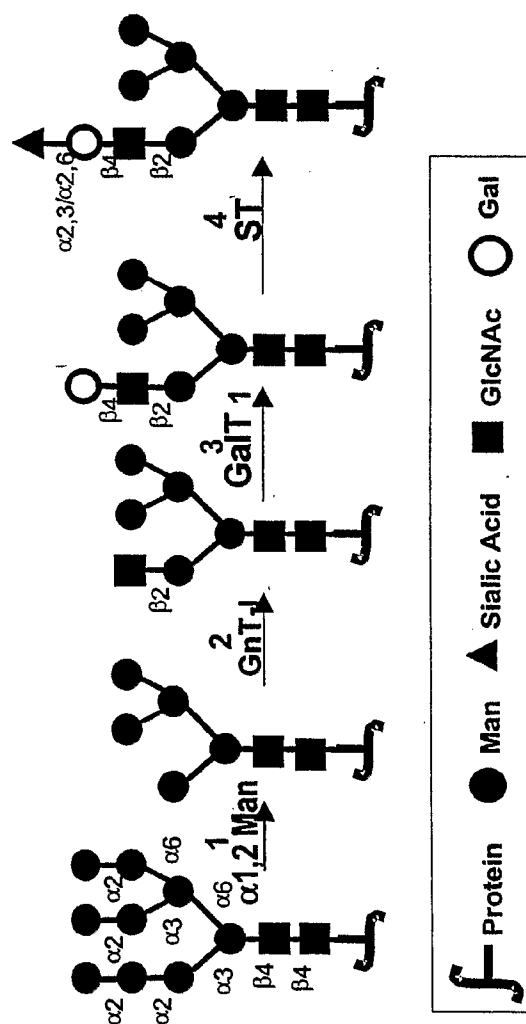


FIG. 181

486/498

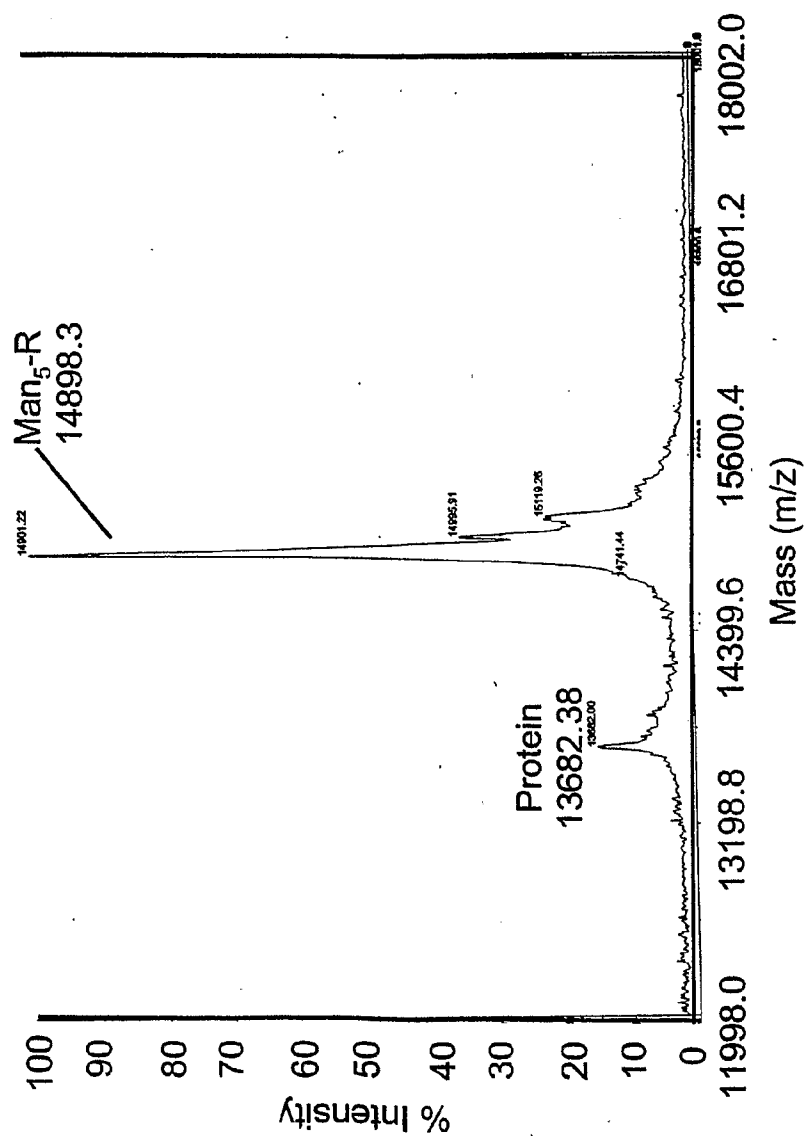


FIG. 182A

487/498

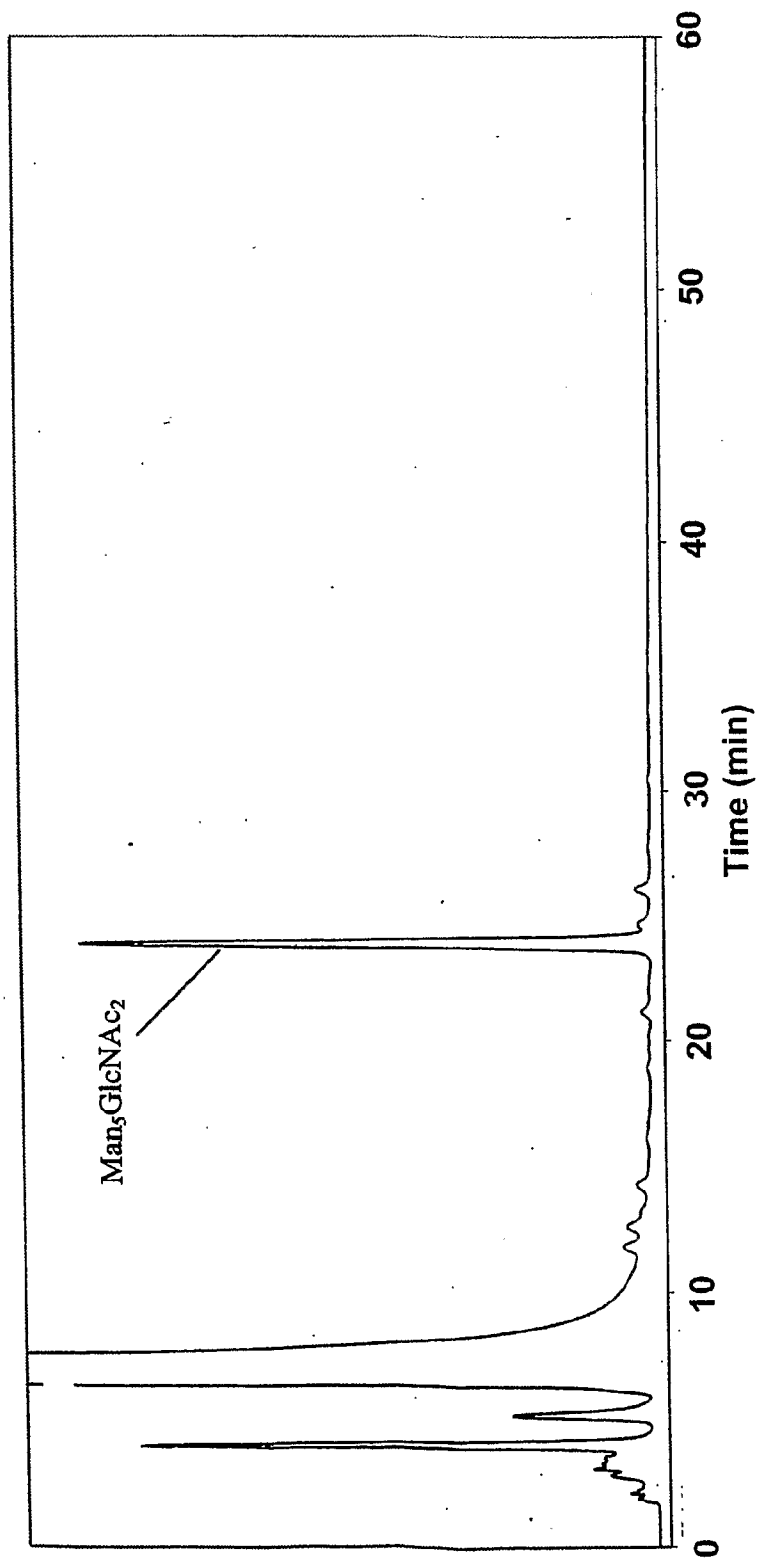


FIG. 182B

488/498

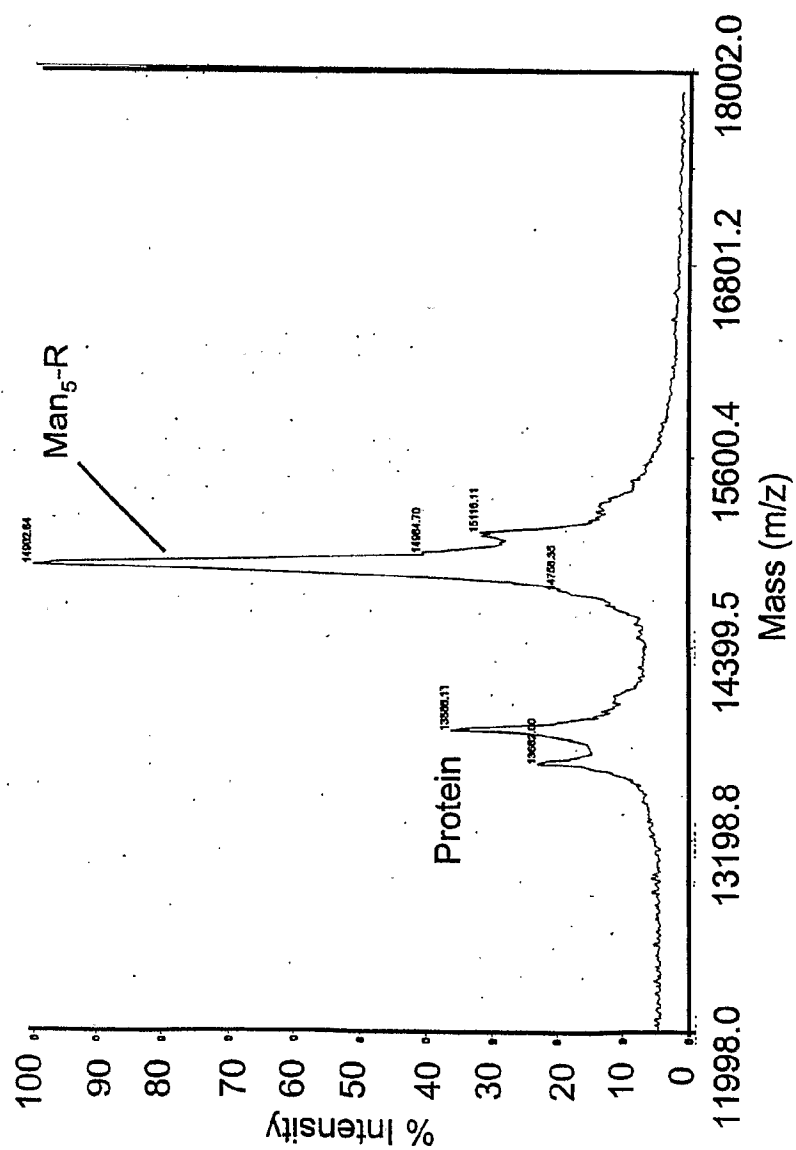


FIG. 183

489/498

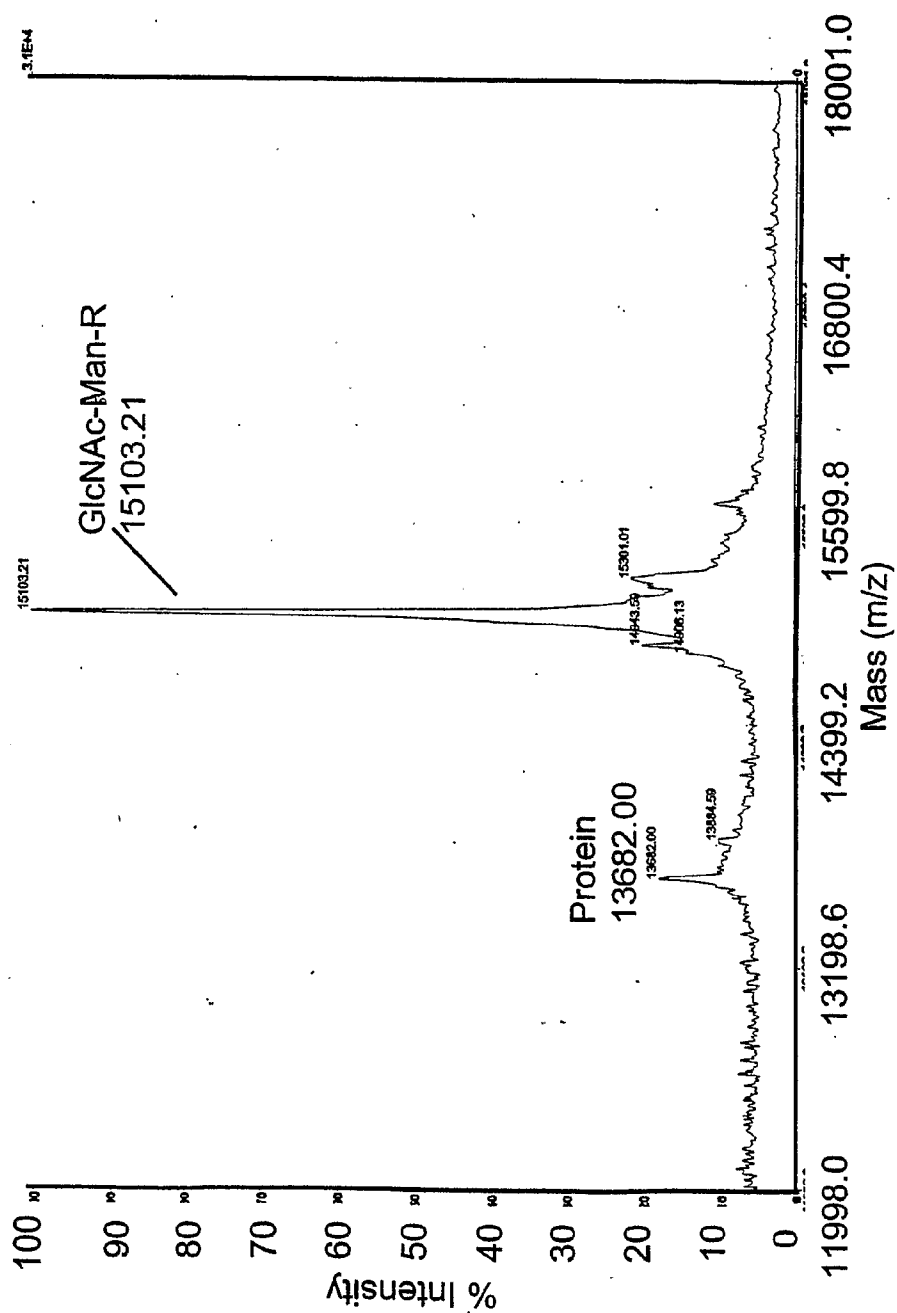


FIG. 184

490/498

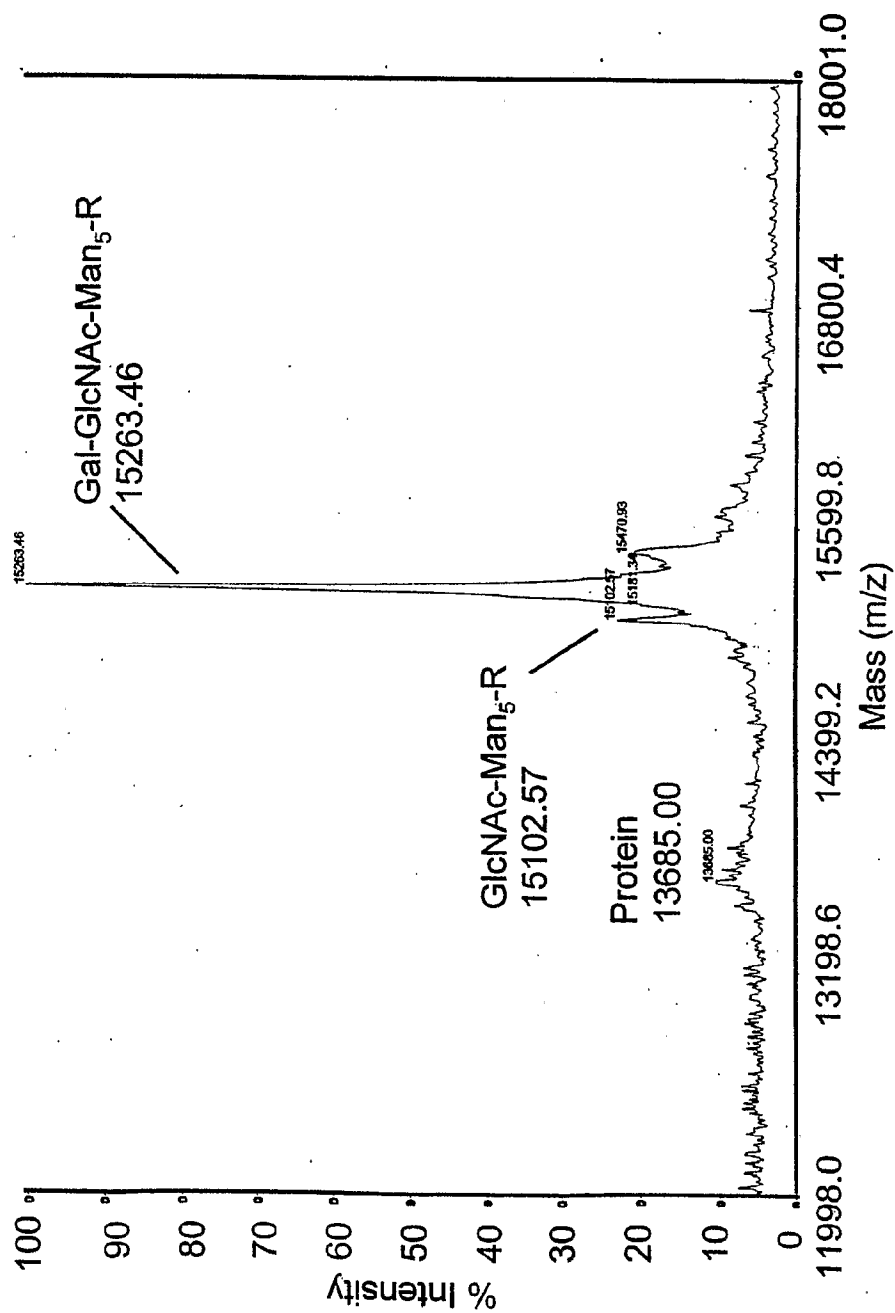


FIG. 185

491/498

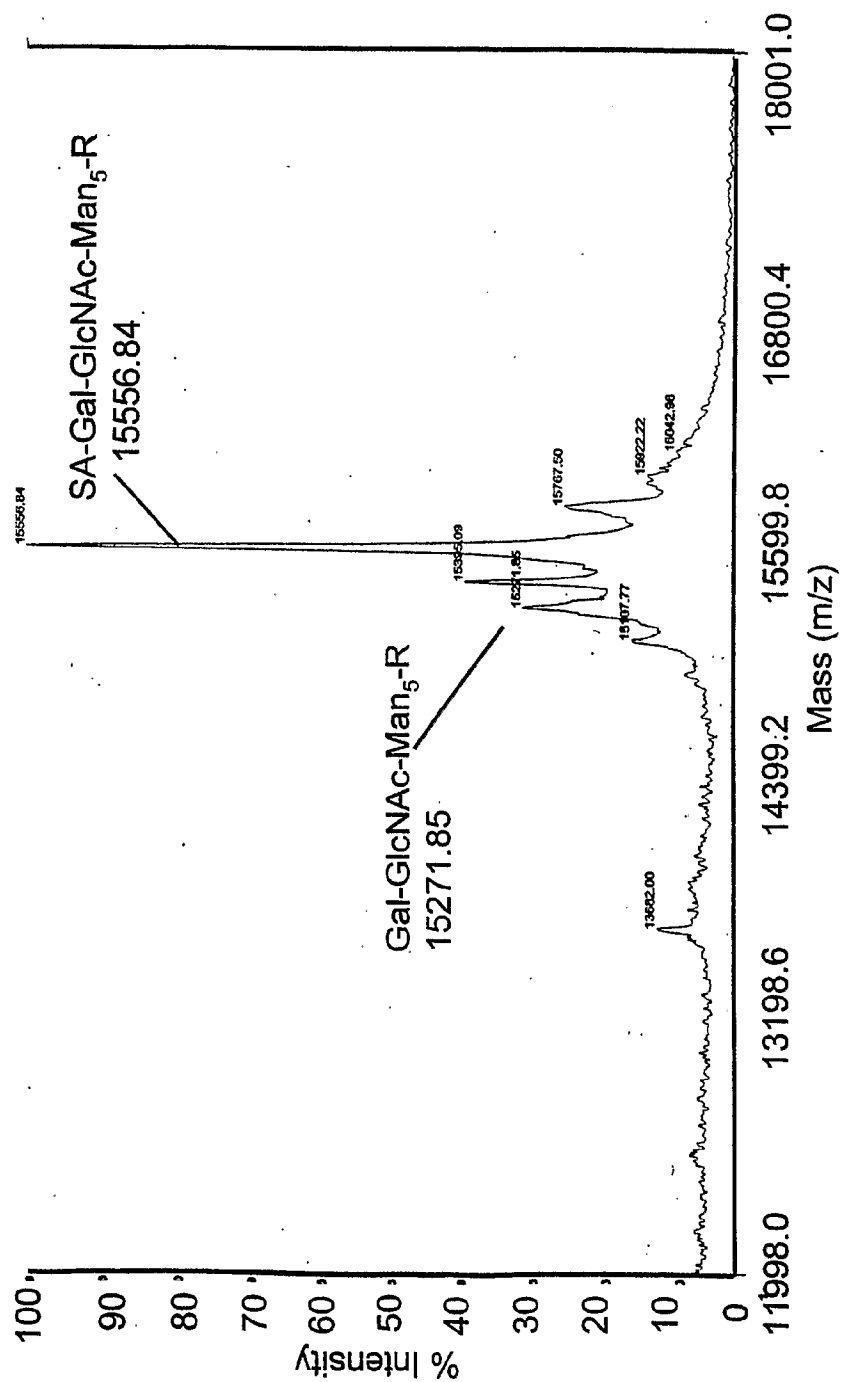


FIG. 186





493/498

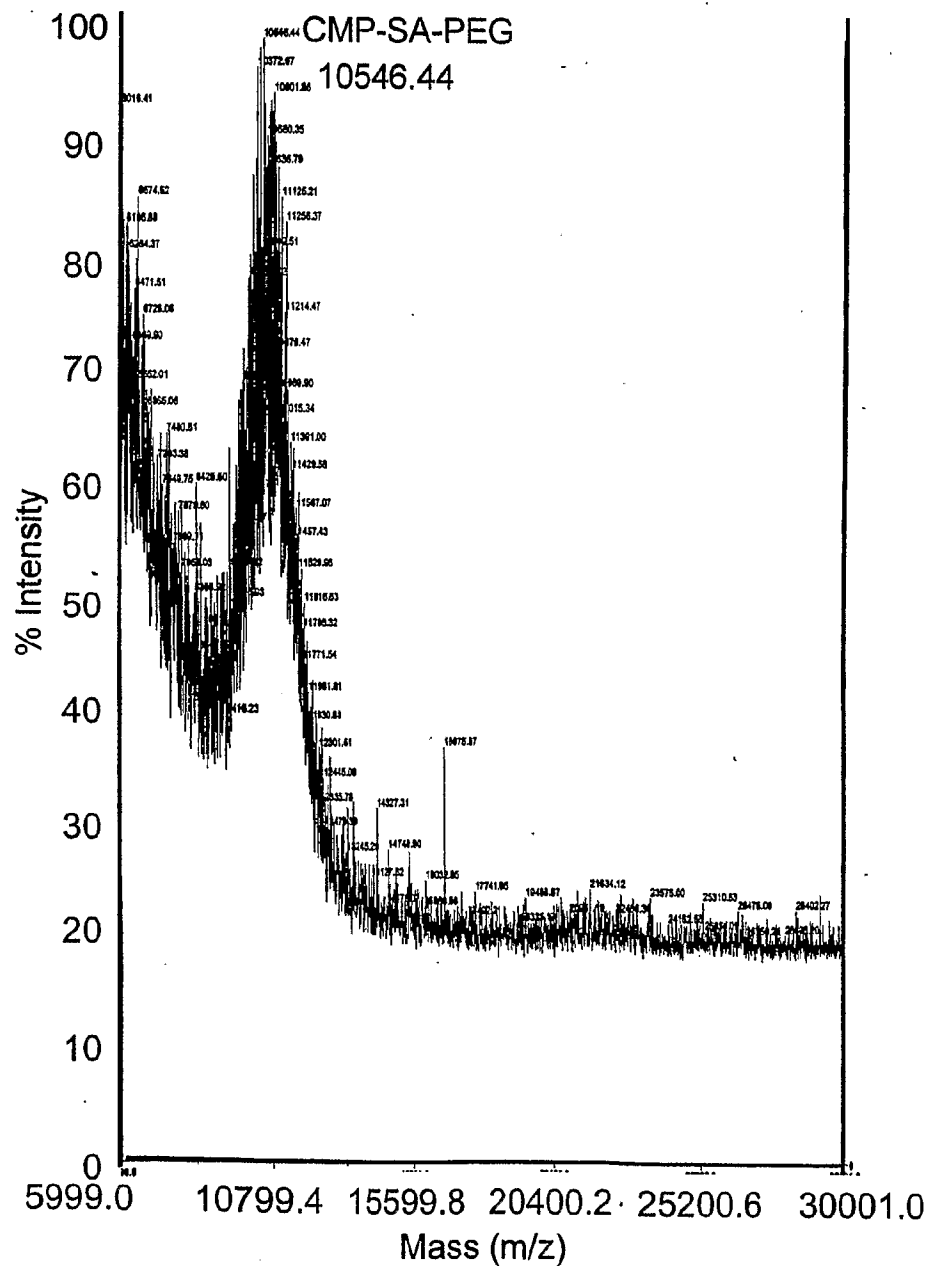


FIG. 187B

494/498

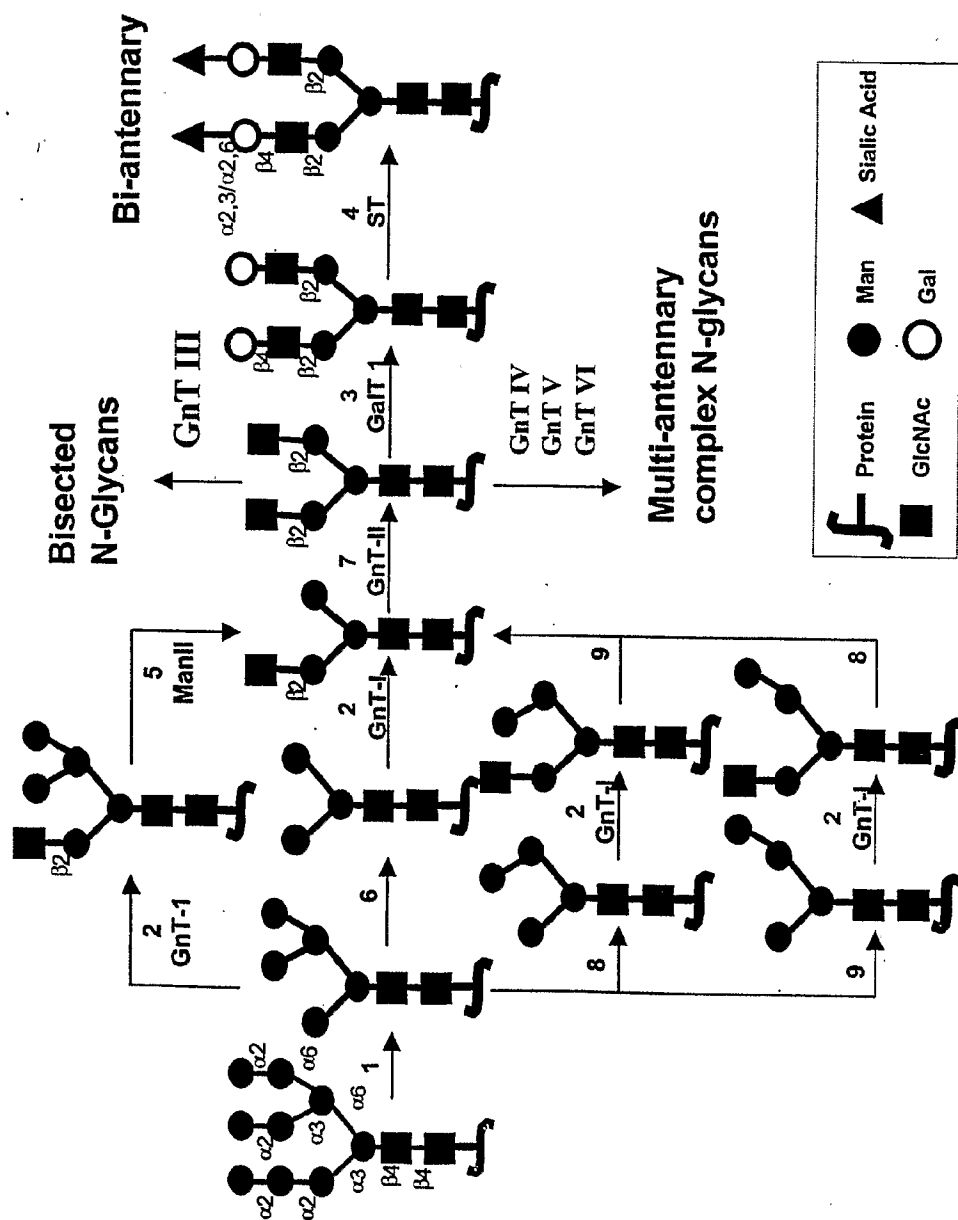


FIG. 188

495/498

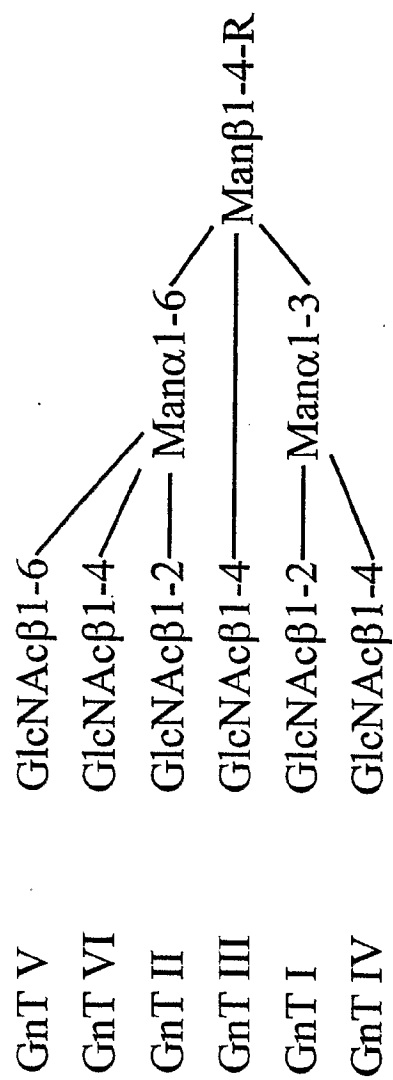


FIG. 189

496/498

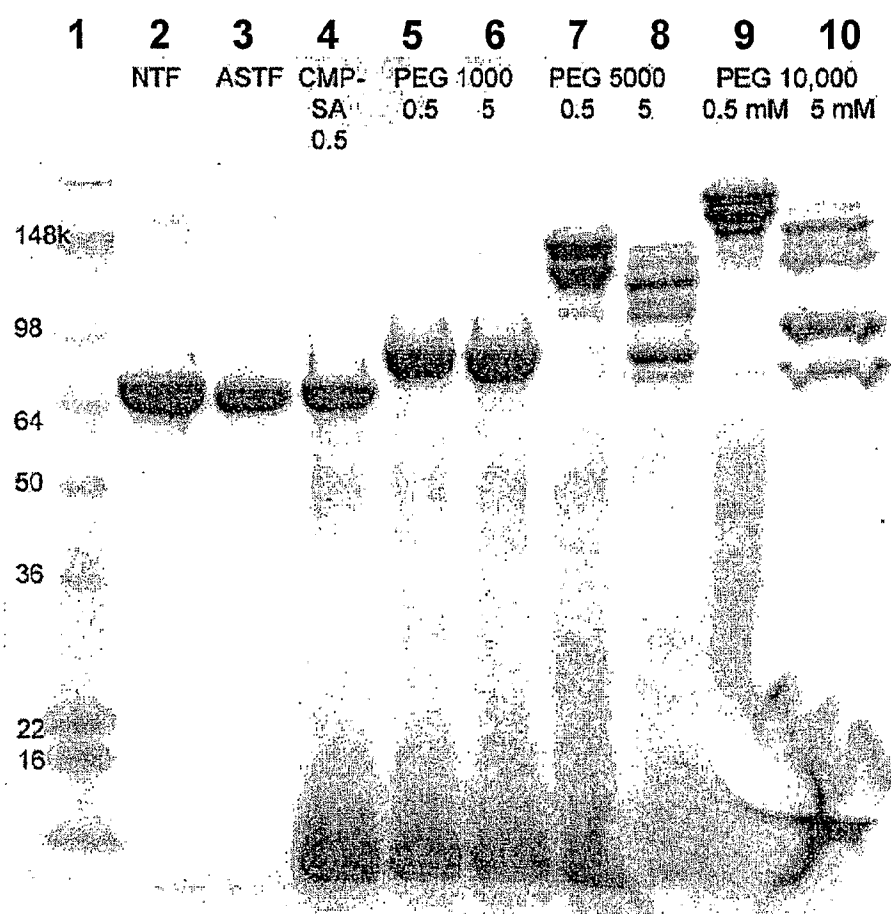


FIG. 190

497/498

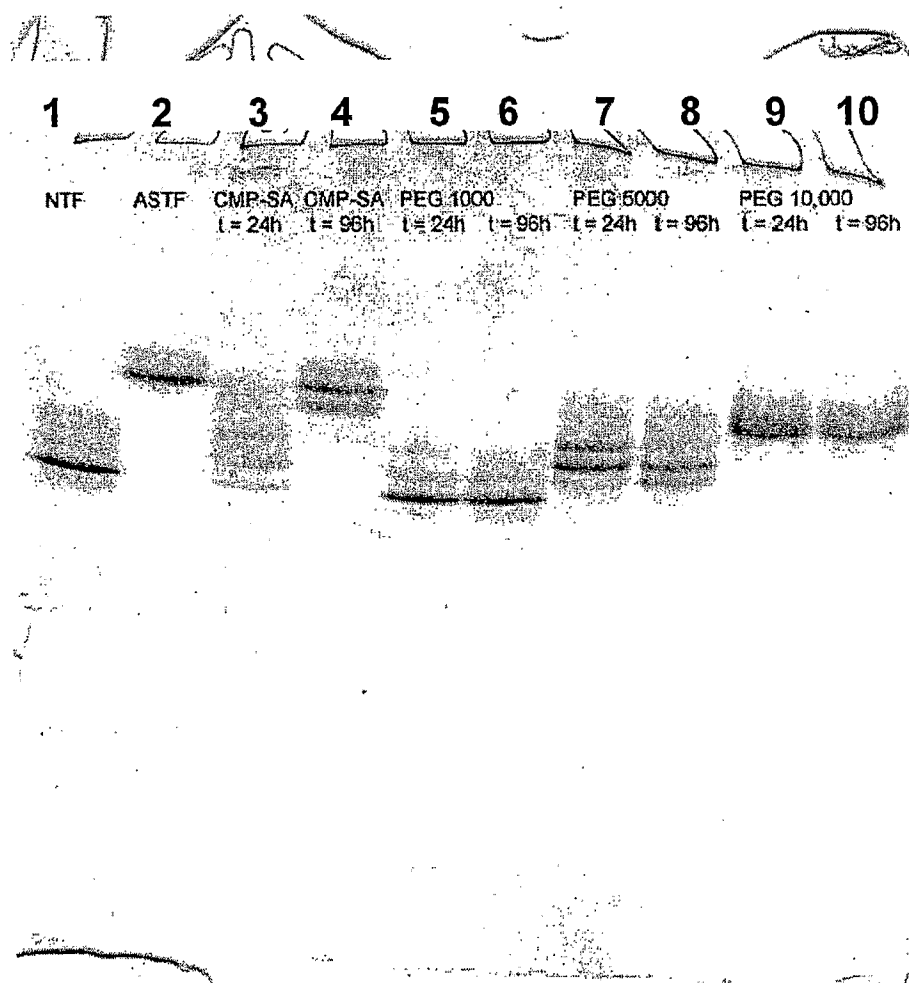
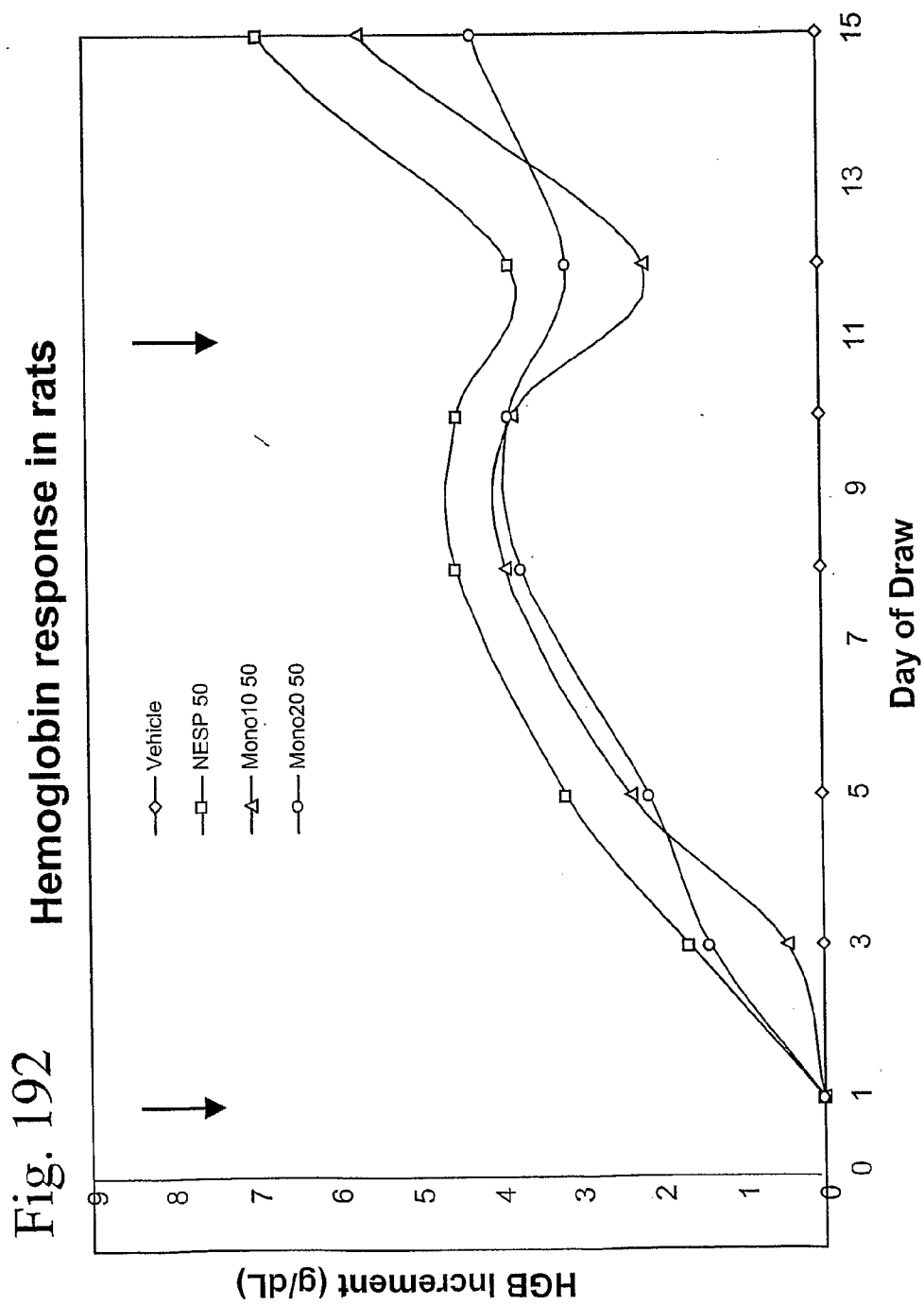


FIG. 191

498/498



## SEQUENCE LISTING

<110> Neose Technologies, Inc.  
 DeFrees, Shawn  
 Zopf, David  
 Bayer, Robert  
 Hakes, David  
 Chen, Xi  
 Bowe, Caryne

<120> ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF  
 ERYTHROPOIETIN

<130> 040853-01-5083WO

<150> PCT/US02/32263  
 <151> 2002-10-09

<150> US 10/287,994  
 <151> 2002-11-5

<150> US 10/360,770  
 <151> 2003-01-06

<150> US 10/369,779  
 <151> 2003-03-17

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 <151> 2003-04-09

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 50 55 60  
 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
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 85 90 95  
 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
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 115 120 125  
 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
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 145 150 155 160  
 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
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&lt;211&gt; 1733

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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 Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser  
 35 40 45  
 Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu  
 50 55 60  
 Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His  
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 Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser

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Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr					
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Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val					
	115		120		125
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys					
	130		135		140
Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro					
	145		150		155
Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu					
	165		170		175
Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu					
	180		185		

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 <211> 757  
 <212> DNA  
 <213> Homo sapiens

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<210> 6  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
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 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg  
 35 40 45  
 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu  
 50 55 60  
 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile  
 65 70 75 80  
 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser  
 85 90 95  
 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
 100 105 110  
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu  
 115 120 125  
 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys  
 130 135 140  
 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser  
 145 150 155 160  
 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr  
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 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn  
 180 185

<210> 7  
 <211> 1332  
 <212> DNA  
 <213> Homo sapiens

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<210> 8  
 <211> 444  
 <212> PRT  
 <213> Homo sapiens

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 Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro  
 35 40 45  
 Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu  
 50 55 60  
 Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile  
 65 70 75 80  
 Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly  
 85 90 95  
 Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro  
 100 105 110  
 Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile  
 115 120 125  
 Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr  
 130 135 140  
 Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala  
 145 150 155 160  
 Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile  
 165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val  
 180 185 190  
 Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu  
 195 200 205  
 Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile  
 210 215 220  
 Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg  
 225 230 235 240  
 Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly  
 245 250 255  
 Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr  
 260 265 270  
 Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln  
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 Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg  
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 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser  
 305 310 315 320  
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met  
 325 330 335  
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser  
 340 345 350  
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala  
 355 360 365  
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly  
 370 375 380  
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val  
 385 390 395 400  
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr  
 405 410 415  
 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu  
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 435 440

<210> 9  
 <211> 1437  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
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 ccatgtttta atggcggcag ttgcaaggat gacattaatt cctatgaatg ttgggtgtccc 360  
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<210> 10

<211> 462

<212> PRT

<213> Homo sapiens

<400> 10

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Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu  
 20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn  
 35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys

50	55	60
Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn 65 70 75 80		
Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln 85 90 95		
Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile 100 105 110		
Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys 115 120 125		
Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe 130 135 140		
Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly 145 150 155 160		
Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe 165 170 175		
Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala 180 185 190		
Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu 195 200 205		
Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe 210 215 220		
Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp 225 230 235 240		
Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile 245 250 255		
Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly 260 265 270		
Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu 275 280 285		
His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His 290 295 300		
Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu 305 310 315 320		
Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys 325 330 335		
Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly 340 345 350		
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu 355 360 365		
Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu 370 375 380		

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe  
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His  
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp  
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val  
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr  
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<210> 11  
 <211> 603  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
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 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
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Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro  
 20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro  
 35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro  
 50 55 60



Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu  
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly  
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr  
100 105 110

Tyr His Lys Ser  
115

<210> 13  
<211> 390  
<212> DNA  
<213> Homo sapiens

<400> 13  
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cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggccagc 360  
tactgctcct ttggtgaaat gaaagaataa 390

<210> 14  
<211> 129  
<212> PRT  
<213> Homo sapiens

<400> 14  
Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile  
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Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys  
20 25 30  
Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly  
35 40 45  
Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys  
50 55 60  
Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg  
65 70 75 80  
Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val  
85 90 95  
Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys  
100 105 110  
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys

115

120

125

Glu

&lt;210&gt; 15

&lt;211&gt; 1342

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

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aaaccaccaa aaaaaaaaaa aa 1342

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&lt;210&gt; 16

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu  
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu  
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu  
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu  
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg  
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu  
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser  
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly  
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu  
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile  
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu  
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
 180 185 190

Arg

&lt;210&gt; 17

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

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435

<210> 18  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp  
 35 40 45  
 Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe  
 50 55 60  
 Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys  
 65 70 75 80  
 Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met  
 85 90 95  
 Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
 100 105 110  
 Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys  
 115 120 125  
 Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu  
 130 135 140

<210> 19  
 <211> 501  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
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 aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360  
 tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg 420  
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 ggtcgaagag catcccagta a 501

<210> 20  
 <211> 166

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu  
 1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu  
 20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn  
 35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp  
 50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe  
 65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile  
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Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg  
 100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val  
 115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser  
 130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg  
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Gly Arg Arg Ala Ser Gln  
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&lt;210&gt; 21

&lt;211&gt; 1352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

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 cttcttctcc ccagttagca tcgtacagc ctttgcaatg ctctccctgg ggaccaaggc 300  
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<210> 22  
 <211> 418  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
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 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn  
 35 40 45  
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln  
 50 55 60  
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser  
 65 70 75 80  
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr  
 85 90 95  
 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro  
 100 105 110  
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn  
 115 120 125  
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu  
 130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys  
 145 150 155 160  
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu  
 165 170 175  
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys  
 180 185 190  
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu  
 195 200 205  
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
 210 215 220  
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val  
 225 230 235 240  
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys  
 245 250 255  
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala  
 260 265 270  
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu  
 275 280 285  
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp  
 290 295 300  
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr  
 305 310 315 320  
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
 325 330 335  
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys  
 340 345 350  
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly  
 355 360 365  
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile  
 370 375 380  
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu  
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Gln Lys

<210> 23

<211> 2004

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 24  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
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 Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe  
 35 40 45  
 Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser  
 50 55 60  
 Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu  
 65 70 75 80  
 Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln  
 85 90 95  
 Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln  
 100 105 110  
 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala  
 115 120 125  
 Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu  
 130 135 140  
 Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val  
 145 150 155 160  
 Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp  
 165 170 175  
 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp  
 180 185 190  
 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln  
 195 200 205  
 Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu  
 210 215 220  
 Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro  
 225 230 235 240  
 Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu  
 245 250 255  
 Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu  
 260 265 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu  
 275 280 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly  
 290 295 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu  
 305 310 315 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr  
 325 330 335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr  
 340 345 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg  
 355 360 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser  
 370 375 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met  
 385 390 395 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly  
 405 410 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp  
 420 425 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp  
 435 440 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys  
 450 455 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys  
 465 470 475 480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val  
 485 490 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys  
 500 505 510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile  
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His Thr Tyr Leu Trp His Arg Gln  
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<210> 25

<211> 1726

<212> DNA

<213> Homo sapiens

<400> 25

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 tacagcgggc ggaggccaga cgccatcagg ctgggcctgg ggaaccacaa ctactgcaga 540  
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&lt;210&gt; 26

&lt;211&gt; 562

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
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 Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met  
 35 40 45  
 Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn  
 50 55 60  
 Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser  
 65 70 75 80  
 Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr  
 85 90 95  
 Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu  
 100 105 110  
 Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr  
 115 120 125  
 Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser  
 130 135 140  
 Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro  
 145 150 155 160  
 Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His  
 165 170 175  
 Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val  
 180 185 190  
 Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys  
 195 200 205  
 Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg  
 210 215 220  
 Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn  
 225 230 235 240  
 Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala  
 245 250 255  
 Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly  
 260 265 270  
 Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp  
 275 280 285  
 Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr  
 290 295 300  
 Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala  
 305 310 315 320  
 Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro

325                      330                      335  
 Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile  
                          340                      345                      350  
 Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu  
                          355                      360                      365  
 Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu  
                          370                      375                      380  
 Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp  
 385    390    395    400  
 Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser  
     405    410    415  
 Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro  
     420    425    430  
 Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly  
     435    440    445  
 Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
     450    455    460  
 Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His  
 465    470    475    480  
 Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr  
     485    490    495  
 Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp  
     500    505    510  
 Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val  
     515    520    525  
 Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly  
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 Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met  
 545    550    555    560

Arg Pro

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 <211> 825  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
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<210> 28
<211> 156
<212> PRT
<213> Homo sapiens

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<400> 28
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35 40 45
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
50 55 60
Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln
65 70 75 80
Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
85 90 95
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
100 105 110
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
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Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
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Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
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<210> 29
<211> 7931
<212> DNA
<213> Homo sapiens

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<400> 29

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 Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg  
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 Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val  
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 Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile  
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 Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser  
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 His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser  
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33

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Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met	Leu	Pro	Ser	Lys	Ala	Gly
2000						2005					2010			
Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly	Glu	His	Leu	His	Ala	Gly
2015						2020					2025			
Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser	Asn	Lys	Cys	Gln	Thr	Pro
2030						2035					2040			
Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile	Thr	Ala
2045						2050					2055			

Ser Gly	Gln Tyr Gly Gln Trp	Ala Pro Lys Leu	Ala Arg Leu His
2060	2065	2070	
Tyr Ser	Gly Ser Ile Asn Ala	Trp Ser Thr Lys Glu	Pro Phe Ser
2075	2080	2085	
Trp Ile	Lys Val Asp Leu Leu	Ala Pro Met Ile Ile	His Gly Ile
2090	2095	2100	
Lys Thr	Gln Gly Ala Arg Gln	Lys Phe Ser Ser Leu	Tyr Ile Ser
2105	2110	2115	
Gln Phe	Ile Ile Met Tyr Ser	Leu Asp Gly Lys Lys	Trp Gln Thr
2120	2125	2130	
Tyr Arg	Gly Asn Ser Thr Gly	Thr Leu Met Val Phe	Phe Gly Asn
2135	2140	2145	
Val Asp	Ser Ser Gly Ile Lys	His Asn Ile Phe Asn	Pro Pro Ile
2150	2155	2160	
Ile Ala	Arg Tyr Ile Arg Leu	His Pro Thr His Tyr	Ser Ile Arg
2165	2170	2175	
Ser Thr	Leu Arg Met Glu Leu	Met Gly Cys Asp Leu	Asn Ser Cys
2180	2185	2190	
Ser Met	Pro Leu Gly Met Glu	Ser Lys Ala Ile Ser	Asp Ala Gln
2195	2200	2205	
Ile Thr	Ala Ser Ser Tyr Phe	Thr Asn Met Phe Ala	Thr Trp Ser
2210	2215	2220	
Pro Ser	Lys Ala Arg Leu His	Leu Gln Gly Arg Ser	Asn Ala Trp
2225	2230	2235	
Arg Pro	Gln Val Asn Asn Pro	Lys Glu Trp Leu Gln	Val Asp Phe
2240	2245	2250	
Gln Lys	Thr Met Lys Val Thr	Gly Val Thr Thr Gln	Gly Val Lys
2255	2260	2265	
Ser Leu	Leu Thr Ser Met Tyr	Val Lys Glu Phe Leu	Ile Ser Ser
2270	2275	2280	
Ser Gln	Asp Gly His Gln Trp	Thr Leu Phe Phe Gln	Asn Gly Lys
2285	2290	2295	
Val Lys	Val Phe Gln Gly Asn	Gln Asp Ser Phe Thr	Pro Val Val
2300	2305	2310	
Asn Ser	Leu Asp Pro Pro Leu	Leu Thr Arg Tyr Leu	Arg Ile His
2315	2320	2325	
Pro Gln	Ser Trp Val His Gln	Ile Ala Leu Arg Met	Glu Val Leu
2330	2335	2340	
Gly Cys	Glu Ala Gln Asp Leu	Tyr	
2345	2350		

&lt;210&gt; 31

<211> 1471  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 atggcgcccg tcgccgtctg ggccgcgctg gccgtcggac tggagctctg ggctgcggcg 60  
 cagccttgc ccgccaggt ggcatTTaca ccctacgcc cggagcccg gagcacatgc 120  
 cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctgcgccggc 180  
 caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac 240  
 agcacataca ccagctctg gaactgggtt cccgagtgtc tgagctgttg ctcccgtgt 300  
 agctctgacc aggtggaaac tcaagcctgc actcgggaac agaaccgcat ctgcacctgc 360  
 agggccggct ggtactgcgc gctgagcaag caggaggggt gccggtgtg cgcgccgctg 420  
 cgcaagtgcc gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg 480  
 tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgagg 540  
 cccaccaga tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc 600  
 acgtccacgt ccccccaccg gagtatggcc ccaggggcag tacacttacc ccagccagtg 660  
 tccacacgat cccaacacac gcagccaact ccagaacca gcactgctcc aagcacctcc 720  
 ttctgtctcc caatgggccc cagcccccca gctgaaggga gcactggcga cttcgtctct 780  
 ccagttggac tgattgtggg tgtgacagcc ttgggtctac taataatagg agtgggtaac 840  
 tgtgtcatca tgaccaggt gaaaaagaag cccttgtgcc tgcagagaga agccaagggtg 900  
 cctcaattgc ctgccgataa ggccgggggt acacagggcc ccgagcagca gcacctgctg 960  
 atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga 1020  
 agggcgccca ctcggaacca gccacaggca ccaggcgtgg aggccagtgg ggccggggag 1080  
 gcccgggcca gcaccgggag ctgagattct tcccctgggt gccatgggac ccagggtcaat 1140  
 gtcacctgca tcgtgaaagt ctgtagcagc totgaccaca gtcacagtg ctctcccaa 1200  
 gccagctcca caatgggaga cacagattcc agcccctcgg agtccccgaa ggacgagcag 1260  
 gtcccccttct ccaaggagga atgtgccttt cggtcacagc tggagacgcc agagacctg 1320  
 ctggggagca ccgaagagaa gccctgccc cttggagtgc ctgatgctgg gatgaagccc 1380  
 agttaaccag gccggtgtgg gctgtgtcgt agccaagggt ggctgagccc tggcaggatg 1440  
 accctgcgaa ggggccctgg tccttcagg c 1471

<210> 32  
 <211> 461  
 <212> PRT  
 <213> Homo sapiens

<400> 32

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
 1 5 10 15  
 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
 20 25 30  
 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln  
 35 40 45  
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
 50 55 60  
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
 65 70 75 80  
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
 85 90 95  
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
 100 105 110  
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
 115 120 125  
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
 130 135 140  
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
 145 150 155 160  
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
 165 170 175  
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
 180 185 190  
 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
 195 200 205  
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
 210 215 220  
 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser  
 225 230 235 240  
 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly  
 245 250 255  
 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly  
 260 265 270  
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys  
 275 280 285  
 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro  
 290 295 300  
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu  
 305 310 315 320  
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser

	325		330		335
Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly					
	340		345		350
Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser					
	355		360		365
Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile					
	370		375		380
Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln					
	385		390		395
Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro					
	405		410		415
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser					
	420		425		430
Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro					
	435		440		445
Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser					
	450		455		460

<210> 33  
 <211> 1475  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
 tccacctgtc cccgcagcgc cggctcgcgc cctcctgccg cagccaccga gccgccgtct 60  
 agcgccccga cctcgccacc atgagagccc tgcctggcgc cctgcttctc tgcgtcctgg 120  
 tcgtgagcga ctccaaaggc agcaatgaac ttcattcaagt tccatcgaac tgtgactgtc 180  
 taaatggagg aacatgtgtg tccaacaagt acttctccaa cattcactgg tgcaactgcc 240  
 caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300  
 atggctactt ttaccgagga aaggccagca ctgacaccat gggccggccc tgccctgccct 360  
 ggaactctgc cactgtcctt cagcaaactg accatgccca cagatctgat gctcttcagc 420  
 tgggcctggg gaaacataat tactgcagga acccagacaa ccggaggcga ccctgggtgct 480  
 atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcac ggtgcatgac tgcgcagatg 540  
 gaaaaaagcc ctctctcct ccagaagaat taaaatttca gtgtggccaa aagactctga 600  
 ggccccgctt taagattatt gggggagaat tcaccaccat cgagaaccag ccctgggttg 660  
 cggccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca 720  
 tcagcccttg ctgggtgatc agcgccacac actgcttcat tgattacca aagaaggagg 780  
 actacatcgt ctacctgggt cgctcaaggc ttaactocaa cagcaaggg gagatgaagt 840  
 ttgaggtgga aaacctcctc ctacacaagg actacagcgc tgacacgctt gctcaccaca 900

acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgcag ccatcccgga 960  
 ctatacagac catctgcttg ccctcgatgt ataacgatcc ccagtttggc acaagctgtg 1020  
 agatcactgg ctttggaaaa gagaattcta cagactatct ctatccggag cagctgaaga 1080  
 tgactgttgt gaagctgatt tcccaccggg agtgtcagca gcccactac tacggctctg 1140  
 aagtcaccac caaaatgctg tgtgctgctg acccacagtg gaaaacagat tcctgccagg 1200  
 gagactcagg gggacccctc gtctgttccc tccaaggccg catgactttg actggaattg 1260  
 tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac 1320  
 acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggg 1380  
 ccccagggag gaaacgggca ccaccgctt tcttgctggg tgcattttt gcagtagagt 1440  
 catctccatc agctgtaaga agagactggg aagat 1475

<210> 34  
 <211> 431  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser  
 1 5 10 15  
 Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp  
 20 25 30  
 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile  
 35 40 45  
 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile  
 50 55 60  
 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly  
 65 70 75 80  
 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser  
 85 90 95  
 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
 100 105 110  
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg  
 115 120 125  
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln  
 130 135 140  
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro  
 145 150 155 160  
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg  
 165 170 175  
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp

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<400> 35
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 36  
 <211> 120  
 <212> PRT  
 <213> Mus musculus

<400> 36  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr  
 20 25 30  
 Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln  
 100 105 110  
 Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 37  
 <211> 120  
 <212> PRT  
 <213> Mus musculus

<400> 37  
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
 1 5 10 15  
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
 20 25 30  
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu  
 35 40 45  
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser  
 50 55 60



Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
 65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
 85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala  
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser  
 115 120

<210> 38  
 <211> 106  
 <212> PRT  
 <213> Mus musculus

<400> 38  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met  
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr  
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
 50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp  
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr  
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 100 105

<210> 39  
 <211> 1039  
 <212> DNA  
 <213> Homo sapiens

<400> 39  
 tcctgcacag gcagtgcctt gaagtgttc ttcagagacc tttcttcata gactactttt 60  
 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120  
 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg 180  
 ggggcgctgc tggcactggc ggccctactg cagggggcgg tgtccctgaa gatcgcagcc 240  
 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 300  
 gtgcagatcc tgagccgcta tgacatcgcc ctgggtccagg aggtcagaga cageccactg 360  
 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420  
 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480

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cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg 540
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgggt cacagaggtc 600
agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac 660
gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggga cgtcatgttg 720
atggggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc 780
ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca 840
cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgcggtt 900
gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg 960
gccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc 1020
cacaccagtt gaactgcag 1039

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&lt;210&gt; 40

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 40

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Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
1          5          10          15
Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
20          25          30
Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35          40          45
Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
50          55          60
Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65          70          75          80
Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
85          90          95
Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
100         105         110
Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
115         120         125
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
130         135         140
Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145         150         155         160
Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
165         170         175
Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
180         185         190

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Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
 195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
 210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
 225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
 245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
 260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys  
 275 280

<210> 41  
 <211> 678  
 <212> DNA  
 <213> Mus musculus

<400> 41  
 gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60  
 ttctcctgca gggccagtca gttcgttggc tcaagcatcc actggtatca gcaaagaaca 120  
 aatggttctc caaggcttct cataaagtat gttcttgagt ctatgtctgg gatcccttcc 180  
 aggttttagtg gcagtggatc agggacagat ttactotta gcatcaacac tgtggagtct 240  
 gaagatatcg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggctcg 300  
 gggacaaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa 360  
 cctggaggat ccatgaaact ctctgtgtt gcctctggat tcattttcag taaccaactgg 420  
 atgaactggg tccgccagtc tccagagaag gggcttgagt gggttgctga aattagatca 480  
 aaatctatta attctgcaac acattatgcg gagtctgtga aaggagggtt caccatctca 540  
 agagatgatt ccaaaagtgc tgtctacctg caaatgaccg acttaagaac tgaagacact 600  
 ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggc 660  
 accactctca cagtctcc 678

<210> 42  
 <211> 226  
 <212> PRT  
 <213> Mus musculus

<400> 42  
 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly  
 1 5 10 15  
 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser  
 20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile  
 35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser  
 65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe  
 85 90 95

Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu  
 100 105 110

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser  
 115 120 125

Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val  
 130 135 140

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser  
 145 150 155 160

Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg  
 165 170 175

Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met  
 180 185 190

Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn  
 195 200 205

Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr  
 210 215 220

Val Ser  
 225

<210> 43  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
 gctgcatcag aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc 60  
 gcctcctgcc cctgctggcg ctgctggccc tctggggacc tgaccagcc gcagcctttg 120  
 tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaac 180  
 gaggcttctt ctacacaccc aagaccgcc gggaggcaga ggacctgcag gtggggcagg 240  
 tggagctggg cgggggccct ggtgcaggca gcctgcagcc cttggccctg gaggggtccc 300  
 tgcaagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg 360  
 agaactactg caactagacg cagcccgag gcagccccc acccgccgcc tctgcaccg 420  
 agagagatgg aataaagccc ttgaaccago 450

<210> 44  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu  
 1 5 10 15  
 Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly  
 20 25 30  
 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe  
 35 40 45  
 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly  
 50 55 60  
 Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu  
 65 70 75 80  
 Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys  
 85 90 95  
 Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn  
 100 105 110

<210> 45  
 <211> 1203  
 <212> DNA  
 <213> Hepatitis B virus

<400> 45  
 atgggagggtt ggtcttccaa acctcgacaa ggcatgggga cgaatctttc tgttcccaat 60  
 cctctgggat tctttccga tcaccagttg gacctgctg tcggagccaa ctcaaacaat 120  
 ccagattggg acttcaaccc caacaaggat cactggccag aggcaatcaa ggtaggagcg 180  
 ggagacttgc ggccagggtt caccacacca caggcggtc ttttggggtg gagccctcag 240  
 gctcagggca tattgacaac agtgccagca ggcctctc ctgtttccac caatggcag 300  
 tcaggaagac agcctactcc catctctcca cctctaagag acagtcattc tcaggccatg 360  
 cagtggaaact ccacaacatt ccaccaagct ctgctagatc ccagagtgag gggcctatat 420  
 tttcctgctg gtggctccag ttccggaaca gtaaaccctg ttccgactac tgtctcacc 480  
 atatcgtcaa tcttctcgag gactggggac cctgcacga acatggagag cacaacatca 540  
 ggattcctag gacctgtgt cgtgttacag ggggggttt tcttggtgac aagaatcctc 600  
 acaataccac agagtctaga ctggtggtg acttctctca attttctagg gggagcacc 660  
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 tga 1203

<210> 46  
 <211> 400  
 <212> PRT  
 <213> Hepatitis B virus

<400> 46  
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 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro  
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 Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn  
 35 40 45  
 Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly  
 50 55 60  
 Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln  
 65 70 75 80  
 Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser  
 85 90 95  
 Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu  
 100 105 110  
 Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His  
 115 120 125  
 Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly  
 130 135 140  
 Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro  
 145 150 155 160  
 Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu  
 165 170 175  
 Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly  
 180 185 190  
 Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
 195 200 205  
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly  
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro  
 225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile  
 245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu  
 260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser  
 275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly  
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Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn  
 305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu  
 325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro  
 340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val  
 355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser  
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Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile  
 385 390 395 400

&lt;210&gt; 47

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

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gctcatccag tcgtggctgg agcccgtag gttcctcagg agtgtcttcg ccaacagcct 420

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 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
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 Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln  
 35 40 45  
 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys  
 50 55 60  
 Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe  
 65 70 75 80  
 Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys  
 85 90 95  
 Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp  
 100 105 110  
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val  
 115 120 125  
 Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu  
 130 135 140  
 Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg  
 145 150 155 160  
 Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser  
 165 170 175  
 His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe  
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 Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys  
 195 200 205  
 Arg Ser Val Glu Gly Ser Cys Gly Phe  
 210 215

<210> 49  
 <211> 963  
 <212> DNA  
 <213> Homo sapiens

<400> 49



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 tga 963

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 <211> 320  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
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 Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg  
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 Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu  
 35 40 45  
 Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro  
 50 55 60  
 Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro  
 65 70 75 80  
 Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr  
 85 90 95  
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
 100 105 110

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg  
 115 120 125  
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
 130 135 140  
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
 145 150 155 160  
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
 165 170 175  
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 180 185 190  
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
 195 200 205  
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
 210 215 220  
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
 225 230 235 240  
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 245 250 255  
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
 260 265 270  
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
 275 280 285  
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 290 295 300  
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 305 310 315 320  
 <210> 51  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens  
 <400> 51  
 Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly  
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 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp

85 90 95  
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 100 105  
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 <211> 107  
 <212> PRT  
 <213> Mus musculus  
 <400> 52  
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 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr  
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 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile  
 35 40 45  
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln  
 65 70 75 80  
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp  
 85 90 95  
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
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 <211> 119  
 <212> PRT  
 <213> Homo sapiens  
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 35 40 45  
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
 50 55 60  
 Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
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 Thr Leu Val Thr Val Ser Ser  
 115

<210> 54  
 <211> 119  
 <212> PRT  
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<400> 54  
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 Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
 50 55 60  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr  
 65 70 75 80  
 Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ala  
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<210> 55  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 55  
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 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr  
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 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala  
 100 105 110  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
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 Phe Asn Arg Gly Glu Cys  
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 <210> 56  
 <211> 448  
 <212> PRT  
 <213> Homo sapiens  
 <400> 56  
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 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
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 Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr  
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 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
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 180 185 190  
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56

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 gtcacaatga cttgcagggc cagctcaagt gtaagttaca tccactgggt ccagcagaag 180  
 ccaggatcct cccccaaacc ctggatttat gccacatcca acctggcttc tggagtccct 240  
 gttcgcttca gtggcagtgg gtctgggact tcttactctc tcacaatcag cagagtggag 300  
 gctgaagatg ctgccactta ttactgccag cagtggacta gtaaccacc cacgttcgga 360



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384

<210> 60  
 <211> 128  
 <212> PRT  
 <213> Mus musculus

<400> 60  
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 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 115 120 125

<210> 61  
 <211> 420  
 <212> DNA  
 <213> Mus musculus

<400> 61  
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 tgcaaggctt ctggctacac atttaccagt tacaatatgc actgggtaaa acagacacct 180  
 ggtcggggcc tggaatgat tggagctatt tatcccgaa atggtgatac ttcctacaat 240  
 cagaagttca aaggcaaggc cacattgact gcagacaaat cctccagcac agcctacatg 300  
 cagctcagca gcctgacatc tgaggactct gcggtctatt actgtgcaag atcgacttac 360  
 tacggcgggtg actggtactt caatgtctgg ggcgagggga ccaagggtcac cgtctctgca 420

<210> 62  
 <211> 140  
 <212> PRT  
 <213> Mus musculus

<400> 62  
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 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu  
 50 55 60  
 Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn  
 65 70 75 80  
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
 85 90 95  
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
 100 105 110  
 Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn  
 115 120 125  
 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala  
 130 135 140

<210> 63  
 <211> 1395  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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 ttgctgctca ttggcttctg ggaactgcgtg acctgtcacg ggagccctgt ggacatctgc 120  
 acagccaagc cgcgggacat tcccatgaat cccatgtgca tttaccgctc cccggagaag 180  
 aaggcaactg aggatgaggg ctccagaacag aagatcccgg aggccaccaa ccggcgtgtc 240  
 tgggaactgt ccaaggccaa ttcccgtttt gctaccactt tctatcagca cctggcagat 300  
 tccaagaatg acaatgataa cattttctctg tcaccctga gtatctccac ggcttttgc 360  
 atgaccaagc tgggtgcctg taatgacacc ctccagcaac tgatggaggt atttaagttt 420  
 gacaccatat ctgagaaaac atctgatcag atccacttct tctttgcaa actgaactgc 480  
 cgactctatc gaaaagccaa caaatcctcc aagttagtat cagccaatcg cctttttgga 540  
 gacaaatccc ttaccttcaa tgagacctac caggacatca gtgagttgggt atatggagcc 600  
 aagctccagc ccctggactt caaggaaaat gcagagcaat ccagagcggc catcaacaaa 660  
 tgggtgtcca ataagaccga aggcogaatc accgatgtca ttccctcgga agccatcaat 720  
 gagctcaactg ttctggtgct ggtaacacc atttacttca agggcctgtg gaagtcaaag 780  
 ttcagccctg agaacacaag gaaggaactg ttctacaagg ctgatggaga gtcgtgttca 840  
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gtgcttgagt tgccttcaa aggtgatgac atcaccatgg tctcatctt gcccaagcct 960  
 gagaagagcc tggccaaggt ggagaaggaa ctcaccccag aggtgctgca ggagtggctg 1020  
 gatgaattgg aggagatgat gctgggtggc cacatgccc gcttccgcat tgaggacggc 1080  
 ttcagtttga aggagcagct gcaagacatg ggccttgctg atctgttcag cctgaaaag 1140  
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 cataaggcat ttcttgaggt aaatgaagaa ggcagtgaag cagctgcaag taccgctgtt 1260  
 gtgattgctg gccgttcgct aaacccaac agggtgactt tcaaggccaa caggcctttc 1320  
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 ccttggttta agtaa 1395

<210> 64  
 <211> 464  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
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 1 5 10 15  
 Tyr Leu Leu Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys  
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 His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro  
 35 40 45  
 Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu  
 50 55 60  
 Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val  
 65 70 75 80  
 Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln  
 85 90 95  
 His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro  
 100 105 110  
 Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn  
 115 120 125  
 Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser  
 130 135 140  
 Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys  
 145 150 155 160  
 Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn  
 165 170 175  
 Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp  
 180 185 190  
 Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys

195					200					205					
Glu	Asn	Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn
210						215					220				
Lys	Thr	Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn
225					230					235					240
Glu	Leu	Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu
				245					250					255	
Trp	Lys	Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr
			260					265					270		
Lys	Ala	Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly
		275					280					285			
Lys	Phe	Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu
	290					295					300				
Pro	Phe	Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro
305					310					315					320
Glu	Lys	Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu
				325					330					335	
Gln	Glu	Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met
			340					345					350		
Pro	Arg	Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln
		355					360					365			
Asp	Met	Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro
	370					375					380				
Gly	Ile	Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe
385					390					395					400
His	Lys	Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala
				405					410					415	
Ser	Thr	Ala	Val	Val	Ile	Ala	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val
			420					425					430		
Thr	Phe	Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro
		435					440					445			
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	450					455					460				

<210> 65  
 <211> 1962  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
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 ccccggtg ccccgccga ggcccgac ctggtgcagg tggacgggc ccgcgcgctg 12  
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gctgaccagt acgtcctcag ctgggaccag cagctcaacc tcgcctatgt gggcgccgtc 240  
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 ggggtccactg gacggggcct gagctacaac ttcaccacc tggacgggta cttggacctt 360  
 ctgagggaga accagctcct ccaggggttt gagctgatgg gcagcgccctc gggccacttc 420  
 actgactttg aggacaagca gcaggtgttt gagtggaagg acttggtctc cagcctggcc 480  
 aggagataca tcggtaggta cggactggcg catgtttcca agtggaactt cgagacgtgg 540  
 aatgagccag accaccacga ctttgacaac gtctccatga ccatgcaagg ctctctgaac 600  
 tactacgatg cctgctcgga ggggtctgcgc gccgccagcc ccgcctgcg gctgggaggc 660  
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 tgccacgaog gtaccaactt cttoactggg gaggcgggcg tgcggctgga ctacatctcc 780  
 ctccacagga aggggtgcgcg cagctccatc tccatcctgg agcaggagaa ggtcgtcgcg 840  
 cagcagatcc ggcagctctt cccaagttc gcggacaccc ccatttaca cgacgaggcg 900  
 gaccgcgtgg tgggctggtc cctgccacag ccgtggaggg cggacgtgac ctacgcggcc 960  
 atggtggtga aggtcatcgc gcagcatcag aacctgctac tggccaacac cacctccgcc 1020  
 tccccctacg cgctcctgag caacgacaat gccttctga gctaccacc gcaccccttc 1080  
 gcgcagcgca cgctcaccgc gcgtctocag gtcaacaaca cccgccgcc gcacgtgcag 1140  
 ctgttgcgca agccggtgct cacggccatg gggctgctgg cgctgctgga tgaggagcag 1200  
 ctctgggccg aagtgtcgca ggccgggacc gtcttgga gcaaccacac ggtgggcgtc 1260  
 ctggccagcg cccaccgcc ccagggcgcg gcgacgcct ggcgcgcgcg ggtgctgac 1320  
 tacgcgagcg acgacaccgc cgcccacccc aaccgcagcg tcgcggtgac cctgcggctg 1380  
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 tgcagccccg acggcgagtg gcggcgccct ggccggcccg tcttccccac ggcagagcag 1500  
 ttccggcgca tgcgcgcggc tgaggacccg gtggccgcgg cgcgccgcc cttaccgcgc 1560  
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 gtccctgtgc caagagggcc cccatccccg ggcaatccat ga 1962

<210> 66  
 <211> 653  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser  
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 Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val  
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 Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg  
 35 40 45  
 Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr  
 50 55 60  
 Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val  
 65 70 75 80  
 Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu  
 85 90 95  
 Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr  
 100 105 110  
 His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro  
 115 120 125  
 Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu  
 130 135 140  
 Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala  
 145 150 155 160  
 Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn  
 165 170 175  
 Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser  
 180 185 190  
 Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly  
 195 200 205  
 Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser  
 210 215 220  
 Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His  
 225 230 235 240  
 Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu  
 245 250 255  
 Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile  
 260 265 270  
 Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro  
 275 280 285  
 Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val

290					295					300					
Gly	Trp	Ser	Leu	Pro	Gln	Pro	Trp	Arg	Ala	Asp	Val	Thr	Tyr	Ala	Ala
305					310					315					320
Met	Val	Val	Lys	Val	Ile	Ala	Gln	His	Gln	Asn	Leu	Leu	Leu	Ala	Asn
				325					330					335	
Thr	Thr	Ser	Ala	Phe	Pro	Tyr	Ala	Leu	Leu	Ser	Asn	Asp	Asn	Ala	Phe
			340					345					350		
Leu	Ser	Tyr	His	Pro	His	Pro	Phe	Ala	Gln	Arg	Thr	Leu	Thr	Ala	Arg
		355					360					365			
Phe	Gln	Val	Asn	Asn	Thr	Arg	Pro	Pro	His	Val	Gln	Leu	Leu	Arg	Lys
	370					375					380				
Pro	Val	Leu	Thr	Ala	Met	Gly	Leu	Leu	Ala	Leu	Leu	Asp	Glu	Glu	Gln
385						390					395				400
Leu	Trp	Ala	Glu	Val	Ser	Gln	Ala	Gly	Thr	Val	Leu	Asp	Ser	Asn	His
				405					410					415	
Thr	Val	Gly	Val	Leu	Ala	Ser	Ala	His	Arg	Pro	Gln	Gly	Pro	Ala	Asp
			420					425					430		
Ala	Trp	Arg	Ala	Ala	Val	Leu	Ile	Tyr	Ala	Ser	Asp	Asp	Thr	Arg	Ala
		435					440					445			
His	Pro	Asn	Arg	Ser	Val	Ala	Val	Thr	Leu	Arg	Leu	Arg	Gly	Val	Pro
		450				455					460				
Pro	Gly	Pro	Gly	Leu	Val	Tyr	Val	Thr	Arg	Tyr	Leu	Asp	Asn	Gly	Leu
465						470					475				480
Cys	Ser	Pro	Asp	Gly	Glu	Trp	Arg	Arg	Leu	Gly	Arg	Pro	Val	Phe	Pro
				485					490					495	
Thr	Ala	Glu	Gln	Phe	Arg	Arg	Met	Arg	Ala	Ala	Glu	Asp	Pro	Val	Ala
			500					505					510		
Ala	Ala	Pro	Arg	Pro	Leu	Pro	Ala	Gly	Gly	Arg	Leu	Thr	Leu	Arg	Pro
		515					520					525			
Ala	Leu	Arg	Leu	Pro	Ser	Leu	Leu	Leu	Val	His	Val	Cys	Ala	Arg	Pro
		530				535					540				
Glu	Lys	Pro	Pro	Gly	Gln	Val	Thr	Arg	Leu	Arg	Ala	Leu	Pro	Leu	Thr
545						550					555				560
Gln	Gly	Gln	Leu	Val	Leu	Val	Trp	Ser	Asp	Glu	His	Val	Gly	Ser	Lys
				565					570					575	
Cys	Leu	Trp	Thr	Tyr	Glu	Ile	Gln	Phe	Ser	Gln	Asp	Gly	Lys	Ala	Tyr
			580					585					590		
Thr	Pro	Val	Ser	Arg	Lys	Pro	Ser	Thr	Phe	Asn	Leu	Phe	Val	Phe	Ser
		595					600					605			
Pro	Asp	Thr	Gly	Ala	Val	Ser	Gly	Ser	Tyr	Arg	Val	Arg	Ala	Leu	Asp
	610					615					620				

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu  
 625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro  
 645 650

<210> 67  
 <211> 1290  
 <212> DNA  
 <213> Homo sapiens

<400> 67  
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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180  
 gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctccagaaggc 240  
 tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga 300  
 gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta 360  
 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420  
 acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatgcca gacctttgct 480  
 gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg 540  
 gcagatgggt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600  
 tcctgtgagt ggctcttcta tatgtggccc tttaaaaagc ccaattatac agaaatccga 660  
 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720  
 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780  
 ggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa 840  
 gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900  
 cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960  
 caggaccctt tgggcaagca agggtagcag cttagacagg gagacaactt tgaagtgtgg 1020  
 gaacgacctc tctcaggctt agcctgggct gtagctatga taaaccggca ggagattggg 1080  
 ggacctcgct cttataccat cgcagttgct tccctgggta aaggagtggc ctgtaatcct 1140  
 gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact 1200  
 tcaagggttaa gaagtcacat aaatcccaca ggcactgttt tgcttcagct agaaaataca 1260  
 atgcagatgt cattaaaaga cttactttta 1290

<210> 68  
 <211> 429  
 <212> PRT  
 <213> Homo sapiens



&lt;400&gt; 68

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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
          20           25           30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
          35           40           45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
          50           55           60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65           70           75           80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
          85           90           95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
          100          105          110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
          115          120          125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
130          135          140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
145          150          155          160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
          165          170          175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
          180          185          190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
          195          200          205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
210          215          220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
225          230          235          240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
          245          250          255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
          260          265          270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
          275          280          285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
          290          295          300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
305          310          315          320

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Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala  
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala  
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile  
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr  
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
 405 410 415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu  
 420 425

<210> 69  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

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 ttctttctccc agccgggtgc cccaatactt cagtgcattgg gctgctgctt ctctagagca 180  
 tatccacttc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240  
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<210> 70  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
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 Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro  
 20 25 30  
 Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro  
 35 40 45  
 Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro  
 50 55 60  
 Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu  
 65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly  
                             85                            90                            95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr  
                             100                            105                            110

Tyr His Lys Ser  
                             115

<210> 71  
 <211> 498  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 gagggctgcc ccgtgtgcat caccgtcaac accaccatct gtgccggcta ctgccccacc 180  
 atgacccgag tgctgcaggg ggtcctgccg gccctgcctc aggtggtgtg caactaccgc 240  
 gatgtgogct tcgagtccat ccggctccct ggctgccgcg gcggcgtgaa ccccggtggtc 300  
 tcctacgcgc tggtctcag ctgtcaatgt gcactctgcc gccgcagcac cactgactgc 360  
 ggggggtcca aggaccacc cttgacctgt gatgaccccc gcttcaggga ctctctttcc 420  
 tcaaaggccc ctccccccag ccttccaagc ccatcccgac tcccggggcc ctcggaacacc 480  
 ccgatacctcc cacaataa 498

<210> 72  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
 Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly  
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 Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile  
                             20                            25                            30  
 Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr  
                             35                            40                            45  
 Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val  
                             50                            55                            60  
 Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg  
 65                            70                            75                            80  
 Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val  
                             85                            90                            95  
 Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu  
                             100                            105                            110  
 Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu

115                      120                      125  
 Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro  
     130                      135                      140  
 Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr  
 145                      150                      155                      160  
 Pro Ile Leu Pro Gln  
                     165

<210> 73  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<400> 73  
 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu  
 1                      5                      10                      15  
 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His  
                     20                      25                      30  
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe  
                     35                      40                      45  
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp  
                     50                      55                      60  
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu  
 65                      70                      75                      80  
 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp  
                     85                      90                      95  
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu  
                     100                      105                      110  
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala  
                     115                      120                      125  
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val  
                     130                      135                      140  
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala  
 145                      150                      155                      160  
 Cys Arg Thr Gly Asp  
                     165

<210> 74  
 <211> 588  
 <212> DNA  
 <213> Homo sapiens

<400> 74  
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 tctctgggct gtgatctgcc tcagaacat ggcctactta gcaggaacac cttggtgctt 120  
 ctgcacaaaa tgaggagaat ctcccttttc ttgtgtotca aggacagaag agacttcagg 180

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ttccccagg agatggtaaa agggagccag ttgcagaagg cccatgtcat gtctgtcctc 240
catgagatgc tgcagcagat cttcagcctc ttccacacag agogetcctc tgctgcctgg 300
aacatgaccc tcctagacca actccacact ggacttcata agcaactgca acacctggag 360
acctgcttgc tgcaggtagt gggagaagga gaatctgctg gggcaattag cagccctgca 420
ctgaccttga ggaggtactt ccaggaatc cgtgtctacc tgaaagagaa gaaatacagc 480
gactgtgcct gggaagttgt cagaatggaa atcatgaaat ccttggttctt atcaacaaac 540
atgcaagaaa gactgagaag taaagataga gacctgggct catcttga 588

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<210> 75
<211> 195
<212> PRT
<213> Homo sapiens

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<400> 75
Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
1 5 10 15
Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
20 25 30
Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
35 40 45
Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
50 55 60
Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65 70 75 80
His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95
Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110
His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140
Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160
Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175
Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190
Gly Ser Ser
195

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